

**The Genetic Legacy of Breast Cancer: Extending the Common Sense Model for Genetics to
High-Risk BRCA1/2 Counselees and their Adolescent Daughters**

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Abstract

Screening, surveillance and preventative medical interventions are being identified as best practices for women at high-risk of developing hereditary breast cancer. Genetic screening for the BRCA1/2 mutations associated with hereditary breast cancer is currently recommended as an appropriate health intervention for younger women who have been affected by breast cancer, as well as for those who have been identified as high-risk due to their family histories of breast cancer. At present, however, little is known about the psychosocial implications of genetic screening for BRCA1/2 mutations on young families. Using the common sense model of self-regulation (Leventhal et al., 1997), adapted for genetics (Cameron, 2003; Marteau & Weinman, 2006) as a guiding framework, the goals of this dissertation were to: (a) examine the relationships between threat representation and psychosocial functioning in BRCA1/2 counselees, (b) explore the impact of fear representation on women's psychosocial functioning, and (c) assess how BRCA1/2 counselees' threat representations and fear representations impact family functioning and the psychosocial adaptation of their adolescent daughters. Results indicated that total threat representation, including risk representation, illness representation and fear representation, was found to add to the prediction of mothers' self-reported levels of anxiety, depressive symptoms and intrusive ideation regarding genetic counseling. Additionally, when the cognitive processes of the threat representation were controlled (i.e., risk representation and illness representation), the subjective-emotional processes (i.e., the fear representation) continued to emerge as a significant predictor of mothers' self-reported anxiety, depressive and intrusive ideation symptoms. Additionally, support for the association between mothers' threat

representations and adolescent daughters' reports of depressive symptoms and self-concept were noted. Cumulatively, these results provide support for the role of fear representation within the CSM framework and suggest that fear representation plays an important role in BRCA1/2 counselees' psychosocial adaptation following genetic counseling.

Statement of Co-Authorship

The work included in this dissertation was prepared in collaboration with my dissertation supervisor. I was the primary author and Dr. Mario Cappelli was the secondary author. As the primary author, I was responsible for conceptualization of the research question and study methods, planning and execution of statistical analyses, and preparation of manuscripts. Dr. Cappelli provided guidance and assistance in all aspects of the project. Monica O'Neill, a former research assistant at the Children's Hospital of Eastern Ontario, was involved with recruitment of study participants and data collection. I prepared this dissertation. Any future publications that may arise from this work will include co-authors identified above.

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General Introduction

Genetic screening is increasingly a priority in oncology. However, our level of preparedness surrounding the health service delivery of genetic test results, as well as our systematic capacity to address the psychological issues associated with risk information for hereditary cancers, are growing concerns (Broadstock, Michie & Marteau, 2000). In order to address future health service delivery needs in genetics, investigators are being encouraged to adopt a more comprehensive approach by including families who share components of their genetic identities with one another and who may be directly impacted by each other's risk estimates (Meiser, 2005; Meiser & Halliday, 2002). To date, however, the psychosocial impact of adult onset hereditary disorders (AOHDs) on the family as a unit of analysis has been limited. Despite accumulating literature on the psychological outcomes of genetic testing, comparatively little is known about the effects of BRCA1/2 screening on family relationships.

Psychosocial research with families undergoing genetic counseling for the BRCA1/2 mutations associated with hereditary breast cancer is important for at least four reasons. First, studies have revealed that public knowledge of genetic testing for BRCA1/2 mutations is suboptimal. Additionally, many people hold inaccurate perceptions relative to the penetrance of BRCA1/2 mutations and how this corresponds with individual (i.e., personal) levels of risk (e.g., Borzekowski, Guan, Smith, Erby & Roter, 2013). Not only is this true in the general population, but amongst BRCA1/2 counselees as well (e.g., Bluman et al., 2003; Kelly et al., 2005; Mellon et al., 2006; Lerman et al., 2000). This discrepancy in perceived risk versus actual risk has important implications for how families understand and communicate about genetic risk (e.g.,

Kelly, et al., 2007; Meiser & Halliday, 2002). Second, people who obtain publicly funded BRCA1/2 screening in Canada represent a high-risk group with personal and familial histories of breast cancer that may impact their psychosocial adaptation to genetic risk results. Accordingly, further study is required to understand the unique contributions of illness history, genetic risk, and fear associated with breast cancer on the psychosocial functioning of high-risk individuals and their families. Third, due to the pattern of autosomal dominance displayed by BRCA1/2 gene mutations, offspring stand to benefit from their parents' risk estimate results. Currently, however, there is a paucity of research investigating the impact of genetic counseling for BRCA1/2 mutation screening on young families. Such research is important with respect to informing clinical interventions and health service delivery for young families (e.g., Bradbury et al., 2009). Finally, genetic testing for BRCA1/2 gene mutations is not absolutely predictive (Cameron & Reeve, 2006). This provides patients with an ambiguous frame of reference in terms of evaluating risk and complicates decision-making regarding preventative strategies and prophylactic options (e.g., Evans, Blair, Greenhalgh, Hopwood & Howell, 1994; Meiser & Halliday, 2002).

This project represents the next component of an ongoing research program designed to refine our understanding of the psychosocial implications of genetic testing for BRCA1/2 mutations on families. The current study focuses on an especially vulnerable population of women, BRCA1/2 counselees who have adolescent daughters. The purpose of this dissertation is to extend research in the area of psychosocial genetics to determine how history of illness (i.e., *illness representation*; Leventhal et al., 1997), eligibility for genetic screening (i.e., *risk*

representation; Marteau & Weinman, 2006) and distress related to breast cancer (i.e., *fear representation*; Leventhal et al., 1997) impact psychosocial functioning. This information will help guide the refinement of current theoretical conceptualizations of illness, risk, and fear. Using the common sense model (CSM) of self-regulation (Leventhal et al., 1997), adapted for genetics (Marteau & Weinman, 2006) as a guiding framework, the goals of this dissertation were to: (a) examine the relationships between *threat representation* and psychosocial functioning in BRCA1/2 counselees, (b) explore the impact of *fear representation* on women's psychosocial functioning, and (c) study how *threat representation* and *fear representation* impact family functioning and the psychosocial adaptation of adolescent daughters from high-risk families. These goals were addressed through a research study detailed in Chapter 4 of this dissertation. The results of this work will provide significant contributions to the psychosocial genetics literature on AOHDs and specifically BRCA1/2 gene mutations. Knowledge gained from this work will be instrumental in assessing the efficacy of clinical interventions predicated on the foundations of CSM that are being developed and applied for high risk families negotiating genetic risk information. This work also holds potential to help inform the further development of interventions based on the CSM framework.

This dissertation itself is divided into five Chapters. In Chapter 1, I provide a brief background describing genetic screening technology, eligibility criteria for BRCA1/2 screening, restrictions on publicly funded genetics services, as well as a broad overview several legal and ethical issues that have emerged in relation to BRCA1/2 screening. Chapter 2 includes an updated literature scan completed by this author, which surveys research documenting the

psychosocial outcomes of BRCA1/2 screening. This review includes 14 studies published between 2007 and 2013 and integrates these findings with the literature published before 2007. Chapter 3 outlines several theoretical models that have guided our current understanding of the relationship between illness and genetic risk and which have provided the backbone for understanding and disentangling the impact of genetic risk on the psychosocial adaptation of women being screened for BRCA1/2 mutations and their families. Chapter 4 includes the rationale and goals, hypotheses, analyses and results of a research study related to psychosocial functioning and adaptation experienced by mothers and their adolescent daughters. The final Chapter, 5, presents a broader discussion of study results, strengths, limitations and implications.

CHAPTER 1

BRCA1/2 Prevalence, Policy and Politics

Psychosocial genetics research, as a field, has traditionally been informed by a variety of professional groups including nursing, psychology, medicine, bioethics, health policy and law. As a result, the literature in this area crosses the landscape between these areas of practice. The following section presents a global introduction to the area of genetic screening for hereditary breast cancer and includes: (a) a discussion of the incidence of hereditary breast cancer, (b) an outline of health policies that underlie genetic screening for the BRCA1/2 gene mutations associated with hereditary breast cancer with particular attention to the Canadian context, (c) an overview of diagnostic information provided by genetic screening for BRCA1/2 gene mutations and the role of individualized medicine, (d) a summary of the current health policies and laws that impact psychological research within this field, and (e) an examination of the role of BRCA1/2 screening with respect to informing individualized medicine and population health.

Incidence and Prevalence of Breast Cancer

In North America, the lifetime prevalence of breast cancer is currently the highest in the world (WHO, 2006). Additionally, since the 1970s, incidence rates of breast cancer have increased dramatically. In Canada, breast cancer has been identified as a major public health concern, chronic, costly, and often resulting in reduced quality of life for individuals diagnosed. Among Canadian women, breast cancer continues to lead cancer incidence rates and it is estimated that in 2012 alone, 22,700 women were diagnosed with breast cancer. Although the specific etiology of breast cancer is unknown, hormonal, reproductive and hereditary influences

have all been identified as risk factors (Canadian Cancer Steering Committee, 2012). National initiatives have been undertaken by Canadian and provincial governments as well as community organizations to promote surveillance behaviours aimed at screening, early detection and prevention of breast cancer. One predictive measure currently available to high-risk Canadian families is genetic screening for the specific deleterious BRCA1 and BRCA2 germline mutations associated with hereditary breast cancer.

BRCA1/2 Gene Mutations

BRCA1 and BRCA2 genes are located on chromosomes 17 and 13, respectively and have been identified as tumor suppressor genes. BRCA1/2 genes normally function to assist in the repair of damaged DNA and the maintenance of cells' stability (Hall et al., 1990; Panchal, Ennis, Canon & Bordeleau, 2008; Wooster et al., 1994). Research conducted over the past twenty years in the area of molecular genetics has demonstrated that specific germline mutations (i.e., the presence of an altered genes within the egg or sperm cells, that can be passed to subsequent generations) in BRCA1 and BRCA2 are associated with increased risks of several types of cancer including breast cancer (e.g., Easton, 1999; Panchal et al., 2008; Petrucelli, Daly & Feldman, 2013).

Increased risk of breast cancer. An estimated 10% to 15% of all breast cancer cases have an hereditary component (Kotsopoulos et al., 2014). Further evidence based on the largest twin study of breast cancer patients has demonstrated that as many as 27% of total breast cancer cases may be due to inherited genes (Lichtenstein et al., 2000). Overall, when the incidence rates of breast cancer are evaluated, the literature reveals that genetic susceptibility makes a modest to

moderate contribution in terms of overall cases (Kotsopoulos, et al., 2014; Czene, Lichtenstein & Hemminki, 2002).

Amongst high-risk families, however, the contributions of germline mutations in BRCA1 and BRCA2 genes account for approximately 20% to 25% of all familial breast cancers (Kostopoulos et al., 2104). When lifetime risk of breast cancer is assessed amongst these high risk women, results reveal that between 55% and 65% percent of women diagnosed with deleterious BRCA1 mutations will develop breast cancer by age 70 years (Chen & Parmigiani, 2007; Howlader, Noone & Krapcho, 2013). Additionally, amongst women identified with harmful BRCA2 mutations, approximately 40% are expected to develop breast cancer by age 70 (Chen & Parmigiani, 2007; Howlader, Noone & Krapcho, 2013). By contrast, the lifetime risk of breast cancer for women of average breast cancer risk is estimated to be just 12% (National Comprehensive Cancer Network, 2013).

BRCA1/2 germline mutations also confer a much higher risk of second primary breast cancers (Metcalf et al., 2008). For example, the risk of being diagnosed with a second primary breast cancer within five years is approximately 27% for BRCA1 carriers as compared with rates between 3.5% and 11% in the general population (Metcalf et al., 2004; Petrucelli et al., 2013).

Autosomal dominance of BRCA1/2. Germline mutations in BRCA1/2 genes are inherited in an autosomal dominant manner. Autosomal dominance is best described as a pattern of inheritance characteristic of some genetic diseases whereby the gene in question is located on a non-sex (i.e., numbered) chromosome and the condition is expressed in persons who have just one copy of the mutant allele (Petrucelli et al., 2013). In other words, when one parent has a

dominant gene mutation, there is a 50% chance that any child they have will also inherit said mutation. In the case of the specific BRCA1 and BRCA2 germline mutations, an offspring of a parent with a deleterious BRCA1 or BRCA2 mutation will have a 50% chance of inheriting the BRCA1/2 mutation (Petrucelli et al., 2013).

BRCA1/2 Mutation Screening

Molecular genetic testing is used to identify BRCA1 and/or BRCA2 germline mutations in individuals and families. According to guidelines produced by several professional societies (e.g., National Comprehensive Cancer Network, 2012; American Society of Breast Surgeons, 2006; US Preventive Services Task Force 2005), an increased likelihood of deleterious mutations in BRCA1 or BRCA2 should be suspected in individuals with a personal or family history of breast cancer (1st, 2nd, or 3rd degree relative) accompanied by any one or more of the following factors: (a) breast cancer diagnosed at age 50 or younger, (b) ovarian cancer, (c) multiple primary breast cancers either in the same breast or opposite breast, (d) breast and ovarian cancer, (e) male breast cancer, (f) triple-negative breast cancer, (g) pancreatic cancer with breast or ovarian cancer in the same individual or on the same side of the family, (h) Ashkenazi Jewish ancestry; (i) two or more relatives with breast cancer, one under age 50, (j) three or more relatives with breast cancer at any age, (k) previously identified BRCA1 or BRCA2 mutation(s) in the family (NCCN, 2012; Petrucelli et al., 2013).

Testing family members for BRCA1/2 germline mutations is considered most informative if the first person to undergo testing is a proband or index case. A proband is defined as “an affected individual through whom a family with a genetic disorder is ascertained”

(Petrucci et al., 2013, para. 8). In the case of BRCA1/2 associated breast cancer, the proband is usually identified by an early personal history of breast cancer (i.e., age < 50 years) since this reduces the chances that the cancer may have been sporadic in nature (e.g., NCCN, 2012). Mutation testing typically begins with a proband (with known BRCA-related cancer) to identify whether a clinically significant mutation may be segregating in the family. Following this, testing of relatives without cancer may occur (NCCN, 2012).

The type of mutation analysis required in BRCA1/2 screening is highly dependent on family history. A small number of clinically significant BRCA1 and BRCA2 mutations have been found in different families and these include the three founder mutations common in the Ashkenazi Jewish population. For individuals who originate from families with these types of mutations (or from ethnic groups with common mutations), testing can occur specifically for these identified mutations (Nelson et al., 2013). For individuals without linkages to known mutations, testing can occur through direct DNA sequencing (Myriad, 2013). It is estimated that 12% of high-risk families without a BRCA1 or BRCA2 coding-region mutation may have other clinically significant genomic rearrangements. Secondary testing for these types of mutations is available through the BRCA Rearrangement Test (BART; Myriad, 2013).

Access to BRCA1/2 screening in Canada. Due to the nature of the publicly funded health care system Canada, BRCA1/2 screening is typically directed through the provincially managed national health insurance system. As a result, genetic testing conducted in Canadian health care settings is currently restricted to pre-screened, high-risk patients (Williams-Jones & Burgess, 2004). In Canada, women referred to genetic counseling and screening for BRCA1/2

mutations must meet stringent criteria developed by the clinical subcommittee of the Predictive Cancer Genetics Steering Committee (2001). Accordingly, referrals for genetic counseling in Canada made via the public health care system are intended to be reserved for high-risk, vulnerable groups of individuals/families. A typical participant receiving publicly funded genetic screening in Canada will have been diagnosed with breast cancer (i.e., proband) and considered high-risk (e.g., breast cancer onset at age 35 or younger) or have clearly defined risk factors (e.g., be a relative of an individual with a known BRCA1/2 mutation; relative of a proband) (e.g., Ontario Ministry of Health and Long Term Care, 2011).

In Ontario, Canada, the Ministry of Health and Long Term Care (MOHLTC; 2011) has developed specific referral guidelines for BRCA1/2 molecular genetic screening programs in the province. These guidelines conform to the criteria outlined by the Predictive Cancer Genetics Screening Committee (2001) and are included in Appendix A of this manuscript. Women included in this research study would have been expected to meet the MOHLTC referral criteria prior to their file being accepted for genetic counseling services by the participating genetics clinic in this project (located at the Children's Hospital of Eastern Ontario in Ottawa, Ontario, Canada). Participants in the present study received genetic counseling for BRCA1/2 germline mutations between 2005 and 2010. This is notable because in 2007 the genetic testing methodology for BRCA1/2 shifted in the province of Ontario from protein truncation testing (PTT) with sequencing of exons 2 and 5 of BRCA1 to denaturing high performance liquid chromatography (DHLC) and multiplex ligation-dependent probe assay (MLPA; Panchal, Ennis, Canon & Bordeleau, 2008). By contrast, the most common methodology used to identify

BRCA1 and BRCA2 mutations in the United States at that time was gene sequencing and large deletion and rearrangement screening (Myriad, 2008).

Presently, women in Ontario with significant family histories of breast cancer and who are eligible for genetic testing can receive screening for either one or both of the BRCA1 and BRCA2 genes. Historically, Canadian women (including those who participated in this study) did not have access to more comprehensive gene panel screening for hereditary breast cancer developed by Myriad (Kotsopoulos et al., 2014). It is expected that new research in this area, along with the dissolution of Myriad patents in the United States, will pave the way for more comprehensive panel testing in Canada in the future (Kotsopoulos et al., 2014). Consistent with recommendations made by the Predictive Cancer Genetics Screening Committee (2001) the health service delivery of publicly funded genetic screening for BRCA1/2 mutations in Canada includes two to three genetic counseling sessions as part of standard care (Predictive Cancer Genetics Screening Committee, 2001). As such, all women included in this study have received genetic counseling.

BRCA1/2 Diagnoses and Penetrance

BRCA1/2 diagnoses. Molecular testing for BRCA1/2 mutations yields four diagnostic categories. The first result is commonly referred to in the literature as BRCA positive, indicating that deleterious mutations in the BRCA1 and/or BRCA2 genes are present. This BRCA1/2 positive result confers an increased risk for BRCA1 and/or BRCA2 associated cancers. For the purpose of this dissertation, women receiving this diagnosis are described as BRCA1/2 positive or BRCA1/2 carriers. The second result category is described as a true negative BRCA1/2 result

(i.e., BRCA negative) and occurs when there is an absence of a mutation in an individual despite that person having relatives with cancer and known BRCA mutations. A person with a BRCA negative test result has the same risk of cancer as someone in the general population. For the purpose of this dissertation, true negatives are described and BRCA1/2 negatives or non-carriers (e.g., Hanoch, Miron-Shatz, Rolison & Ozanne, 2014).

The third diagnostic category that can result from genetic screening for BRCA1 and/or BRCA2 gene mutations are variants of uncertain significance (VUS). VUS results commonly occur when abnormalities of the BRCA gene are identified, but it is unknown if these abnormalities are associated with an increased risk for breast cancer. Between 2.9% and 10% of all BRCA1/2 screeners will receive a VUS result (Eggington et al., 2014; Nelson et al., 2013). The fourth and final possible result of BRCA1/2 screening is referred to in the broader literature as an uninformative negative. This diagnosis is said to occur when there is an absence of a mutation in an individual and information about relatives is not definitive (because either a mutation was not detected by relatives' tests or they have not been tested). Recent estimates indicate that between 56% and 70% of BRCA1/2 screeners will receive uninformative negative BRCA test results (Graves et al., 2012; Weitzel et al., 2012).

Based on recommendations made in the literature, uninformative negative and VUS results are represented under the heading BRCA1/2 uncertain in Chapter 4 of this manuscript (e.g., Hanoch et al., 2014; Frost Venne, Cunningham, Gerritsen-McKane, 2004). Rationale for combining these risk estimates into one category include: (a) VUS and uninformative negative risk estimates share commonalities in that these types of results are unable to provide any

conclusive information about heritable breast cancer risk and (b) information about penetrance is either limited or unavailable (Hanoch et al., 2014).

Table 1.

BRCA 1/2 Diagnoses and Study Labels

BRCA Diagnosis	Dissertation Label
BRCA Positive	BRCA Positive or Carriers
BRCA Negative	BRCA Negative or Non-carriers
Uninformative Negative	BRCA Uncertain or Uncertain
Variant of Uncertain Significance	BRCA Uncertain or Uncertain

BRCA1/2 penetrance. Genetic testing for BRCA1/2 mutations is not absolutely predictive (Cameron & Reeve, 2006). The penetrance of BRCA1/2 mutations is defined as the probability or likelihood of developing breast cancer among people who have a known deleterious BRCA1/2 mutation (Hanoch et al., 2014). Of note, BRCA1/2 penetrance is genotype specific and age dependent. Additionally, estimates of the penetrance of BRCA1/2 mutations differ by test result (Nelson et al., 2013).

In general, a positive BRCA1 or BRCA2 mutation result provides information about a person's potential risk of developing breast cancer. However, an individual identified as having a BRCA1 and/or BRCA2 gene alteration will not always develop inherited breast cancer. Due to the incomplete penetrance of BRCA1/2, people who inherit the gene may not develop breast cancer due to other genetic or environmental factors (Domchek & Weber, 2006). Likewise, a

true negative BRCA1/2 test result suggests that an individual will not develop heritable breast cancer. However, a negative result cannot provide information about non-heritable breast cancer risk. Moreover, a negative BRCA1 and/or BRCA2 test result cannot always provide information about other gene alterations that may or may not be responsible for heritable cancers (Meiser, 2005).

A recent meta-analysis completed by Nelson et al. (2013) demonstrated that in BRCA positive women, risk for breast cancer to age 70 years was 46% for BRCA1 and 50% for BRCA2 when one family member was tested, and 70% for BRCA1 and 71% for BRCA2 when multiple family members were tested. Among women with true negative test results (i.e. non-carriers or BRCA negative), results from a meta-analysis of ten studies indicated that standardized incidence ratio for breast cancer was 1.13 95% CI [0.81, 1.58]. This result was not significantly different from risk estimates of breast cancer in the general population (Nelson et al., 2013). At this time, there is limited information regarding penetrance for those receiving uncertain BRCA1/2 results. With respect to uninformative negative test results, a recent meta-analysis study conducted by Nelson et al. (2013) identified only three studies available for review. Based on the available information, the standard incidence ratio for breast cancer in the uninformative negative BRCA group was calculated to be 3.81 95% CI [3.06, 4.75]. At this time, no breast cancer penetrance studies exist documenting the standard incidence ratio of breast disease in women who obtain a VUS BRCA test result.

BRCA1/2 Politics

Patents. In 2013, a number of ethical and legal developments related to BRCA1/2 genes occurred. The first issue concerned patents on BRCA1/2 genes held by Myriad Genetics in the United States. The patents, 9 in all, were obtained between 1995 and 1998 and included one patent that covered 47 separate mutations in the BRCA1 gene (US 5,693,47323), five patents that covered the BRCA1 gene and associated diagnostic tests (US 5,709,999; US 5,747,282; US 5,710,001; US 5,753,441; and US 6,162,89723), two additional patents that covered methods of detecting BRCA1 mutations and the entire sequence of the BRCA1 gene and tools used in this work, as well as a patent claiming BRCA2 DNA, mutations, and diagnosis (US 5,837,49223). An additional patent over the method of detecting BRCA2 mutations and antibodies was also obtained (US 6,124,10423). These patents enabled Myriad to effectively acquire control over the use of diagnostic tests based on those genes (Gold & Carbone, 2010). However, following a lengthy legal battle, in June, 2013, the United States Supreme Court unanimously ruled that “products of nature,” including genes, could not be patented (United States Supreme Court, 2013).

Myriad filed similar patents over BRCA1/2 genes in Canada that were approved by the Canadian Intellectual Property Office (CIPO) in the 1990s. These patents covered BRCA1 and mutations of BRCA1 (patent numbers 2,196,797 and 2,196,79031) and BRCA2 (patent number 2,239,73331), as well as, all associated diagnostic procedures. Due to the nature of the publicly funded health care system in Canada, and a piece of legislation, the Canada Health Act (R.S., 1985, c.C-6), which requires that accessibility to health care be maintained for all Canadians

through a ban on private financing, a series of legal battles between Myriad and several Canadian provinces ensued. The central issue was that Myriad's patents over human genes created a monopoly that restricted access to care. In 2004, the province of Ontario made arguments to the Supreme Court of Canada in a case regarding biotechnology patents and the impact on the health system; however, that case was unsuccessful and Myriad retained their patents over BRCA1/2 in Canada (Gold & Carbone, 2010). Despite this ruling, and threats made by United States government on behalf of Myriad related to trade sanctions, Myriad's patents have been widely disregarded in Canada since they directly contradict health policy and legislation protecting publicly funded health care (Gold & Carbone, 2010).

The outcome of the United States Supreme Court ruling against Myriad has important implications for the patents currently retained in Canada, as well as, future health policies and laws more globally. From a scientific perspective, this ruling has been viewed quite favourably. For example, Dr. Frances Collins, Director of the US National Institutes of Health stated:

I am very pleased with today's ruling by the U.S. Supreme Court in the case of Assoc. for Molecular Pathology Et Al. v. USPTO and Myriad Genetics, Inc. Et Al. that genes isolated from the human body are not patentable. The decision represents a victory for all those eagerly awaiting more individualized, gene-based approaches to medical care. The right to control exclusively the use of a patient's genes could have made it more difficult to access new tests and treatments that rely on novel technologies that can quickly determine the sequence of any of the estimated 20,000 genes in the human genome. Such approaches form the cornerstone of the rapidly emerging field of

personalized medicine, in which diagnostic, therapeutic, and preventive strategies can be tailored to each person's unique genetic makeup. (Collins, 2013, para 4.).

Direct-to-consumer (DTC) BRCA1/2 screening. The United States Supreme Court ruling has had a number of cascade effects, including the opening of a competitive market for BRCA1/2 screening. During the same week that this ruling was delivered, prices for BRCA1/2 screening dropped from \$4500 to \$995 among direct-to-consumer (DTC) genetic screening companies (e.g., <https://www.genebygene.com/products/brca12>, 2013). With the addition of more affordable DTC genetic screening products for BRCA1/2 mutations, greater choices are now available to all women. Despite the increased accessibility and popularity of genetic screening for BRCA1/2 mutations, DTC products are not without controversy.

In a 2010 review of DTC genetic technology completed by the National Institutes of Health (NIH) in the United States, four important limitations of DTC genetic technologies were highlighted including: (a) lack of Federal oversight of direct to consumer genetic testing, including promotional materials, (b) concerns related to evidence of clinical validity and/or clinical utility for most direct to consumer genetic tests, (c) issues related to privacy and protection of consumers using these services, and (d) knowledge levels about genetics among many consumers (NIH, 2010). Concerns identified by the NIH regarding DTC genetic technology are ongoing. For example, on November 28, 2013, the United States Food and Drug Administration sent a notice to the DTC genetic screening company, 23andme, ordering them to cease marketing their products over concerns related to the validity, clinical utility and reliability of their technology (FDA, 2013). In Canada, DTC genetic screening for BRCA1/2 mutations

currently falls out of the scope of the Canadian food and drug act and is an unregulated practice (Sarazin, Health Canada, nd).

Compared to the United States and Canada, the European Union (EU) generally has more advanced policies supporting regulations for DTC technologies. Within the EU, Germany currently has the most stringent piece of national legislation, the Human Genetic Examination Act (2009), which both regulates predictive and diagnostic genetic testing and requires involvement of physicians in genetic screening, effectively eliminating most DTC genetic screening products (Borry et al., 2012). Similar pieces of legislation exist in both Switzerland and France (Loi n°. 2004-800 relative à la bioéthique, 2004; Loi n°. 2011-267 d'orientation et de programmation pour la performance de la sécurité intérieure, 2011), and specify that genetic testing can only be executed by a medical doctor and can only occur after careful review of certain information, including family history. However, there are no provisions in these countries regarding obtaining this testing abroad (Borry et al., 2012). In the Netherlands, the legislation is more complex and considers the clinical validity of DTC genetic technology, as well as, professional medical practice standards and expected health benefit-risk analyses as important variables in approving DTC genetic technologies (Borry et al., 2012). In general, however, guidelines for the use of DTC products vary considerably across the EU despite attempts to propose uniform regulations (European Academies Science Advisory Council, 2012).

The only known published material investigating outcomes of DTC genetic screening was a recent case study by Doheny et al. (2012) who reported an unexpected psychosocial reaction in a patient as a result of learning her BRCA1/2 carrier status from a DTC product. In

their discussion of that case example, Doheny et al. (2012) suggested that genetic mutation results that produce fear or anxiety based responses in consumers may result in the avoidance of important surveillance and health management behaviours. Doheny et al. cautioned against the use of DTC in the absence of an informed genetic counseling process and recommended in favour of additional research to investigate the psychological impact of DTC genetic screening on consumers (2012).

BRCA1/2 celebrity. The advent of increased accessibility to DTC BRCA1/2 products occurred concurrently with a surge in media attention on BRCA1/2 gene mutations. In large part this had to do with the fact that celebrities like Angelina Jolie started to come forward to discuss their personal experiences of undergoing BRCA1/2 genetic screening (Jolie, New York Times, May 14, 2013). Jolie recently wrote an editorial in the New York Times in which she discussed her rationale for undergoing BRCA1/2 screening saying, “I have always told [my kids] not to worry, but the truth is I carry a ‘faulty’ gene, BRCA1, which sharply increases my risk of developing breast cancer and ovarian cancer” (New York Times, May 14, 2013, para. 3). As part of this piece, Jolie also discussed how learning of her BRCA1 mutation status led her to undergo a prophylactic double mastectomy as a surveillance measure.

A study of 2,572 adults in the United States taken three weeks following publication of Jolie’s editorial indicated that the majority of respondents (75%) knew about her story. However, fewer than 10% of respondents accurately interpreted Ms. Jolie’s risk of developing breast cancer relative to a woman unaffected by the BRCA1 gene mutation. In addition, of the women surveyed in this sample, most overestimated their personal risk of carrying the BRCA1 gene

mutation and the majority of these women expressed an interest in participating in genetic screening as a result of learning of Jolie's BRCA1 status (Borzekowski et al., 2013). Results of a document analysis study which reviewed media publication of Jolie's story, suggested that while Jolie accurately communicated information about her own personal risk for breast cancer, the media's representation ignored the rarity of her situation, and was especially positive about her decision to undergo a prophylactic mastectomy (Kamenova, Reshef & Caulfield, 2013). The authors of that study pointed to Jolie's story as an example of "celebrity medicine," whereby people often misinterpret their personal risk due to affiliation with a celebrity (Kamenova, Reshef & Caulfield, 2013). This finding is consistent with an emerging literature that suggests celebrities have the propensity to influence people's medical decisions because they are perceived as highly trustworthy (Hoffman & Tan, 2013). At the current time, there is a lack of understanding in the field regarding "how to effectively communicate with the public about the complex interplay among genomics, behavior, and health" (Tercyak, O'Neill, Rotter & McBride, 2012, p. 568).

BRCA1/2, Personalized Medicine, and Translational Genomics

As genetic screening tools have evolved, this technology has been applied to better understand risk, promote early detection, and develop targeted therapies. These advancements represent the continuing evolution of personalized medicine within genetics. The primary objective of personalized medicine is to tailor medical intervention to the needs of given individuals in order to achieve better health-care outcomes (Tercyak, 2011). BRCA1/2 screening to identify persons at risk of breast cancer and provide preventive therapies treatments to assist in

the reduction of the risk profiles of these individuals is an example of preventative medicine in action (Janssens & van Duijn, 2008).

In the area of breast cancer, medical genetics and personalized medicine have informed surveillance practice guidelines such as those developed by the National Comprehensive Cancer Network (2012) for women identified as BRCA mutation carriers. NCCN recommendations can include: (a) monthly breast self-examinations beginning by age 18 years, (b) annual or semiannual clinician breast examinations starting at age 25 years, and (c) annual mammography and breast magnetic resonance imaging (MRI) beginning at age 25 years. These recommendations also specify that individualized preventative screening may be developed according to on the earliest age of breast cancer onset within the family (NCCN, 2012). In addition to these screening practices, the NCCN (2012) also recommends that BRCA1/2 positive women consider risk-reducing mastectomy, salpingo-oophorectomy, testing of cancer antigen-125 levels (CA-125) and risk-reducing medications. As noted above, however, personalized medicine and the advancement of scientific discovery can be hijacked by unregulated procedures that may detract from utility of genetic test results. Additionally, preliminary research suggests that public knowledge can be easily shifted based on representations from celebrities (Hoffman & Tan, 2013).

Although personalized medicine is continuing to evolve, the highly anticipated potential for personalized medicine to actually assist in the prevention of disease states has yet to be attained (Tercyak, 2011). Khoury et al. (2011) have identified a critical and widening gap “between the promise of cancer genomics and the current reality of its impact on cancer care and

prevention” (p. 2110). In part, this disconnect has occurred because comprehensive and integrative translation of the science of molecular genetics into improved population health outcomes has been slow and impeded by several factors including a lack of population sciences research (Khoury, et al., 2011; Schully, Benedicto, Gillanders, Wang & Khoury, 2011).

According to Khoury et al. (2007), translational genomics, as a field, is characterized by five nonlinear phases including: discovery and replication phase; first phase of translation (“bench to bedside”); second phase of translation including evidenced based recommendations and policies; third phase of translation including implementation and dissemination science; and fourth phase of translation including population level study of effectiveness, cost effectiveness and outcomes (Khoury et al., 2007; Khoury et al., 2011). A recent analysis of the National Cancer Institute (NCI) cancer genomics research portfolio in the United States demonstrated that less than 2% of funded research was considered translational beyond the discovery and “bench to bedside” phases (Schully et al., 2011). This concentrated focus on discovery and “bench to bedside” level of research is limiting and problematic since it exacerbates the gap between genomics and breast cancer care and prevention (e.g., Khoury et al., 2011). Expanding the scope of current research programs to more inclusively promote and involve population science disciplines (e.g., epidemiology, behavioural social and communication sciences) is expected to provide a more integrative and complete approach to reducing the burden associated with breast cancer and improving translational genomics (Khoury et al., 2011).

While the literature investigating the psychosocial implications of BRCA1/2 genetic testing has traditionally focused on individuals at increased personal risk for breast cancer, little

is known about the impact of genetic screening on families as a unit of analysis, particularly young families. One of the aims of the current research study is not to close the gap described above entirely but, instead, to provide a more nuanced understanding of patients with young families who are participating in genetic counseling for BRCA1/2 mutations in the context of their roles as mothers. The goal of this dissertation is to add to the current knowledge in a theoretically informed manner that could support advancements in the areas of genetic counseling, risk communication, and health behaviours of high-risk families.

BRCA1/2 Screening and Families

A necessary step in determining whether or not genetic technology will provide useful information for family members is to assess how families interpret their genetic risk, whether or not they communicate about this risk, and how they negotiate genetic risk in the presence of histories of illness directly related to this risk. Increasingly, decision-making models for medical interventions are predicated on preventative health care philosophies. The primary objectives of preventative medicine are to extend health-related quality of life for current patients and to identify patients of the future (Gordon, 1987). As a result, the identification of risk factors for disease and the establishment of appropriate protocols to monitor high-risk populations are essential in promoting efficacious preventative models.

Molecular genetics and the predictive risk estimates derived from genetic technology represent a health service where the potential for knowledge translation of preventative models into action oriented health care strategies has enormous potential. However, the success of predictive screening for genetically based illnesses rests both in the dissemination of information

to patients and the implementation of cost-effective medical and psychological aftercare (Khoury et al., 2011; Esplen et al., 2013). At present, protocols for aftercare in genetics are developing but the implementation of guidelines is inconsistent across provincial and territorial health care systems in Canada (e.g., Avard et al., 2007; Kotsopoulous et al., 2014). A critical step in the development of aftercare programs designed to assist patients negotiating lifelong, irreversible risk information is to understand the psychosocial implications of genetic testing on both the individual undergoing screening and family members who stand to benefit from risk information.

Oncology is one area where the predictive screening of high-risk families has become a priority. Investigations of women's attitudes towards predictive genetic testing, prophylactic options, and other breast health behaviours in adult populations indicate that a large majority of women are embracing preventative medicine. For instance, research regarding interest in BRCA1/2 screening has indicated that between 60% and 87% of high-risk women offered screening expressed an interest in undergoing BRCA1/2 screening (Cappelli et al., 1999; Lerman & Shields, 2004). These rates are considerably higher than those associated with other adult onset hereditary disorders (AOHDs; Cameron & Reeve, 2006). The literature on BRCA1/2 counselees has generally identified four primary reasons underlying interest in this technology including: (a) learning about children's future risk (Bluman et al., 1999; Lerman et al., 1994; Lerman et al., 1997; Struewing et al., 1995), (b) providing relief from uncertainty regarding risk status (Bluman et al., 1999; Chaliki et al., 1995; Jacobsen et al., 1997; Lerman et al., 1997; Struewing et al., 1995), (c) enhancing the ability to make informed decision about prophylactic options to prevent cancer and/or increasing uptake of cancer screening practices (Bluman et al.,

1999; Chaliki et al., 1995; Jacobsen et al., 1997; Lerman et al., 1994; Lerman et al., 1997; Struewing et al., 1995), and (d) informing important life decisions such as marriage. Although other sociodemographic variables such as age, education, marital status, and ethnicity have frequently been studied in the literature examining interest in genetic screening, conclusive relationships have not been determined between these variables and uptake of BRCA1/2 screening (e.g., Pasacreata, 2003).

Hereditary breast cancer cases are more likely to occur in women under the age of 50, many of whom have adolescent children. Not surprisingly, the genetic legacy of breast cancer appears to be a salient issue for this group of women. For instance, our research group has demonstrated that concerns about an adolescent daughter's breast cancer risk are particularly important in determining whether or not a mother will undergo genetic testing (Cappelli et al., 1999; Cappelli et al., 2001; Cappelli et al., 2005). These results have been corroborated by many of our colleagues investigating this phenomenon (e.g., Bodd, Reichelt, Heimdal & Moller, 2003; Lodder et al., 2001; Tessaro, Borstelmann, Regan, Rimer & Winer, 1997). In fact, researchers have reported that up to 80% of women in a breast cancer genetic screening program elected to be tested because they wanted to know if they may have passed on a gene mutation to their pediatric-aged children (e.g., Tercyak et al., 2007). However, what remains to be seen is how the psychosocial adaptation of families undergoing genetic screening is influenced by threat variables including illness history, eligibility for genetic screening, and fear associated with breast cancer (Marteau & Weinman, 2006).

Although the knowledge provided by predictive screening may be beneficial, it also comes with great personal responsibility. Due to the shared components that underlie genetics, risk estimates for breast cancer affect the individual but also have the potential to impact family members. In previous work, our research group has observed that women with breast cancer are especially concerned about the implications of genetic testing for their adolescent daughters (Cappelli et al., 1999; Cappelli et al., 2001; Cappelli et al., 2005). Adolescent daughters of women being screened for BRCA1/2 mutations are at risk themselves for developing breast cancer and are viewed by many oncologists as “the patients of the future” (Cappelli et al., 1999). To date, however, investigations surrounding the implications of genetic testing for breast cancer susceptibility in highly relevant groups of families participating in genetic counseling for BRCA1/2 mutations have been limited.

CHAPTER 2

Scan of Literature on BRCA1/2 Screeners: Psychosocial Distress, Psychological Outcomes and Family Effects Associated with BRCA1/2 Screening

Over the last twenty years, there have been dramatic technological advances in genetic screening for BRCA1/2 mutations as well as increased accessibility to this screening. However, the psychosocial literature has failed to keep pace with these innovations as evidenced by the fact that the research has traditionally focused on (a) interest in genetic technology and (b) utilization of screening services for BRCA1/2 mutations. At the current time, advances in genetic technology and increased availability of genetic screening have eclipsed the issues of interest in and utilization of BRCA1/2 screening. The evidence from both the academic and popular literature clearly demonstrates that people are interested in investigating these technologies and that uptake rates for BRCA1/2 screening are generally high.

The high demand for BRCA1/2 screening, combined with established prevention strategies for breast cancer, explain why individuals being screened for BRCA1/2 alterations have been identified as a “clinically important group” (Meiser, 2005, p. 1060). However, the pattern of incomplete gene penetrance associated with BRCA1/2 mutations is theorized to produce unique emotional consequences for people at risk of carrying these mutations. For instance, potential BRCA1/2 counselees may encounter uncertainty about: (a) whether to undergo genetic screening, (b) if they will develop breast cancer, (c) how severe their disease may be, and (d) whether available prevention strategies will be effective. Additionally, BRCA1/2 results may have implications for interpersonal relationships, future plans including reproductive

decisions, and insurance availability/discrimination (Lerman & Shields, 2004; Marteau & Richards, 1996). Much of the literature in this domain has focused on investigating psychosocial distress and whether BRCA1/2 screening may result in clinically significant anxiety, depressive symptoms, and/or worry (Croyle, Smith, Botkin, Baty & Nash, 1997; Lerman, Croyle, Tercyak, & Hamann, 2002). Cumulatively, the broad findings in this area have determined that, overall, the vast majority of BRCA1/2 counselees cope well with risk information although a minority do experience clinically significant psychosocial distress (e.g., Hamilton, Lobel & Moyer, 2009; Tercyak et al., 2012). More recently, the patterns in the literature have shifted toward building understanding of (a) the subclinical distress experienced by BRCA1/2 counselees and (b) how susceptibility for BRCA1/2 may result in adaptive responses aimed at disease prevention. Rather than addressing psychosocial distress, researchers are now moving toward an understanding of psychosocial functioning in the presence of genetic risk for BRCA1/2 mutations.

Given the scope of the current study, as well as the number of existing literature reviews completed before 2007 (i.e., Broadstock et al., 2006; Meiser, 2005; Pasacreta, 2003; Schlich-Bakker, ten Kroode & Ausems, 2006a), an updated literature review was undertaken to examine the recent research regarding the psychosocial functioning of women being screened for BRCA1/2 gene mutations. The purpose of the current review was to explore recent findings and integrate this information with results obtained from the peer-reviewed literature published before 2007. Bibliographic databases (PsycINFO, MedLine, PubMed) were searched in March 2010 and again in June, 2013 using the keywords: (*breast cancer or BRCA**) and (*gene* test**, *gene* counsel**, *gene* screen**) and (*psycholog**, *psychosocial*, *distress*, *anxiety*, *depression*, or

worry). Studies were considered eligible for this scan if they were: (a) published in a peer-reviewed journal between 2007 and 2013, (b) included participants older than 18, (c) used at least one emotional distress variable measured using a standardized quantitative instrument, (d) included individuals participating in BRCA1/2 genetic counseling, and (e) were published in either English or French languages. Before the inclusion criteria were applied, the search produced 219 total studies published between 1995 and 2013. Following the application of the inclusion criteria, 14 studies (i.e., Bennett et al., 2008; Cukier et al., 2013; Dagan & Shocat, 2009; Foster, Watson & Eeles, 2007; Geirdal & Dahl, 2008; Graves et al., 2012; Julian-Reynier et al., 2011; Lapointe et al., 2012; Low, Bower, Kwan & Seldon, 2008; Metcalfe et al., 2012; Mikkelsen, Sunde, Johansen & Johansen, 2009; O'Neill et al., 2012; Pieterse, Ausems, Spreuwenberg & van Dulman, 2011; Wevers et al., 2011) and 1 meta-analysis (Hamilton, Lobel & Moyer, 2009) were identified as appropriate for inclusion in this scan.

Defining Psychosocial Distress and Psychosocial Functioning

Psychosocial research is commonly used as an umbrella term by a variety of health research domains (e.g., psychology, oncology, medicine, epidemiology). While the term encourages a common, multifactorial understanding of pathways that lead to ill-health, concerns have been articulated by various researchers about how we define, understand, operationalize, and study psychosocial outcomes (e.g., Martikainen, Bartley & Lahelma, 2002). Previous studies that have assessed psychosocial distress following participation in AOHD screening using standardized instruments (e.g., global measures of anxiety, depression symptoms) have demonstrated that between 8% and 25% of people undergoing screening for AOHD mutations

will experience clinically significant levels of distress (e.g., Esplen et al., 2013). However, within the psychosocial genetics literature, there has been considerable debate over the issue of how we define and understand psychosocial distress. Much of this debate has been related to issues surrounding operationalization and measurement of distress (e.g., Biesecker et al., 2008).

The current understanding and operationalization of the term psychosocial distress in the BRCA1/2 literature has been coopted from psychosocial oncology research where distress is understood to mean, “an unpleasant experience of an emotional, psychological, social, or spiritual nature that interferes with the ability to cope it extends along a continuum, from common normal feelings of vulnerability, sadness, and fears, to problems that are disabling, such as true depression, anxiety, panic, and feeling isolated” (NCCN, 2012, para. 5). Research on the topic of psychosocial distress is considered important since results can inform methods of detecting and identifying distress. Additionally, this research can translate into interventions and programming to assist clinicians in determining which patients may benefit from further assessment or referral for supportive care (e.g., Esplen et al., 2013). In fact, the study of psychosocial distress is acknowledged as a key priority area in Canada as evidenced by the fact that distress is recognized by Accreditation Canada (2012) as the sixth vital sign (following heart rate, blood pressure, respiratory rate, temperature and pain).

Over the last twenty-five years, the field of psychosocial genetics has developed into a proper research domain. During this time, the findings from the literature have revealed that the continuum of distress described above is especially salient in this population of patients undergoing genetic counseling as only a minority of these genetic counselees will experience

clinically significant levels of distress. As such, the term *psychosocial functioning* has been applied more frequently in the literature and clinical practice. The term psychosocial functioning has broader utility as a concept since it accounts for the continuum of responses, including subclinical levels of distress, and captures wellness and resiliency in addition to symptoms and coping. The primary goal of psychosocial genetics research has been to investigate the “psychological outcomes, interpersonal and familial effects, and cultural and community responses” related to genetic screening (NCCN, 2012, para. 9). Psychosocial genetics literature generally focuses on three outcome variables including: psychological outcomes, functional outcomes, and behavioural outcomes. Given that the concentration of this thesis is on the psychosocial functioning outcomes of BRCA1/2 counsees, rather than the behavioural outcomes (e.g., surveillance behaviours), review of the recent literature will focus primarily on psychological and functional outcomes of BRCA1/2 counsees.

Psychosocial Functioning Variables

In her seminal review, Pasacreta (2003) identified fourteen studies (i.e., Biesecker et al., 2000; Croyle et al., 1997; Dorval et al., 2000; Dudok deWit et al., 1997; Dudok deWit, et al., 1997; Dudok deWit et al., 1998; Lerman, Schwartz, Miller, Daly & Rimer, 1996; Lerman et al., 1997; Lerman et al., 1998; Lodder et al., 1999; Lodder et al., 2001; Smith et al., 1999; Wagner et al., 2000) that discussed the impact of BRCA1/2 screening on psychological functioning. Although there was considerable variability in the operationalization and measurement of psychological distress across these studies, the research generally looked at four outcome variables (i.e., measures of psychosocial distress) including: depressive symptoms, anxiety,

breast cancer worry, and risk perception. In the interest of consistency, the present review followed a similar format by grouping study findings according to psychosocial outcome variables including depressive symptoms, anxiety, breast cancer worry and risk perception.

Depressive symptoms. Studies assessing depressive symptoms as a measure of psychosocial distress in response to BRCA1/2 counseling and screening have utilized a variety of measurement scales including the Beck Hopelessness Scale (BHS; Beck, Steer & Garbin, 1988), the Brief Symptom Inventory (BSI; Derogatis & Melisaratos, 1983), the Beck Depression Inventory (BDI; Beck et al., 1998), the Center for Epidemiologic Studies-Depression Scale (CES-D; Radloff, 1977) and the Hospital Anxiety and Depression Scale (HADS; Zigmond & Snaith, 1983). While some of these measures are designed to specifically capture depressive symptoms, others included a variety of subscales measuring anxiety and worry in addition to depressive symptoms. For many of the studies reviewed, separate depressive symptom scales were not available or depressive and anxiety symptoms were collapsed making it challenging to assess depressive symptoms (isolated from anxiety) as experienced by BRCA1/2 counselees. For studies that did include separate depressive symptom scales or measures, the operational definition of mood-related distress was sometimes poorly defined and typically based on clinical cut-offs. These clinical ratings may not be the most appropriate way to understand psychosocial distress as experienced by BRCA1/2 counselees. As a result of the methodological issues highlighted above, interpretation of the findings related to depressive symptoms was rather difficult and further research is likely needed to help fully explain the impact of BRCA1/2

screening on subclinical depressive symptoms experienced by BRCA1/2 counselees (e.g., Esplen et al., 2013).

Of the four prospective studies published between 2007 and 2013 that have reported on depressive symptoms in response to BRCA1/2 screening, three obtained non-significant results, suggesting that BRCA1/2 screening does not impact mood (Bennett et al., 2008; Mikkelsen et al., 2009; Reichelt, Moller, Heimdal & Dahl, 2008). This is consistent with the majority of the literature published between 1995 and 2007 that found no significant impact of BRCA1/2 screening on mood (e.g., Arver, Haegermark, Platten, Lindholm, & Brandberg, 2004; Bowen, Burke, McTiernan, Yasui & Andersen, 2004; Cull et al., 1998; Lobb et al., 2004; Watson et al., 1998).

While much of the previous research on BRCA1/2 counselees has indicated that no clinically significant differences exist between depressive symptom ratings of BRCA1/2 carriers, non-carriers, and age-matched controls, subclinical differences in depressive symptoms have been documented in the literature (e.g., Bennett et al., 2008; Dagan & Shocat, 2009). Additionally, findings from one of the most methodologically sound studies in this research domain have suggested that subclinical depressive symptoms experienced following BRCA1/2 screening may be linked with carrier results (Meiser et al., 2002). In their prospective cohort study, Meiser et al. (2002) compared BRCA1/2 negatives (i.e., non-carriers) with BRCA1/2 carriers as well as women who had family histories of breast cancer but who were not tested for the BRCA1/2 mutations. Findings from that study indicated that depressive symptom scores, as measured by the Beck Depression Inventory, at 4 months post-screening were significantly lower

for BRCA1/2 non-carriers as compared to both BRCA1/2 carriers and women who were not tested for the mutations (Means were 3.6, 6.2, 6.4, respectively, $p = 0.024$). While differences between the groups were observed, it should be noted that scores did not reach the threshold for clinical depression and that these differences were not sustained over time (i.e., at 12 month follow up). However, these findings suggest that further research is needed to understand the impact of BRCA1/2 carrier status on sub-threshold depressive symptoms.

In addition to carrier status, some preliminary research suggests that family histories of breast cancer may play a role in depressive symptoms experienced in response to BRCA1/2 screening. For example, Geirdal, Reichelt and Dahl (2005) conducted a prospective cohort study that measured depressive symptoms (using the Hospital Anxiety and Depression Survey; HADS). Results from that study demonstrated that women who did not receive genetic testing but who had a family history of breast cancer endorsed significantly more depressive symptoms compared with women receiving positive BRCA1/2 test results. Once again, however, mean scores from these groups did not meet clinical cutoffs for depression (Geirdal, Reichelt & Dahl, 2005).

More recently, research by Graves et al. (2012) revealed that, BRCA1/2 screeners with personal histories of breast cancer who received positive BRCA1/2 mutation results experienced lower rates of positive experiences compared with women who had never been diagnosed with breast cancer and who had received BRCA1/2 uncertain results. Another recent study by Cukier et al. (2013) found that BRCA1/2 screeners with personal histories of cancer, reported significantly higher rates of depressive symptoms on the Center of Epidemiological Studies

Depression scale (CES-D; $\beta = .17$, $SE = .28$, $p = .04$). While these results are compelling, it is important to note the measure of depressive symptoms in this study has excellent sensitivity with respect to mood fluctuations and this may have contributed to these findings (e.g., Verdier-Taillefer et al., 2001). At the present time, further investigation is required to determine the complex interplay between breast cancer history and BRCA1/2 carrier results on depressive symptoms. However, results from this review indicate that illness variables play a role in depressive symptoms, while the impact of BRCA1/2 risk is not well-established at this time. Comparatively less is known about how eligibility for BRCA1/2 screening impacts psychological functioning in high-risk women who participate in genetic counseling for BRCA1/2 but are determined to be ineligible for screening. One of the purposes of the current study is to understand how eligibility for BRCA1/2 screening in the public health care context impacts BRCA1/2 counselees' psychosocial functioning.

Anxiety. Studies of psychosocial functioning in BRCA1/2 screeners have often measured anxiety using a variety of scales including the State Anxiety subscale of the Spielberger State-Trait Anxiety Inventory (STAI; Spielberger, Gorsuch, Lushene, Vagg, & Jacobs, 1983), the General Health Questionnaire (Goldberg & Hillier, 1979), the short form of the Hopkins Symptom Checklist (Derogatis, Lipman, Rickels, Uhlenhuth, & Covi, 1974), the Anxiety subscale of the Hospital Anxiety and Depression Scale (Zigmond & Snaith, 1983), the Anxiety subscale of the Brief Symptom Inventory (Derogatis & Melisaratos, 1983), and the Anxiety subscale of the Profile of Mood States (McNair, Lorr, & Droppleman, 1971). In some cases, multiple measures were applied to assess anxiety (Hamilton et al., 2009). The methodological

limitations identified in the assessment of depressive symptoms (as described above) also extend to the research on BRCA1/2 counselees' anxiety.

Of the five studies published since 2007 that have explicitly assessed anxiety, two (i.e., Ertmanski et al., 2009; Reichelt et al., 2008) reported no impact of BRCA1/2 screening on anxiety symptoms, while three studies (Foster et al., 2007; Low et al., 2008; Shochat & Dagan, 2010) reported increases in anxiety related to BRCA1/2 screening or risk results. A recent meta-analysis completed by Hamilton, Lobel and Moyer (2009) has more clearly identified the relationship between BRCA1/2 screening and reports of anxiety. Results from that study indicated that BRCA1/2 carrier status was associated with short-term increases in anxiety reported by BRCA1/2 screeners, as well as, significant differences in the degree of anxiety changes experienced by carriers, non-carriers, and those with uncertain BRCA1/2 results at short-term follow up (mixed effects; $Q(2) = 22.41, p < .001$). More specifically, the results of Hamilton, Lobel and Moyer's (2009) work demonstrated that BRCA1/2 carriers experienced significantly higher increases in anxiety during the short-term (i.e., immediately following BRCA1/2 diagnosis).

Several research groups who have investigated the impact of BRCA1/2 mutation status on anxiety have also suggested that effects of BRCA1/2 screening on anxiety can be observed when controlling for mutation status. For instance, two prospective cohort studies (Low et al., 2008; van Dijk et al., 2006) reported significantly higher anxiety scores amongst women who received positive BRCA1/2 results compared with women receiving BRCA1/2 negative test results or uncertain test results. These findings are consistent with results obtained from a

prospective cohort study where non-carriers of BRCA1/2 mutations were compared with carriers and women who did not get tested. Results from that research indicated that non-carriers endorsed significantly fewer anxiety symptoms at 7 to 10 days follow-up (Meiser et al., 2002). However, as Hamilton et al. (2009) have noted, many of the short-term increases in anxiety that have been identified in the literature have not been sustained over time and were subclinical in nature. In addition to research on carriers and non-carriers, a recent study by O'Neill and colleagues (2012) demonstrated that while depressive symptoms and anxiety (as measured by the Brief Symptom Inventory) in their overall sample declined significantly from pretesting to 1-month post-disclosure ($t(206)=3.99, p < .001$), women who received uncertain BRCA1/2 results experienced higher levels of anxious and depressive symptomatology at 1 and 6 months follow up compared to all other women ($t(17)=2.88, p = .01$).

The impact of BRCA1/2 uncertainty on psychological distress has also been studied by Geirdal and colleagues (2008, 2005) who found that women who had family histories of breast cancer, but who had not undergone genetic testing were significantly more anxious and endorsed significantly higher levels of general distress than women who had been identified as BRCA1/2 mutation carriers. This study represents one of only a few research projects (e.g., Foster et al., 2007; Meiser et al., 2002) that have endeavoured to study populations of high-risk BRCA1/2 counselees who are ineligible for screening.

At the present time, results regarding the anxiety experienced by BRCA1/2 counselees appear inconclusive. There do seem to be associations between uncertain and positive carrier status and reports of anxiety. However, many studies lack control groups of women with breast

cancer histories who have undergone genetic counseling but are ineligible for screening or who have elected not to be tested despite having either personal or familial histories of breast cancer. As such, the relationships between illness, risk and eligibility for BRCA1/2 screening and their associations with patients' reports of anxiety are not well understood at this time.

Breast cancer worry. Of the six observational, prospective cohort/case-control studies published between 1995 and present which have examined the issue of breast cancer worry (i.e., Dagan & Shocat, 2009; Foster et al., 2007; Julian-Reynier et al., 2011; Mesier et al., 2002; Metcalfe et al., 2013; van Dijk et al., 2006), five have identified breast cancer worry as an adverse outcome associated with BRCA1/2 screening. In their study of BRCA1/2 screeners, van Dijk and colleagues (2006), tracked participants' levels of breast cancer worry at three time intervals: pretest, one month following genetic screening and seven months following BRCA1/2 diagnosis. Their results indicated that breast cancer worry was significantly higher among women who tested positive for BRCA1/2 mutations as compared to all other groups (which included true negatives, high-risk uncertain and low-risk uncertain). Similar results were reported by Meiser and colleagues (2002) who conducted a cohort study comparing BRCA1/2 screeners with women who did not receive BRCA1/2 testing. Findings from that study revealed significant increases in breast-cancer worry among BRCA1/2 screeners at one-week and 12 month follow up, compared with women who did not receive BRCA1/2 testing (Meiser et al., 2002). Results of these studies suggest that BRCA1/2 screening may play an important role in BRCA1/2 counselees' levels of breast cancer worry.

Of the studies identified for review since 2007, several have reported significant increases in breast cancer specific distress among BRCA1/2 mutation carriers. Results from a study conducted by Metcalfe et al. (2012), indicated that mutation carriers reported significant increases in breast cancer worry from baseline to 1 year following receipt of genetic test results; however, decreases in breast cancer worry were reported amongst mutation carriers from the 1 year follow up mark to the two year follow up assessment. Of note, this study included a small number of participants (N=17) and while significant increases were reported in breast cancer worry, as measured by the Impact of Events Scale, results remained in the mild range. Despite the small sample size, these findings are consistent with results of a larger case-control study (Dagan & Shochat, 2009) that found mutation carriers experienced significantly higher rates of breast cancer worry than controls. Additionally, in their study of 246 people screened for BRCA1/2 mutations, Julian-Reynier et al. (2011), reported significant increases in breast cancer worry for people who received positive BRCA1/2 results and significant decreases in breast cancer anxiety for non-carriers. Finally, results from a 2012 study conducted by Wevers et al. (2011) provided further evidence for the relationship between BRCA1/2 mutation status and breast cancer distress, with BRCA1/2 mutation carriers endorsing significantly higher scores on a measure of breast cancer distress than patients without a pathogenic mutation. Additionally, BRCA1/2 carriers in this sample also demonstrated higher levels of avoidance. While results of Wevers et al.'s study are consistent with the broader findings, results should be interpreted with caution due to the retrospective nature of the reports and the small sample size (N=26; Wevers et al., 2011).

With respect to the impact of illness history on breast cancer worry, several investigators have studied this variable in the context of their BRCA1/2 research. For instance, in a recent study of 148 high-risk, African-American women undergoing BRCA1/2 counseling, Cukier et al. (2013) examined the relationship between the total score on the measure of cancer-specific distress and several sociodemographic and clinical variables. Findings indicated that women who had been diagnosed with breast cancer reported significantly higher rates of intrusive thoughts on a measure of cancer specific distress ($\beta = -.20$, $SE = 1.52$, $p = .02$; Cukier et al., 2013). Similar results were reported in a 2011 study conducted by Wevers et al. who surveyed BRCA1/2 screeners who had been affected by breast cancer. Findings from that sample indicated that 19% of women surveyed reported being often or always worried about the possibility of developing cancer again on a self-report measure, the Cancer Worry Scale. In addition to general cancer distress, Wevers et al. also examined breast cancer specific distress and found that 23% of their sample reported clinically significant levels of ongoing distress related to a recurrence of breast cancer (2011).

Other studies published since 2007 have reported decreases in breast cancer worry following receipt of BRCA1/2 test results. For example, in their prospective cohort study, Foster Watson, and Eeles (2007) reported significant decreases among BRCA1/2 carriers with respect to breast cancer worry, as measured by the Cancer Worry Scale – Revised Version, at three years post-disclosure. These results are consistent with research conducted by other groups (i.e., Bennett et al., 2008; Braithwaite, Sutton, Mackay, Stein & Emery, 2005; Helmes, Culver & Bowen, 2006; Hopwood et al., 2004; Mikkelsen et al., 2009). Of note, the research conducted by

Foster et al. (2007) presents data from longer-term follow up data with women and suggests that time since BRCA1/2 screening may impact patients' levels of breast cancer distress.

A number of studies have been published between 1995 and 2013, assessing the impact of genetic counseling on rates of breast cancer worry or distress. Of these, many revealed no significant increases or decreases in breast cancer worry among BRCA1/2 screeners who receive genetic counseling (e.g., Bowen et al., 2000; Bowen, et al., 2004; Bloom, Stewart, Chang & You, 2006; Brain et al., 2011; Burke et al., 2000; Lerman et al., 1996; Lerman et al., 1999; Fry et al., 2003; Pieterse et al., 2011; Watson et al., 1998). However, a recent meta-analysis completed by Hamilton et al. (2009) has helped to clarify the impact of BRCA1/2 screening on breast cancer worry. According to Hamilton et al. (2009), significant differences were reported in ratings of breast cancer distress by BRCA1/2 carriers, non-carriers, and those with uncertain results over the short (mixed effects $Q(2) = 25.37, p < .001$) medium (mixed effects; $Q(2) = 15.71, p < .001$) and long term (mixed effects $Q(2) = 7.40, p < .03$). Based on their review and analyses, results suggest that BRCA1/2 carriers experienced a small increase in cancer-specific distress immediately following receipt of genetic results ($d = 0.27, p < .001$) but this distress returned to pretesting levels at both medium ($d = -0.01, p > .94$) and long term follow up ($d = -0.15, p = .18$). Non-carriers continued to experience modest to moderate decreases in cancer-specific distress at short, medium and long term intervals following obtaining their mutation status (i.e., $d = -0.25, p < .008$; $d = -0.42, p < .001$; $d = -0.47, p < .001$, respectively). Importantly, BRCA1/2 screeners who obtained uncertain results reported small decreases in

distress after a short period of time ($d = -0.18, p < .04$), followed by a small to medium decrease at medium ($d = -0.34, p < .001$) and long term follow up ($d = -0.39, p < .001$).

BRCA1/2 risk distress. Although most of the research in this domain has investigated psychosocial outcomes including depressive symptoms, anxiety and breast cancer worry, few studies have addressed the role of BRCA1/2 risk distress. In order to develop a more complete understanding of the familial impact of BRCA1/2 counseling, it is critical to first understand how risk information is interpreted and understood by patients themselves. Results of general population studies have indicated that genetic risk for hereditary breast cancer is poorly understood and that the vast majority of people overestimate their personal risk for hereditary breast cancer (Borzekowski et al., 2013; Kamenova, Reshef & Caulfield, 2013). However, across studies of BRCA1/2 counselees, the evidence suggests that genetic counseling improves patients' understanding of their objective risk of hereditary breast cancer (e.g., Mikkelsen et al., 2007; Pieterse et al., 2011; Roshanai, Rosenquist, Lampic & Nordin, 2009).

A systematic review collated results from the 21 studies published prior to 2007 that assessed the impact of genetic counseling on patients' accuracy ratings of their breast cancer risk (Smerecnik, Mesters, Verweij, de Vries & de Vries, 2009). Results of that study revealed that the patients' accuracy of their risk for hereditary breast cancer increased from an average of 42% accuracy before genetic counseling to 58% after counseling (Smerecnik et al., 2009). Despite the improvements in patients' accuracy ratings associated with genetic counseling, the available evidence suggests that women who undergo genetic counseling for BRCA1/2 alterations overestimate their risk of hereditary breast cancer by an average of 25 percentage points (Bloom

et al., 2006). In addition, a prospective study of 246 BRCA1/2 screeners revealed that learning of one's BRCA1/2 risk significantly affected the risk perceptions of both carriers and non-carriers (Julian-Reynier et al., 2011). Among BRCA1/2 carriers, genetic risk information was associated with significant increases in the proportion of carriers with high/very high breast cancer risk perceptions whereas it decreased breast cancer risk perceptions for non-carriers (Julian-Reynier et al., 2011). In another recent investigation by Graves et al. (2012) that assessed genetic risk distress, logistic regression bivariate analysis revealed significant associations between positive genetic test results and distress associated with BRCA1/2 screening.

Collating these findings together, the overall message seems to be that, while genetic counseling helps improve perceived risk estimates for hereditary breast cancer, there is considerable work to be done to help understand discrepancies between perceived and objective levels of risk. Given the complexities associated with accurately interpreting one's risk estimate, however, risk perception is unlikely to provide a good operational definition of distress related to BRCA1/2 test results.

BRCA1/2 eligibility. As mentioned above, few studies have investigated the impact of BRCA1/2 eligibility on psychosocial functioning. In fact, a recent meta-analysis completed by Nelson et al., (2013) which identified sixteen studies published between 2007 and 2012, that assessed the impact of genetic counseling on psychosocial functioning demonstrated that none of these investigations had assessed the impact of eligibility on BRCA1/2 counselees' psychosocial functioning. In other words, eligibility for BRCA1/2 screening was not controlled in assessment of patients' psychosocial functioning following BRCA1/2 counseling in any of the published

literature. Despite this, these same studies often controlled for mutation status and breast cancer history. As a group, the evidence demonstrates that patients who received genetic counseling do not demonstrate clinically significant increases in breast cancer worry, depressive symptoms, or anxiety (Nelson et al., 2013). However, as described above, given that mutation status and breast cancer history are theorized to impact psychosocial functioning, it would stand to reason that eligibility may also be an important variable to consider. Based on the evidence indicating that approximately 20% to 33% of individuals who receive genetic counseling feel their emotional needs are not met within the BRCA1/2 counseling process, it is important to understand the role of eligibility in psychosocial adaptation of BRCA1/2 counselees (Douma et al., 2010; Pieterse et al., 2011). This is especially true based on the existing literature which has demonstrated that counselees who perceived their needs to be fulfilled in the genetic counseling process, demonstrated significantly higher perceived personal control and the significantly lower their anxiety ratings following counseling (Pieterse et al., 2011).

Family Functioning in the BRCA1/2 Context

Research in the area of BRCA1/2 has generally focused on index patients who have undergone genetic screening. As a result, the issue of genetic risk within families as a unit of analysis has traditionally been a major shortcoming within this field of research. According to several researchers who have conducted reviews of psychosocial outcomes of BRCA1/2 screeners (e.g., Schlich-Bakker et al., 2006b; Meiser, 2005, & Pasacreta, 2003), a paucity of literature exists examining the functional implications of BRCA1/2 Screening. Currently, there is a scant empirical research available that discusses the functional impact of risk information on

BRCA1/2 screeners with adolescent daughters. A search of bibliographic databases (PsycINFO, PubMed, and Web of Science) in January 2013 using the keywords: (*breast cancer or BRCA**) and (*gene* test*, gene* counsel*, gene* screen**) and (*adolescent, family, teen**) was conducted. Studies were considered eligible for this scan if they were: (a) published in a peer-reviewed journal between 1995 and 2013, (b) included BRCA1/2 screeners who had adolescent children, (c) were published in either English or French languages, and (d) assessed an aspect of family functioning or communication as part of the study. Nine studies were identified as appropriate for inclusion in this scan. The limited research in this area is due, in part, to ethical restrictions surrounding research with vulnerable populations as well as genetic screening of minors. Of the studies that were identified for review, the sample contained two qualitative (e.g., Clarke, Butler & Esplen, 2008; Bradbury, Dignam & Ibe, 2007) and seven quantitative or mixed-methods investigations (Segal et al., 2004; Patenaude et al., 2006; Bradbury et al., 2012; Tercyak et al., 2001a; Tercyak et al., 2001b; Tercyak et al., 2002; Tercyak et al., 2007).

Given that investigations of the implications of genetic testing for breast cancer susceptibility in highly relevant groups of families negotiating genetic risk have been limited, this literature review begins with a discussion of the broader research on the impact of breast cancer on families since this literature also informed the project background and design.

Summary of parental breast cancer research.

It is estimated that, of the total number of patients diagnosed with breast cancer each year, 19% will be women under the age of 50. In 2012, this number translated to approximately 4,260 young, Canadian women newly affected by breast cancer (Canadian Cancer Statistics,

2012). Research has indicated that at least 18% of all cancer patients reside with their minor children (Weaver et al., 2010). Applied to the Canadian context, it is estimated that 4,086 of the 22,700 Canadian women who were diagnosed with breast cancer in 2012 will be living with minor aged, dependent children (Cancer Research UK, 2012; Canadian Cancer Statistics, 2012; Weaver et al., 2010).

Hereditary breast cancer cases are more likely to occur in women under the age of 50, many of who have adolescent children. In fact, studies of BRCA1/2 positive women, indicate that, approximately 30% to 50% will be diagnosed with breast cancer before age 50 (American Society of Clinical Oncology, 2014). Not surprisingly, the genetic legacy of breast cancer appears to be a salient issue for this group. Due to the inheritance pattern of BRCA1/2 mutations (i.e., autosomal dominant), adolescent daughters of young women with breast cancer are at higher risk for developing breast cancer and are viewed by many oncologists as “the patients of the future” (Cappelli et al., 1999).

Studies investigating the impact of maternal breast cancer on families have, by and large, indicated that the vast majority of children and adolescents cope well with parental cancer. However, as described in the research, a significant minority of young people have been identified as being more vulnerable to developing psychosocial problems secondary to their parents’ breast cancer diagnosis (Faulkner & Davey, 2002, Grabiak, Bender & Puskar, 2007; Visser et al., 2004). Vulnerability of these young people has been linked to several variables including: parental factors, family variables, and youth factors.

Parental factors. Studies of families affected by breast cancer have produced inconsistent results regarding associations between parental factors and children's adjustment. More specifically, several research groups have reported higher internalizing problems and stress responses in adolescents of breast cancer patients (e.g., Compas et al. 1994; Grant & Compas 1995; Huizinga et al., 2011; Welch et al. 1996) as well as significant associations between parental distress and children's emotional and behavioural problems (e.g., Gazendam-Donofrio, 2007; Huizinga et al., 2005). Conversely, other investigations have described no significant associations of parental distress on children's functioning (e.g., Nelson & While et al., 2002; Vannatta, Ramsey, Noll, & Gerhardt, 2010). While results regarding the impact of parental cancer on youth anxiety and distress are mixed, investigations surrounding the impact of parental depressive symptoms have produced more uniform results. As described in several reviews (e.g., Grabiak et al., 2007; Osborn, 2007), there is strong and consistent evidence that children's psychosocial adjustment is related to parents' mood. More specifically, parent depressive symptoms consistently emerged as significant predictor of emotional and behavioural problems (e.g., Edwards et al., 2008; Hoke, 2001; Lewis & Darby, 2004; Sigal, Perry, Robbins, Gagne & Nassif, 2003) as well as distress in children of breast cancer patients (e.g., Watson et al., 2006). Reviews of the impact of parents' cancer stage and prognosis have yielded inconsistent results (Grabiak et al., 2007; Krattenmacher et al., 2012; Osborn, 2007); however, several recent, good quality studies in the area have suggested that advanced cancer stage and poorer prognosis are associated with psychosocial distress in youth (Sigal et al., 2003; Visser et al., 2005).

Family factors. In studies of families affected by parental cancer, general family dysfunction was associated with higher rates of externalizing and internalizing problems (Lindqvist, Schmitt, Santalahti, Romer & Piha, 2007; Thastum et al., 2009, Watson et al., 2006). However, research on specific aspects of family functioning including communication, marital status, and socioeconomics, has produced inconsistent results with respect to the impact of these factors on youth adjustment. For instance, Huizinga and colleagues (2005) found significant associations between open communication patterns and adaptive coping behaviours of youth. Conversely, a study by Nelson and While (2006) found no relationship between parent–child communication and youth adjustment in the context of parental cancer. Similar inconsistencies were observed in the literature with respect to the impact of marital status, marital satisfaction and socioeconomic status (Krattenmacher et al., 2012).

Youth factors. In studies of children of breast cancer patients, gender and age differences have been observed. According to several studies, daughters reported more emotional and behavioural problems and higher stress responses as compared to sons (e.g., Edwards et al., 2008; Welch et al., 1996). Additionally, adolescent daughters have been identified as a particularly vulnerable group (e.g., Compas et al., 1994; Hoke, 2001; Welch et al., 1996). However, findings regarding the impact of age and gender are mixed, with other research groups suggesting that these variables are not associated with children’s psychosocial adaptation to illness (Visser et al., 2007; Watson et al., 2006).

Despite the evidence indicating that a subset of children affected by parental cancer will experience clinically significant levels of psychosocial distress, there is currently a lack of child-

centered interventions for families affected by parental cancer (Niemela , Hakko & Rasanen, 2010). According to Krattenmacher and colleagues (2012), one of the most significant barriers to the development of such interventions has been the lack of systematic study of risk factors and protective factors for children and families affected by breast cancer.

High-Risk Families, Ethical Issues and Important Developmental Considerations

The rapid introduction of BRCA1/2 mutation screening raised several ethical dilemmas, not the least of which is the testing of minors. Many professional organizations have produced policy statements that discourage genetic testing in children for adult-onset diseases (Clarke, 1994; Kodish, 1999). Opponents of BRCA1/2 mutation screening in minors have traditionally cited potential adverse psychological consequences to early testing, including increased cancer distress, anxiety, distortion of family relationships and interference in normal development of self-concept (Wertz et al., 1994). However, to date, there is virtually no empirical data to support arguments against the testing of minors for BRCA1/2 mutations (likewise, there is limited investigation to support the opposing position; e.g., Wade, Wilfond & McBride, 2010).

To date, no known medical benefits to communicating breast cancer risk to minor children have been identified (Bradbury et al., 2012) and current, clinical guidelines suggest that prophylactic surgery and radiographic screening for BRCA1/2 mutation carriers are generally not recommended until individuals are 25 years old (Borry, Stuliens, Nys, Cassiman & Dierickx, 2006). However, breast cancer risk is considered relevant in adolescence for several important reasons. First adolescence has been identified as critical period of carcinogenic vulnerability within the life cycle and there is accumulating research in this area investigating the potential for

early-life events might modify risks for adult breast cancer (e.g. Maruti et al., 2005; Okasha, McCarron, Gunnell & Smith, 2003; Warri, Saarinen, Makela & Hilakri-Clarke, 2008; Wild, 2011). Second, a number of health and risk behaviours begin to develop while others are firmly establishing during this developmental period (e.g., Holmbeck, 2002; Mulye et al., 2009). Third, breast cancer media reporting, promotion, and educational agendas increasingly target youth (e.g., Orenstein, 2010). For example, our previous work has suggested that adolescent girls of mothers with breast cancer are aware of, and concerned about their risk (Cappelli et al., 2005). However, as described by Bradbury et al. (2012), “what high-risk and population-risk girls know and perceive of breast cancer risks, its impact on their psychosocial well-being and adoption of preventive health and risk behaviors and how these change over time remains unknown” (p. 750).

Within the breast cancer literature, adolescent daughters have been theorized to be more vulnerable to psychosocial distress (e.g., Lewis & Hammond, 1996; Spira & Kenemore, 2000). For example, Spira and Kenemore (2000) have asserted that a disconnect occurs between the developmental needs and demands of the adolescent and the needs of the family when a mother is diagnosed with breast cancer. They noted that, based on results of their qualitative study, that adolescents’ emerging self may be impacted by a fear of being diagnosed with breast cancer. They further explained that for many young women, this developmental period is also associated with onset of puberty and development of breasts which they posited could increase fear responses. According to Spira and Kenemore (2000) the threat of losing mother may be associated with the threat of losing the emerging self. While this work is supported by some of

the research in parental breast cancer (e.g., Krattenmacher et al., 2012; Compas et al., 1994; Compas et al., 1996), there is virtually no evidence based on limited studies of adolescents who undergo other types of predictive screening for genetic conditions that knowledge of genetic risk results in poorer psychological functioning (e.g., Wade et al., 2010). However, self-concept is emerging within the BRCA1/2 counselee literature as an important concept warranting further study with several recent investigations of BRCA1/2 counselees demonstrating that lower self-concept in BRCA1/2 counselees was associated with increased psychosocial distress and vulnerability (e.g., den Heijer et al., 2011; Esplen et al., 2011).

Although research indicating that adolescence represents a critical time in the development of self-concept (e.g., Sabastian, Burnett & Blakemore, 2008), this variable has not been well-studied in offspring of high-risk breast cancer families (e.g., Krattenmacher et al., 2012). From both developmental and theoretical perspectives, there are gaps surrounding the study of how offspring respond and adapt to parental risk for breast cancer. Further research is required to address self-concept as well as the interpersonal and relational aspects of risk of hereditary breast cancer as these aspects are poorly understood. Such research will have broad implications for genetic counseling and screening of elementary families.

Research on BRCA1/2 Screening and Families

As described above, investigations of the psychosocial distress experienced by BRCA1/2 screeners with minor children, as well as, familial outcomes represents a critical gap within the field of health psychology. However, the limited research in this domain suggests that the

majority of adolescents in high-risk families learn of familial and genetic risks for breast cancer at a young age (e.g. Tercyak et al., 2001; Bradbury et al., 2012).

Disclosure. Much of the research in the area of psychosocial genetics and the study of offspring has generally focused on communication of risk. Findings have indicated that approximately 50% to 63% of mothers share their BRCA1/2 test results with their minor-age children within one month of diagnosis (Tercyak et al 2001b; Tercyak et al., 2009). Preliminary studies of BRCA1/2 disclosure in parent-child dyads have indicated that disclosure was associated with elevated levels of maternal psychosocial distress (Tercyak, et al., 2001b). However, further analyses revealed that baseline distress in that study influenced disclosure (Tercyak et al., 2001b). Research since that time has revealed that open patterns of family communication are associated with BRCA1/2 disclosure (e.g., Lapointe et al., 2011; Tercyak et al., 2001b; Tercyak et al., 2009).

With respect to the issue of disclosure of BRCA1/2 status, results from one qualitative study with BRCA1/2 screeners indicated that BRCA1/2 mutation carriers who disclosed their positive test results to their children did so primarily because of concerns related to heritability (Clarke, Butler & Esplen, 2008). According to Clarke, Butler & Esplen (2008), disclosure was described as a dynamic process, wherein BRCA1/2 screeners experienced a dilemma (i.e., wanting to protect their children and, at the same time, wanting to provide important health information that could benefit them). Across studies, variables associated with disclosure of BRCA1/2 status in families included age of offspring and family communication style (e.g., Bradbury, Dignam & Ibe, 2007; Bradbury et al., 2012; Patenaude et al., 2006; Segal et al., 2004).

While many of these studies included small samples or surveyed parents of adult children, a more recent investigation completed by Bradbury et al. (2012), surveyed 253 parents of children younger than 21 years. According to parents' reports, 364 offspring (i.e., 66%) were informed of their parent's test result BRCA1/2 status. Variables significantly associated with BRCA1/2 disclosure included age of offspring, gender of offspring (with daughters being significantly more likely to be informed), negative BRCA1/2 results, and parents' education level (Bradbury et al., 2012). Mean age of offspring at time of parental disclosure was 17.04 years (SD = 4.80).

Disclosure and psychological adjustment. Comparatively less literature exists documenting the impact of BRCA1/2 disclosure on the psychosocial adaptation of offspring. To date, only two research groups have published data on this topic. In their small, retrospective, study of 22 adult children, Bradbury et al. (2009) found that 77% of those surveyed felt that learning of their parents' BRCA1/2 status had no significant impact on their emotional health, while 18% reported a negative impact. Of the 22 adult children who were surveyed, 31.8% of the sample had also gone through BRCA1/2 screening themselves (Bradbury et al., 2009). Additionally, in a larger survey of BRCA1/2 screeners with offspring, parents' reports indicated that offspring distress was more common among children learning of a BRCA1/2 positive or uncertain result (Bradbury et al., 2012). Based on a preliminary study that investigated offspring understanding of parental risk, initial results suggested that most young people appeared to understand the BRCA1/2 risk as communicated by their parents (Bradbury et al., 2009). Although some offspring reported negative reactions to parental communication of familial risk

(Bradbury et al., 2007), the majority of young people reported that they were neither surprised nor distressed by the risk information that was disclosed (Bradbury et al., 2009).

Research from the Tercyak group (2001a, 2001b, 2002, 2007) has provided some additional information about the adjustment of young people to genetic risk information. In their 2001(a) study of children age 11 to 17 years of mothers with deleterious BRCA mutations, no clinically significant elevations were reported on measures of anxiety and depressive symptoms following learning of a parent's BRCA1/2 carrier status. Despite this, findings from that study indicated that children who worried about their own cancer risk were significantly more likely to be withdrawn and have somatic problems. Additionally, children who worried about a family member's cancer risk were significantly more likely to have thought problems (Tercyak et al., 2001a).

Relationship effects. Of the few studies that have addressed the impact of genetic screening on families, positive relationship effects have been reported more frequently than negative outcomes (e.g., Bradbury et al., 2007; Esplen et al., 2001; Liede et al., 2000; Manne et al., 2004; Metcalfe et al., 2002; Roshanai et al., 2009). However, these studies have several methodological limitations including: small sample sizes, variability in measurement of family communication, and considerable differences related to time since genetic risk disclosure. Only a small number of studies have conducted quantitative research regarding the effects of the genetic testing process on family relationships (i.e., Lapointe et al., 2011; McInerney-Leo et al., 2005; Stroup & Smith, 2007; Tercyak et al., 2001; van Oostrom et al., 2007) and none have specifically addressed issues related to family functioning of women with minor children. One of the primary

aims of the present dissertation is to address the relational outcomes of BRCA1/2 screening by studying family functioning. Due to the fact that BRCA1/2 counselees who had female adolescent daughters were particularly interested in participating in genetic testing and the implications for their role as mothers may be more salient in the face of the developmental needs of their daughters, mother and adolescent daughters were selected for this study (e.g., Cappelli et al., 2005).

CHAPTER 3

Theoretical Models for Understanding Psychosocial Distress and Predictors of Distress Related to BRCA1/2 Screening

Behavioural factors have been identified as the “most prominent contributors to death and disease in the United States and globally” (Glanz & Bishop, 2010, p. 400). In order to address these factors, interventions and programming have been developed to improve health outcomes and reduce the burden of disease and disease risks at various levels (e.g., individual, family, community). Systematic reviews have demonstrated that the most successful interventions and effective programs are grounded in theory (Ammerman, Lindquist, Lohr, and Hersey, 2002; Glanz, Rimer & Vaswanath, 2008). Theories of health behaviour have acted as roadmaps to (a) understand why people may or may not practice health-promoting behaviours, (b) guide investigations of particular problems in order to inform intervention strategies, and, (c) direct the development and evaluation of appropriate and successful interventions and health programs (Glanz, Rimer & Su, 2005; Glanz, Rimer, Viswanath, 2008).

Explanatory and Change Theories

In general, two powerful assumptions have steered the development of much of the theoretical landscape of health psychology. First, as described by Strobe and Strobe (1995), a substantial proportion of the mortality from the leading causes of death is attributable to the health behaviour of individuals. This assumption has played an important role in driving the development of explanatory theories of health behaviour that seek to: (a) describe factors that influence health behaviours and (b) identify why potential problems/barriers exists. Explanatory

theories of health behaviour have directed the search for modifiable factors (e.g., knowledge, attitude, self-efficacy, social support, lack of resources) that can contribute to a problem. Examples of explanatory theories include: the Health Belief Model, Theory of Planned Behaviour, and Social Cognition Theory (Glanz & Bishop, 2010).

The second important assumption that has driven much of the theoretical development within the domain of health psychology is that behaviour is modifiable (Stroebe & Stroebe, 1995). The notion of behaviour being modifiable has inspired much of the work on change theory. Change theory has been applied to (a) identify the determinants of change, (b) develop health interventions that promote change, and (c) delineate strategies, tools and concepts that can be translated into program messages to help change behaviour (Glanz and Bishop, 2010). The Transtheoretical Model is an example of a change theory.

Explanatory theories and change theories are actually considered quite complementary and there is a good degree of overlap between their associated constructs (Rimer, 2008). In fact, while many theories of health behaviour were conceived of as either explanatory or change oriented by nature, most have potential to function as both explanatory and change models, depending on the specific purpose (Glanz & Bishop, 2010; see Figure 1, page 59). In the case of mammography screening breast cancer, for example, Saywell et al. (2003) combined Health Belief Model constructs with the Transtheoretical Model's (TTM) staging of outcome behaviour to determine which groups required more intensive interventions to improve screening practices.

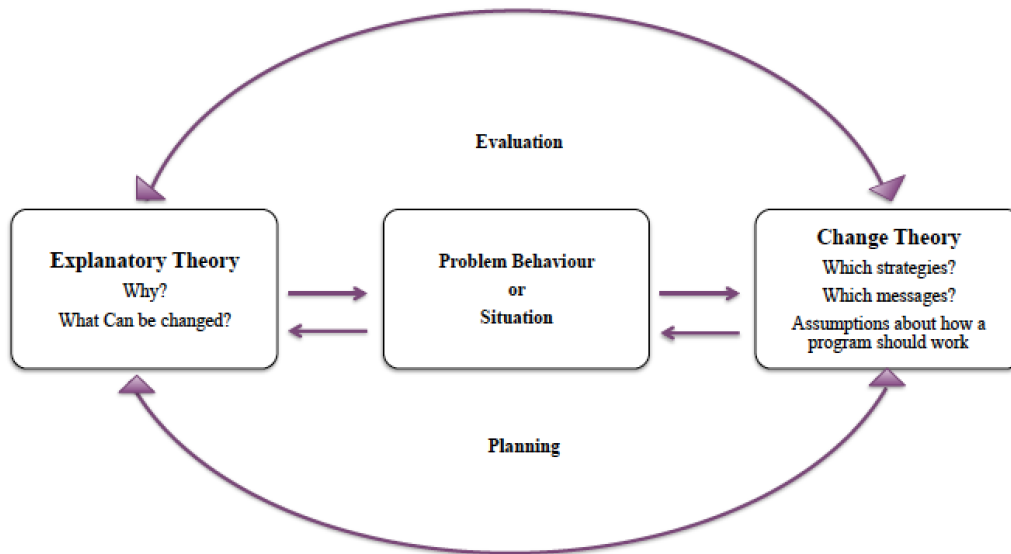


Figure 1. Relationship Between Explanatory and Change Theories (Glanz et al., 2005).

As preventative models of health have been advanced and technologies have been developed to help create predictive genetic risk estimates, theoretical shifts have also taken place in an effort keep up with an evolving understanding of the definition of illness. Four of the most commonly used health behaviour change theories within psychosocial genetics include (e.g., Gooding, Organista, Burack & Biesecker, 2006; Van Riper, 2010): the (a) Health Belief Model (HBM), (b) Transactional Models (e.g., Model of Stress and Genetic Testing), (c) Family Systems Models (e.g., Family Systems Genetic Illness Model), and (d) Transtheoretical Models (TTM), (e.g., Common Sense Model Adapted for Genetics). What immediately follows is a detailed explanation of the four most common theoretical models that have been applied in the field of breast cancer research and psychosocial genetics.

Theoretical Models

The health belief model. The HBM originated in the United States in the 1950s in response to the failure of people to participate in programs to prevent and detect disease (Hochbaum, 1958; Rosenstock, 1960, 1974). By the 1970s, the model had been extended and applied to study people's responses to symptoms as well as their behaviours in response to a diagnosed illness and adherence to medical routines/treatments (Becker, 1974). The HBM attempts to predict and explain health behaviours by focusing on attitudes and beliefs of individuals. The HBM originally used four key concepts to represent the perceived threat and net benefits of engaging in a particular health behaviour. These included: (a) perceived susceptibility, (b) perceived severity, (c) perceived benefits, and (d) perceived barriers.

According to HBM, several modifying variables (e.g., individual, psychosocial and structural variables) affect health-related behaviours by indirectly impacting the perceptions identified above (Rosenstock, 1974). HBM also posits that engagement in health-promoting behaviours requires a trigger or a cue to activate the health seeking behaviour (Rosenstock et al., 1988). The concept of self-efficacy was added to HBM to provide a more parsimonious explanation of more complex, habitual unhealthy behaviours (Rosenstock et al., 1988).

Originally, research groups studying genetic testing and breast cancer selected the Health Belief Model (HBM; Becker, 1974) as the theoretical guide of choice to explain behaviours related to genetic risk and breast cancer (Gooding et al., 2006). According to the HBM, increased perception of susceptibility to a disease should be associated with an increased likelihood of engaging in behaviours that will prevent, detect, or cure the problem (Janz, Champion &

Strecher, 2002). Initially, the HBM, applied within a research context in psychosocial genetics, demonstrated some predictive value and helped explain the influence of perception on health behaviours in the area of breast cancer, as well as, in determining interest in genetic screening for BRCA1/2 mutations (Croyle & Lerman, 1993; Helmes, 2002). For example, studies applying the HBM model have confirmed that perceived high susceptibility to illness is associated with increased interest in genetic testing (e.g., Culver, Burke, Yasui, Durfy, & Press, 2001; Durfy, Bowen, McTieren, Sporleder & Burke, 1999; Meiser et al., 2000).

As the HBM continued to be applied within breast cancer and psychosocial genetics research, however, mixed results emerged and the predictive value of this model for uptake of screening behaviours and BRCA1/2 mutation testing began to be challenged by researchers in the field. Closer examination revealed that a subset of the research examining screening practices for breast cancer indicated that individuals who identified as most threatened by their risk for breast cancer were significantly more likely to avoid detection procedures (Consedine, Magai, Krivoshekova, Ryzewicz & Neugut, 2004; Lerman et al., 1993; Lindberg & Wellish, 2001; Schwarz, Taylor & Willard, 2003). Investigators suggested that when screening practices result in outcomes that are more ambiguous (as is the case in genetic testing for breast cancer), the likelihood of avoidance behaviours may be augmented. For example, even when individuals were identified as BRCA1/2 positive, compliance with surveillance was problematic (e.g., Lerman et al., 2000). These findings conflicted with the predictive value of HBM and suggested that, perhaps, health behaviours of women undergoing genetic screening for BRCA1/2 mutations are not fully explained according to the theoretical tenants of the HBM.

The dissonance described above may, in part, be due to the fact that the HBM, as an explanatory model, may not fully capture the nuances of genetics for several reasons. First, HBM favours a cognitive perspective (Shiloh, Vinter & Barak, 1997; Slovic, Finucane, Peters, & MacGregor, 2004). As such, this model, while accounting for cognition and behaviour, may not fully explain psychosocial distress and the emotional sequelae that result from encountering a health threat. Implicit in the HBM is the assumption that individuals act on their beliefs in a logical and applied manner. For this reason, HBM may not be the most suitable model to study genetics because results are not always actionable in the same way a diagnosis might be. Second, the HBM does not explain other variables that significantly influence health behaviours (e.g., coping). More specifically, in HBM, a health behaviour is conceptualized as a singular event. With respect to genetic testing and breast cancer, however, the literature suggests that individuals (particularly those who are identified as at risk as a result of genetic predispositions) encounter health threats and illness on more than one occasion and that numerous health behaviours may follow from this dynamic process (Gooding et al., 2006). Third, the HBM places emphasis on the intrapersonal rather than the interpersonal (Rimer, 2008). In the context of genetics research, the impact of molecular medicine on individuals as well as their families suggests that intrapersonal scope of HBM may be too limited and that an interpersonal approach may be more suited to help explain health behaviours in this context. Finally, HBM has received significant criticism and has not held up to the rigorous scientific examination of longitudinal study. For example, a meta-analysis of studies using HBM constructs to predict various health behaviours over time concluded that this model may not be particularly useful owing to the fact that two of its primary

constructs (perceived severity and perceived susceptibility) only weakly predict longitudinal behavioural outcomes (Painter, Borba, Hynes & Glanz, 2008).

Transactional models. The Transactional Model of Stress and Coping (TSC) is a framework for assessing coping with stressful events (Lazarus & Cohen, 1977; Cohen, 1984). Within TSC theory, stressful experiences are described as transactions between people and environments such that the impact of an external stressors are mediated by appraisals of these stressors as well as the immediate resources accessible at the time (psychological, social, and cultural; Lazarus & Cohen, 1977; Cohen, 1984). In other words, when encountering a stressor, a person evaluates potential threats or harms (primary appraisal), as well as his or her ability to change the situation and manage adverse emotional reactions (secondary appraisal). According to Lazarus and Folkman (1984), these primary appraisals inform coping behaviours. In general, according to TSC theory, learning about an illness and its treatments is typically considered more effective than seeking distractions and avoiding thinking and talking about stressful life events, especially when something can be done about the events (Lazarus & Lazarus, 1994). A more recent extension of this theory has been advanced to include positive psychological states since these states are theorized to account for meaning-based coping processes (Lazarus, Folkman, & Moskowitz, 2000). While HBM typically focuses on intrapersonal factors, one of the relative advantages of TSC as it applies to the area of genomics, is that it also considers the interpersonal context (Viswanath, 2008).

Model of stress and genetic testing. The model of stress and genetic testing proposed by Baum, Friedman & Zakowski (1997) is an expansion of the original transactional stress and

coping model developed by Lazarus & Folkman (1984), adapted for genetics. This model proposes that stressor characteristics in the context of genetic screening are represented by the risk estimate obtained (i.e., in the case of genetic screening for breast cancer mutations, the stressor characteristics would be represented by BRCA1/2 positive, BRCA1/2 negative BRCA1/2 uncertain risk estimates). According to the model, these stressor characteristics interact with personal factors (i.e., variables such as social support, psychosocial resources and coping) to determine whether the risk result is interpreted as a threat (thereby increasing feelings of uncertainty). More specifically, the model proposes that the level of distress experienced by BRCA1/2 screeners will vary as a function of six variables including: (a) the results of the genetic screening, (b) the disease characteristics, (c) the level of uncertainty following screening, (d) the degree of uncertainty reduction, (e) the availability of active coping resources; and (f) personal variables (as described above). As an explanatory framework, this model has been successful in helping to provide explanations as to why risk estimates do not always translate into preventative surveillance behaviours and has primarily addressed four outcomes (i.e., mental health, physiological effects, behavioural change and health behaviour change). However, one of the shortcomings of this model is the reliance on the accuracy of patients' risk perceptions. As described in the literature, patients' accuracy regarding genetic risk estimates improves with genetic counseling but is still somewhat unreliable (Smerecnik et al., 2009); as such, given the discrepancies reported in patients' risk accuracy may impact study designs and conclusions that can be drawn from the findings.

Family systems models. According to family systems theorists, frameworks applied to study families are essentially tools to help understand, explain, and give meaning to research and clinical data (Bengtson, Accock, Allen, Dilworth-Anderson, & Klein, 2005). Bengtson, Accock, Allen, Dilworth-Anderson and Klein (2005) suggest that by theorizing, family systems researchers are able to build cumulative knowledge that informs intervention, programming and policy. Most family systems models applied in genetics are conceptually linked through their interpersonal approaches to understanding illness and genetic risk.

Family systems genetic illness model. One of the most promising theories for families encountering genetic illness is the Family Systems Genetic Illness Model (FSGI; Rolland & Williams, 2005). The FSGI is a modernized and expanded version of Rolland's original Family Systems Illness (FSI; Rolland 1984; Rolland 2003). The original model was developed according to the family systems tradition and applied a strength-based framework by focusing on families as potential resources. Major dimensions addressed by the FSI included: (a) psychosocial "typologies" of illness, (b) developmental phases over time and (c) important family system variables. The strength of this interpersonal theory is that it focuses on the psychosocial demands of an illness over time as well as in the context of family systems dynamics (Rolland, 2003).

The FSGI model has been updated to reflect advances in genomic medicine. Consistent with the foundational dimensions of the original FSI framework, the FSGI applies the typology dimension to group genetic conditions that impact individuals and families over the lifespan (Rolland & Williams, 2005). More specifically, the psychosocial typology of genomic illness is used to define groups of genetic disorders according to four key characteristics including: (a)

likelihood of developing a condition that is associated with a genetic mutation (levels include: low, variable high), (b) clinical severity (low or high), (c) timing of onset in the life cycle (childhood, early to mid adulthood and later life) and (d) whether effective treatment or screening options exist to alter onset and/or progression (yes or no). Based on this categorization system, thirty-six separate typologies have been identified. These typologies can be used to examine the relationships between individuals and family dynamics within the context of specific genomic disorders (Rolland & Williams, 2005).

With advancements made in genetics, the traditional demarcations between health and chronic illness have become less clear. As such, risk estimates are now being considered more carefully in the theoretical literature. Currently, individuals and families are learning they are at increased risk for a genetic condition, often long before the clinical onset of symptoms (e.g., Rolland & Williams, 2006). The original FSI model included time phases for illnesses that occurred following the onset of symptoms. However, the more contemporary FSGI to include time phases beginning prior to the onset of symptoms. Rolland and Williams (2005) have identified four nonsymptomatic time phases: (a) awareness, (b) crisis I pretesting, (c) crisis II/posttesting, and (d) long-term adaptation. Each of the nonsymptomatic phases identified by Rolland and Williams have associated individual and family developmental tasks (Rolland & Williams, 2006).

According to Van Riper (2010), use of the FSGI can assist in the development of precise conceptualizations of the different types of genetic conditions. The utility of these conceptualizations is that they can inform the development and execution of psychosocially

sound interventions for individuals and families living with genetic conditions. While the FSGI holds promise as a theory that can be integrated with other models, one of the weaknesses of this framework is that the empirical research base supporting the FSGI framework has not been systematically evaluated (Van Riper, 2010).

Transtheoretical Model (TTM). Prochaska and DiClemente (1983) originally developed the Transtheoretical Model (TTM). According to TTM, long-term changes in health behaviour involve multiple adaptations over time. It is this view of behaviour change as a process rather than a discrete event which helps distinguish TTM from other health behaviours theories like HBM. TTM is recognized by its focus on stage of change and includes five different stages including: (a) precontemplation, (b) contemplation, (c) preparation, (d) action, and (e) maintenance. TTM theories have been described as change-based frameworks that have intuitive appeal and can be easily linked to practice (Armitage & Conner, 2000). In fact, a recent review of the literature on genetic screening for cancer revealed that the Transtheoretical Model (TTM) has provided the theoretical foundations for the majority of the program development and intervention studies in this domain (Albada, Ausems, Bensing & van Dulmen, 2009).

The common sense model (CSM). The common sense model of self-regulation of health information (CSM) was developed based on the foundations of TTM. CSM describes how information about a health threat is conceptualized within an individual's pre-existing cognitive schemas. CSM theory posits that specific cognitive schemas are activated in the presence of a health threat. This activation yields cognitive representations of illness that are then interpolated by the individual. This phenomenon is referred to as the objective-cognitive process and is

characterized by five key concepts: (a) identification of the health threat (i.e., the name of the health condition), (b) determination of cause(s), (c) investigation of its consequences, (d) exploration of the timeline of the illness (both immediate and delayed; Leventhal et al., 1992; Leventhal & Cameron, 1987; Leventhal, Leventhal & Cameron, 2001; Brisette & Leventhal, 2003), and (e) health behaviours or action plans, referred to in the model as control or cure (Decruyenaere, Evers-Kiebooms, Welkenhuysen, Denayer & Claes, 2000). What distinguishes CSM from HBM, however, is a co-occurring process described as the subjective-emotional process.

According to CSM, emotional processes occur within the context of illness and illness-related experiences (Cameron & Jago, 2008). Based on the dynamic experience of encountering a health threat and cycling through the five concepts illustrative of the cognitive process, it is posited that a parallel emotional reaction takes place within the individual. As described by Cameron (2003), the emotion regulation arm of the CSM, at a conceptual level, is entirely consistent with the “behavioural inhibition system” (BIS; e.g., Carver & Scheier, 1998; Carver, Sutton, & Scheier, 2000; Gray, 1987) and the stress and genetic testing model proposed by Baum Friedman & Zakowski (1997).

A review of the empirical evidence from research on BIS processes and studies guided by the CSM has demonstrated that fear has a powerful motivational influence on cognitive risk representations as well as psychosocial functioning (Cameron, 2003). Additionally, a number of researchers have identified conditions in which fear predicts health behaviour whereas risk judgments do not (Diefenbach, Miller, & Daly, 1996; McCaul, Schroeder, & Reid, 1996). As

described by Cameron (2003) “there is substantial evidence that risk representations and worry independently influence information processing and behaviour” (p. 4).

Evident within this description is the interactional nature of the cognitive and emotional processes. The CSM posits that these two processes are reciprocal in nature and that their interaction ultimately results in the production of coping strategies. Based on the interplay of cognitive and emotional processes, a variety of coping strategies may be enacted with the purpose of appraising and then accommodating the perceived health threat (e.g., Leventhal , 1997, Cameron & Reeve, 2006). However, a caveat made explicit within the CSM is that the coping strategies employed by the individual may result in “mutually interfering or facilitating” appraisals (Decruyenaere et al., 2000). It is this caveat that “delineates the reciprocal influences of emotions and cognitions and how anxiety influences information processing in ways that shape representations” (Cameron & Jago, 2008, p. 217). This caveat also helps explain both the congruence and discordance of illness perception, emotional regulation, and actions within the context of a health threat (Cameron, 2003).

The advantages of the CSM and why it was considered for use in this project are that it accounts for the cognitive processes and resulting health behaviours outlined by the HBM while mapping onto constructs including problem focused coping (i.e., the cognitive processes of CSM) and emotion focused coping (i.e., the emotional processes of CSM) as conceptualized within the Transactional Model of Stress and Coping (TSC) proposed by Lazarus and Folkman (1984). Additionally, as a self-regulation theory, it is one of several theories in this domain that makes a distinction between cognitive and emotional processes (Epstein, 1994; Teasdale, 1997).

In essence, this model provides the most comprehensive theoretical view of health threats currently available by incorporating both objective risk and subjective fear into the understanding of threat representation.

The adapted CSM for genetics. Research has demonstrated that people tend to view health conditions associated with genetic causes as less controllable than those with psychosocial or environmental origins (Senior, Marteau, & Peters, 1999; Shiloh, Rashuk-Rosenthal, & Benyamini, 2002). Based on the evidence which suggests that greater level of perceived control is a predictor of motivation for and achievement of health behaviour change, concerns regarding the implications of conveying or reinforcing the possibility that a health outcome is not controllable have been identified within the field of psychosocial genetics (Luszczynska & Schwarzer, 2005; Shiloh, 2006; Marteau et al., 2004; Wright et al., 2007; Wright, Weinman, & Marteau, 2003). As described by McBride et al. (2010), “whether and how genetic information might add positively to existing interventions or produce counterproductive responses is still largely unknown” (p. 561). The National Human Genome Research Institute (2008) has identified the issue of the ability of genetic information to translate into improved adoption of healthy behaviours as a top research priority and psychological theory has been recognized as a catalyst in assisting in the development a better understanding of the impact of genetic information on health behaviour (McBride et al., 2010).

Recently, the CSM for genetic risk information was proposed by Marteau and Weinman (2006) as an expansion of Leventhal’s original framework (see Figure 2 located on page 72). Genetic risk information is considered a unique health threat because it targets perceived risk, or

the expectancy one has of being diagnosed with a specific illness during one's lifetime (van Korlaar, Cameron, Vossen, van der Meer, & Rosendaal, 2007). The adapted CSM evaluates risk both within and apart from traditional health threats (i.e., illness).

This model has been applied to existing genetics research (Lau, Bernard, Hatrman, 1989; Marteau et al., 2004; Michie, McDonald, & Marteau, 2003; Shiloh, Rashuk-Rosenthal & Benyamini, 2002), and has recently been used in the execution of several studies examining the threat of genetic testing (Michie et al., 2002; Marteau et al., 2004). While, one of the relative strengths of the CSM is that it delineates two parallel and partially independent processes (i.e., the cognitive processes are aimed at regulating the objective health threat – the danger control and the emotion-focused processes aimed at regulating the emotional consequences of health-related information – the fear control), its application to genetic risk is in its infancy.

As described by Marteau & Weinman (2006) there is a paucity of research regarding the emotional regulation arm (i.e., the fear control pathway) of the CSM for genetics. In fact, research on the CSM, like many other self-regulation theories, has yet to fully integrate the emotional processes (i.e., fear representation) into the model using empirical evidence (Slovic, Finucane, Peters, & MacGregor, 2004). For example, of the three other studies on genetics and breast cancer that have utilized this model (e.g., Kelly et al., 2005; Kelly et al., 2007; van Oostrom, 2007), all have focused primarily on illness and risk representation and did not explicitly consider the impact of fear representation as an important component of threat representation within CSM.

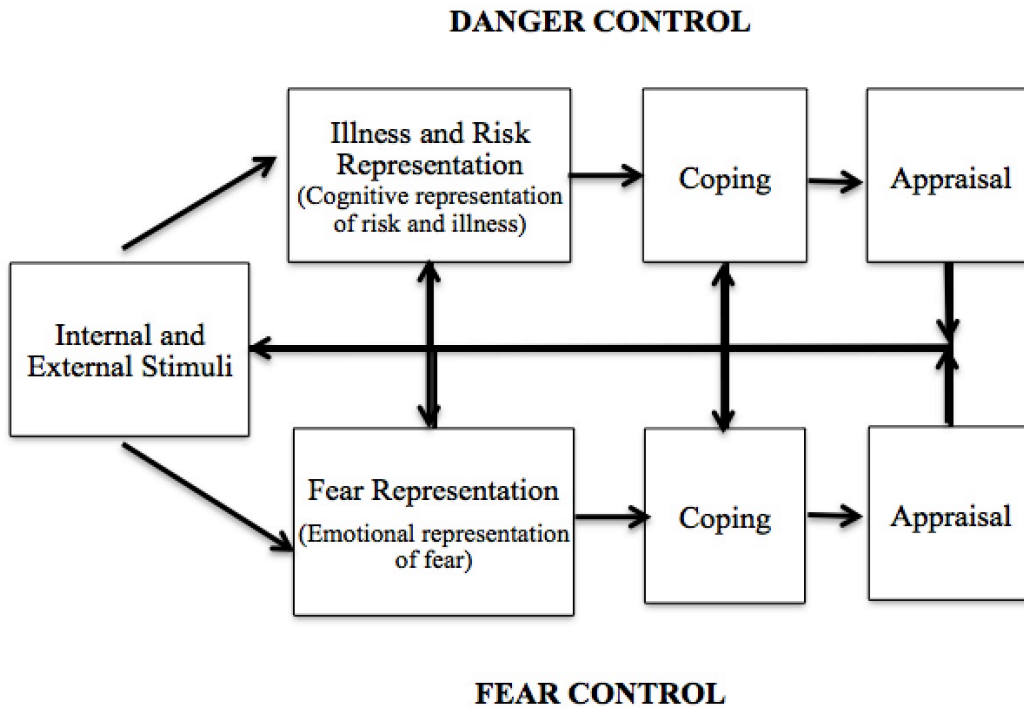


Figure 2. Common Sense Model for Genetics (Cameron, 2003; Marteau & Weinman, 2006)

CSM and BRCA1/2. Several recent studies have applied the adapted CSM (Marteau & Weinman, 2006) as a guiding framework in order to study discrepancies between perceived and objective risk for hereditary breast cancer among BRCA1/2 Screeners (e.g., Kelly et al., 2005; Kelly et al., 2007; van Oostrom, 2007). Results of these investigations indicated that BRCA1/2 counselees' perceived levels of risk are often higher than their actual (i.e., objective) risk for hereditary cancer. Additionally, these studies have demonstrated that risk perceptions are often

resistant to modification even in the presence of objective risk information (Kelly et al., 2005; Kelly et al., 2007; van Oostrom, 2007).

One of the major limitations of these studies, however, is that they that they have focused on accuracy ratings as a way to account for subjective risk estimates (e.g., Kelly et al., 2005; van Oostrom et al., 2007). While accuracy ratings represent an important way to describe and measure discrepancies, they do not fully explain threat representation as articulated in the CSM, adapted for genetics (e.g., Cameron, 2003; Marteau & Weinman, 2006). Accuracy ratings do provide information about an individual's level of perceived risk; however, these ratings do not adequately map onto the concept of the fear representation since they largely ignore the emotional component of threat representation as described in the CSM. It is this subjective-emotional component which is theorized to play a critical role in the overall threat representation, discrepancies between perceived and objective levels of risk, and, ultimately, in psychosocial adaptation to the health threat (e.g., Cameron, 2003).

Although vulnerability has not yet been formally identified as a CSM domain, preliminary research using the CSM to study future health threats has suggested that vulnerability may play a critical role with respect to expanding our understanding of psychosocial responses to health threats. According to Brownlee et al. (2001), perceived vulnerability to illness, will inform patients' threat representations which, in turn, will impact both psychosocial functioning and coping strategies. To date, however, while researchers have invested resources in understanding the relationship between BRCA1/2 screeners' personal and family histories of cancer, as well as their carrier statuses on threat representations, the notion

that patients' subjective-emotional assessments (i.e., fear representation) may impact their threat representations has not been evaluated. This represents an important limitation in the development of the adapted CSM framework given that distress associated with the health threat is posited to play a central role in the development patients' threat representation and their resulting coping and appraisal processes (Cameron, 2003).

From a theoretical perspective, this view of the subjective-emotional process as an important factor in predicting psychological distress is consistent with recent models of psychological vulnerability that have suggested that understanding the psychological meaning of events is central to predicting psychological outcomes (e.g., as cited in Beausoleil, 2012; Reis et al., 2000). Given the potential impacts of threat representation on psychosocial functioning, it is critical that the emotion regulation arm of this model be studied more carefully. This is especially important at this time as the development of psychological and genetic counseling interventions based on the CSM are currently underway (e.g., Beyamini, 2009; Wearden & Peters, 2008; Gooding et al., 2006; McAndrew et al., 2008).

Summary

There is no guiding framework or theoretical model that is superior when studying psychosocial phenomena in genetics (e.g., Van Riper, 2010). Previous studies conducted by our group (Cappelli et al., 2005; Cappelli et al., 2001) have applied the Health Belief Model (HBM) to better understand how individuals respond to genetic risk for the BRCA1/2 mutation associated with breast cancer. However, given the focus of the current study and the movement in the field of psychosocial genetics toward the CSM, this framework was considered for use in

the present study. Based on findings from our previous research and the high-risk nature of this group of study, we felt that having a better understanding of fear associated of breast cancer, particularly in the context of risk ambiguity, may provide us with a more complete understanding of how threat representation is impacted by subjective-emotional influences. More specifically, the CSM for genetics was considered especially relevant from a design perspective given that the many of participants would have been considered ineligible for BRCA1/2 screening and may be negotiating arguably more ambiguous risk. Shifting toward the CSM for this project was considered advantageous since our goals for this project were aimed at developing a better understanding the subjective-emotional aspects of BRCA1/2 genetic counseling and screening for mothers as well as their adolescent daughters.

As researchers, we recognize that genetic counseling and screening for BRCA1/2 mutations is both an individual and a family experience. As such, we wanted to include daughters as this was consistent with our previous research direction and, based in the literature on breast cancer, would be a relevant starting point in developing a better understanding of the impact of BRCA1/2 mutations on vulnerable, young families. Although the CSM is the general theoretical model that underscores this thesis, in studying dyads of mothers and daughters, we explicitly acknowledge that there is a parallel theoretical understanding of family systems that exists within the context of this study and will be returned to more explicitly in the discussion (please see Chapter 5).

CHAPTER 4

The Genetic Legacy of Breast Cancer: Extending the Common Sense Model for Genetics to High-Risk BRCA1/2 Counselees and their Adolescent Daughters

This project was approved by the institution's Research Ethics Board in conformity with the Canadian Tricouncil Policy Statement: Ethical Conduct for Research Involving Humans. The project itself was not part of standard care or the regular clinical research associated with the participating genetics department. As such, the study protocol was subject to a number of ethical boundaries guided by legislation contained in the Personal Health Information Act of Ontario (2004; https://www.elaws.gov.on.ca/html/statutes/english/elaws_statutes_04p03_e.htm).

Study Parameters and Implications for Design

Several important ethical considerations informed the conceptualization of this project and are delineated here since they impact the rationale, goals and hypotheses of this work. First, the research ethics approval for this project specified that investigators were not able to abstract information from medical charts regarding participants' proband status, dates of diagnoses for women with personal histories of breast cancer or dates of genetic counseling. Files were identified based on specified parameters described in the methods section by a professional staff member of the genetics department and data abstraction from medical records was limited to the following variables: history of breast cancer (i.e., personal or family) and BRCA1/2 eligibility (i.e., eligible for screening or ineligible for screening). Second, linkage of data specific to mothers' BRCA risk between parents and offspring was

not permitted by the Research Ethics Board and information regarding participants' risk status was made available to the investigators for the purposes of demographic analyses, *only* (Dr. G. Graham, personal communication, 2008). For this reason, the conceptual framework of the thesis focuses on eligibility for BRCA1/2 screening as the measure of risk perception, rather than the conventional BRCA risk status that is reported in the broader literature. Third, investigators in this study were not permitted to request information from mothers or daughters about the status of maternal risk disclosure. Fourth, investigators were also unable to inquire about daughters' awareness of their mothers' participation in genetic counseling for BRCA1/2 mutations.

Study Rationale

Objective-cognitive. Drawing on the psychosocial research in genetics, including findings from the only known systematic review to assess the impact of genetic screening on women's accurate reporting of their genetic risk (i.e., Smerecnik et al., 2009), information suggests that, while genetic counseling improves accuracy of risk understanding, there is considerable variability in BRCA1/2 counselees' precise understanding of their risk. This is potentially more complicated in the Canadian context where BRCA1/2 screening is reserved for women originating from high-risk families and genetics services are delivered in the context of a publicly funded health care system. Given the demands on this system, access to genetic screening may be more limited for Canadian women. Additionally, the strong cultural values that exist in this country supporting public health care may result in fewer people considering direct-to-consumer or other privatized screening for the BRCA1/2 germline mutations (e.g.,

Mendelson, 2002). Based on this information, eligibility for BRCA1/2 screening is theorized to impact perceptions of risk in the Canadian context.

At present, little is known about the impact of BRCA1/2 eligibility on psychosocial functioning of BRCA1/2 counselees and their families. For example, a recent meta-analysis completed by Nelson et al., (2013) demonstrated that the impact of eligibility for BRCA1/2 screening on BRCA1/2 counselees' psychosocial functioning was not assessed in any of the included studies. In other words, eligibility for BRCA1/2 screening was not controlled for in assessment of patients' psychosocial functioning following BRCA1/2 counseling in any of the published literature. Despite this, these same studies often controlled for mutation status and breast cancer history as factors that were theorized to impact perception of risk. Given that mutation status and breast cancer history have been theorized to impact psychosocial functioning in the extant literature, it would stand to reason that eligibility for BRCA1/2 may also be an important variable to consider in investigating risk perception in a publicly funded health care system.

Goal 1. The first aim of this study was to develop an exploratory study, using the adapted common sense model for genetics (CSM) as a guiding framework, to investigate how threat representation including objective-cognitive information (e.g., breast cancer history, eligibility for BRCA1/2 genetic screening) impacts the psychosocial functioning of BRCA1/2 counselees.

Subjective-emotional. Another major oversight in the field, as identified in this Chapter 3 of this dissertation, is that research utilizing the CSM framework has tended to focus on objective-cognitive information as a predictor of psychosocial distress and coping and virtually

ignored the subjective-emotional aspects of the model. More specifically, there is a paucity of empirical study that has focused on BRCA1/2 counselees' fear representations and the role of the fear control pathway in the CSM. According to Russell and Barrett (1999), fear, at a conceptual level, is different than anxiety or worry. More specifically, whereas fear is more immediate and intense, worry, in contrast, is typically carried out over time. Additionally, the affect attached to fear is stronger than for worry (McCaul & Goetz, nd). As described by Champion et al. (2004) breast cancer fear is "the emotional and physiologic response to the threat of breast cancer (and) is conceptually different from the cognitive processing . . . when responding to perceived threat to breast cancer" (p. 754).

Goal 2. The second goal of the current study was to apply the adapted common sense model for genetics (CSM), as a guiding framework to investigate the subjective-emotional experience of BRCA1/2 counselees and, more specifically, how fear impacts psychosocial functioning of BRCA1/2 counselees.

Family effects. Based on the previous review of the existing literature (see Chapter 2), investigators also noted that research with minor aged offspring of BRCA1/2 counselees was limited. The gap in the literature in this area is significant as there is currently sparse data documenting the impact of BRCA1/2 genetic counseling on young people or how mothers' threat representations impact offspring psychosocial functioning and health behaviours. Currently, familial and group-level behaviour change interventions have rarely been applied in the context of genetic susceptibility testing. This has been identified as an underutilized approach to health promotion and preventative medicine that is well-suited to genetics (Krattenmacher et

al., 2012; Nelson et al., 2013). However, additional information regarding the psychosocial functioning of young people from high-risk families is needed to inform the development of such interventions and preventative strategies.

Goal 3. Although the CSM is oriented around the intrapersonal, molecular genetics by its very nature is an interpersonal experience due to the shared components that surround genetics. Researchers were interested in integrating families in this project and obtaining a better sense of relational functioning and the psychosocial adaptation of BRCA1/2 counselees' minor aged daughters. The third aim of the study was to investigate how mothers' threat representations and fear representations impacted daughters' psychosocial functioning.

Summary. The primary goal of this study was to examine the role of *threat representation* (i.e., objective-cognitive information + subjective-emotional information) on the psychosocial functioning of BRCA1/2 counselees (who were also mothers) and their adolescent daughters. Threat representation including: (a) *risk representation*, defined as BRCA eligibility (tested vs. not eligible), (b) *illness representation*, defined as breast cancer history (affected vs. non-affected), and (c) *fear representation* (i.e., breast cancer fear), were identified as predictors of psychosocial functioning (see Table 2, page 81). Psychosocial functioning in this study was defined as separate dependent variables including: (a) depressive symptoms in both mothers and daughters, (b) anxiety in mothers and daughters, (c) intrusive ideation in mothers, (d) self-concept in daughters, and (e) dyadic functioning (i.e., mother-daughter relationship quality) as rated by both mothers and daughters.

The secondary goal of this study was to investigate the impact of the subjective-emotional information of *fear representation* over and above the objective-cognitive information of risk and illness representations on psychosocial functioning of the same BRCA1/2 counselees and their adolescent daughters using the same dependent variables. Terminology is clarified in Table 2 while Figure 3 (see page 82) explicitly illustrates how the CSM framework is typically described and Figure 4 (see page 82) explains how the framework is applied in the context of this exploratory study.

Table 2

Literature, CSM and Study Labels

Terminology in Literature	CSM Construct	Study Labels and Definitions
Breast Cancer History	Illness representation	<i>Affected</i> : Personal History of Breast Cancer <i>Unaffected</i> : Family History of Breast Cancer
Eligibility for BRCA1/2 screening	Risk representation	<i>Tested</i> : Received genetic counseling and screening for BRCA1/2 mutations <i>Not Eligible</i> : Received genetic counseling but no screening for BRCA1/2 mutations
Breast Cancer Fear	Fear representation	Fear representation

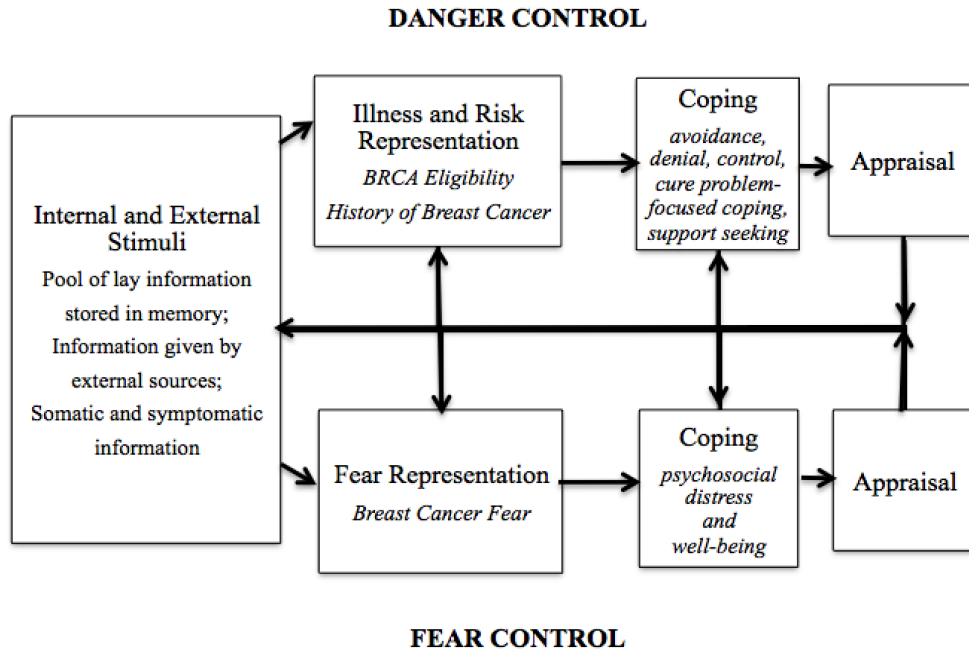


Figure 3. Common Sense Model Applied for Genetics (Cameron, 2003; Marteau & Weinman, 2006; Hagger & Orbell, 2003)

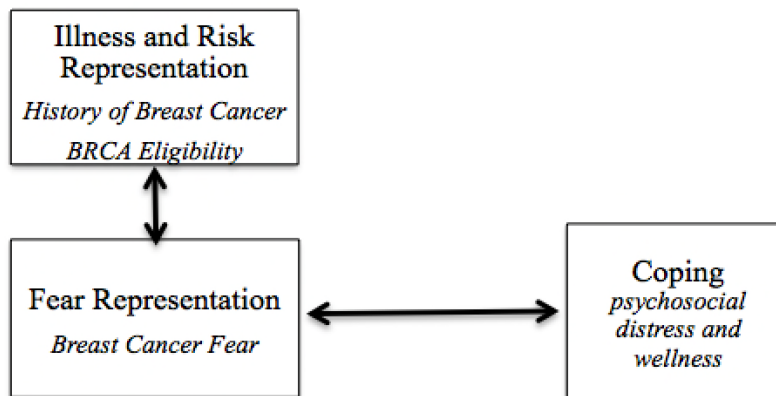


Figure 4. Applied Elements of the Common Sense Model for Genetics in the Current Study (Cameron, 2003; Marteau & Weinman, 2006; Hagger & Orbell, 2003).

Hypotheses

Hypothesis 1. It was hypothesized that mothers' *threat representations* (i.e., *risk representations*, *illness representations*, and *fear representations*) would be associated with maternal psychosocial functioning as indicated by:

Hypothesis 1a: Threat representation would predict maternal depressive symptoms.

Hypothesis 1b: Threat representation would predict maternal anxiety symptoms.

Hypothesis 1c: Threat representation would predict maternal intrusive ideation related to the genetic counseling experience.

Hypothesis 1d: Threat representation would predict problems related to mother-daughter dyadic functioning as rated by mothers.

Hypothesis 2. It was also hypothesized that higher levels maternal *fear representation* would be predictive of increased difficulties in the area of psychosocial functioning over and above *risk representation* and *illness representation* in the final model as indicated by:

Hypothesis 2a: Fear representation would predict maternal depressive symptoms.

Hypothesis 2b: Fear representation would predict maternal anxiety symptoms.

Hypothesis 2c: Fear representation would predict intrusive ideation related to the genetic counseling experience.

Hypothesis 2d: Fear representation would predict problems related to mother-daughter dyadic functioning as rated by mothers.

Hypothesis 3. It was hypothesized that mothers' *threat representations* (i.e., *risk representation, illness representation, and fear representation*) would be associated with daughters' psychosocial functioning as indicated by:

Hypothesis 3a: Threat representation would predict daughters' depressive symptoms.

Hypothesis 3b. Threat representation would predict daughters' anxiety symptoms.

Hypothesis 3c. Threat representation would predict lower self-concept in daughters.

Hypothesis 3d. Threat representation would predict problems related to mother-daughter dyadic functioning, as rated by daughters.

Hypothesis 4. It was also hypothesized that higher levels of maternal *fear representation* would be predictive of daughters' psychosocial functioning difficulties over and above maternal *risk representation* and *illness representation* in the final model as indicated by:

Hypothesis 4a: Fear representation would predict daughters' depressive symptoms.

Hypothesis 4b. Fear representation would predict daughters' anxiety symptoms.

Hypothesis 4c. Fear representation would predict lower self-concept in daughters.

Hypothesis 4d. Fear representation would predict problems related to mother-daughter dyadic functioning, as rated by daughters.

Method

Participants

Participants in this study were considered high-risk, vulnerable women who met stringent criteria outlined by the Ministry of Health and Long Term Care (MOHLTC) for referral to BRCA1/2 molecular genetic counseling programs in the province of Ontario (see

Appendix A for specific referral and screening criteria). Participants included women who had previously been patients of the BRCA1/2 genetic counseling service at the Children's Hospital of Eastern Ontario and all had adolescent daughters. A total of 166 families were originally identified by the Molecular Laboratory at the Children's Hospital of Eastern Ontario as eligible for this study but upon further review, only 142 of these families actually met study criteria. Of the remaining 142 families, 21 families declined participation. Of the families who agreed to participate in the study, response rate was 64% ($N_{mothers} = 77$, $N_{daughters} = 99$). Please see Table 3 for sample demographic information.

In total, 77 women participated in this study ($M_{age} = 48.8$ years, $SD = 5.2$, range = 36 - 61). In terms of history of breast cancer history, 46.8% of participants ($N = 36$) had been diagnosed with breast cancer, while 53.2% of the sample ($N = 41$) had never been diagnosed with breast cancer. With respect to genetic risk, 16% ($N=12$) of the sample reported testing BRCA1/2 positive, 13% ($N=10$) reported testing BRCA1/2 negative while 35% ($N=27$) reported testing BRCA1/2 uncertain and another 36% of respondents ($N= 28$) reported that they were ineligible for screening. The vast majority of the sample, 88%, reported that they were married. With respect to religious affiliation, 81% of the sample reported affiliations with an organized religion and 53% of total respondents indicated that they attended religious services several times a year or more. All women in the sample reported having at least one daughter between ages 11 and 18.

In total, 99 daughters participated in this study ($M_{age} = 15.24$ years, $SD = 2.59$, range = 11 - 18). Participants were children of mothers who had previously been patients of the BRCA1/2 genetic counseling service at the Children's Hospital of Eastern Ontario. In terms of history of breast cancer history, 49.5% of participants ($N = 49$) had mothers who had been diagnosed with breast cancer, while 50.5% of the sample ($N = 50$) had mothers who had never been diagnosed with breast cancer. With respect to genetic risk, 69.7% ($N = 68$) of daughters had mothers who had been *tested* for BRCA1/2 gene mutations and 31.3% ($N = 31$) had mothers who were *not eligible* for BRCA1/2 screening but had received BRCA1/2 counseling.

Table 3

Demographic Characteristics of Study Sample

	<i>M</i>	<i>SD</i>	<i>N</i>	<i>%</i>
<i>Maternal Age</i>	48.8	5.2	77	
History of Breast Cancer				
Affected (i.e., personal history of breast cancer)			36	46.8
<i>Diagnosed ≤ 2 years ago</i>			(8)	(22.2)
<i>Diagnosed > 2 and ≤ 5 years ago</i>			(12)	(33.3)
<i>Missing</i>			(16)	(44.4)
Unaffected (i.e., family history of breast cancer)			41	52.2
Eligibility for BRCA1/2 Genetic Screening				
Eligible for BRCA1/2 Screening			49	63.6
<i>Positive</i>			(12)	(15.6)
<i>Negative</i>			(10)	(13.0)
<i>Uncertain</i>			(27)	(35.0)
Ineligible for BRCA1/2 Screening			28	36.3
Ethnicity				
Caucasian			75	97.4
Other			2	0.03
Married				
Yes			68	88.3
Religious Affiliation/ Spiritual				
Yes			62	80.5
Education				
< College			14	18.2
≥ College			55	71.4
Missing			8	10.4
Daughter Age	15.2	2.9	99	
Daughters per family				
1			39	39.3
2 or more			60	60.6

Procedure

Mothers. Participants were recruited through the Molecular Genetics Laboratory at the Children's Hospital of Eastern Ontario (CHEO) located in Ottawa, Ontario. The Personal Health Information Protection Act (2004) prohibits the use of patient contact information for the purposes of recruitment into a research study without the express consent of the patient. As a result, information regarding patient eligibility was obtained through a chart review conducted by medical geneticists and genetics counselors who had access to such information in the provision of clinical care. Only those women who had previously consented to have their files forwarded on to the research arm of the department were contacted regarding the present study. A letter was sent to eligible women providing a brief overview of the study and advising them that a member of the research team would be telephoning within two weeks to discuss the project, answer questions, and invite participation. Participants were informed that they could withdraw from recruitment or study participation at any time, without penalty.

Inclusion criteria for this project specified that women must have: English fluency, previously participated in genetic counseling within the last five years to determine eligibility for BRCA1 and/or BRCA2 gene mutations, and have daughters between the ages of 11 and 18. For those diagnosed with breast cancer, date of diagnosis had to be within the last five years. Women diagnosed with breast cancer and who were awaiting or undergoing treatment were excluded from participating in the study because previous research has demonstrated that these women differ significantly from women who are who are in partial or full remission (Lerman et al., 1996). These criteria were established to help ensure the internal and external validity of the study. Women who agreed to participate were sent questionnaires, along with return postage.

Daughters. Due to the sensitive nature of the project, mothers were asked to invite participation from their daughters in advance of the research assistant contacting daughters. Once confirmation was received from the mother regarding the daughter's interest, the research assistant telephoned the daughter to discuss the project, the voluntary nature of participation, and answer any questions. Daughters were provided a 35 dollar honorarium for their time whether they completed the questionnaires or not.

Inclusion criteria for this project specified that daughters must have: English fluency, have mothers who previously participated in genetic counseling within the last five years to determine eligibility for BRCA1 and/or BRCA2 gene mutations, and be between the ages of 11 and 18. Inclusion criteria for this study specified that daughters must be aware of the history of breast cancer in their extended families. However, they did not have to demonstrate knowledge of their mothers' personal histories of breast cancer or knowledge of their mothers' participation in genetic counseling and/or risk estimate results in order to be considered eligible for participation. Families in which mothers were currently diagnosed with breast cancer and who were awaiting or undergoing treatment were excluded from participating in the study because previous research has demonstrated that these women differ significantly from women who are in partial or full remission (Lerman et al., 1996).

Illness and risk representation.

Breast cancer status. Mothers in this study either had clearly defined risk factors (e.g., been a relative of an individual with a known BRCA1/2 mutation) or had been diagnosed with breast cancer themselves (e.g., breast cancer onset at age 35 or younger), to be eligible to participate in this study. Mothers who had an identifiable risk factor but have never been diagnosed with breast cancer were counted as belonging to the unaffected group. Mothers who

received a medical diagnosis of breast cancer in the past and who were in either partial or full remission were counted as belonging to the affected group.

Daughters in this study were offspring of mothers who either had clearly defined risk factors (e.g., a relative of an individual with a known BRCA1/2 mutation) or had been diagnosed with breast cancer previously (e.g., early onset breast cancer). Daughters of mothers who had an identifiable risk factor but have never been diagnosed with breast cancer were counted as belonging to the unaffected group. Daughters of mothers who received a medical diagnosis of breast cancer in the past and who were in either partial or full remission were counted as belonging to the affected group.

BRCA Eligibility. Mothers were also separated into groups according to their eligibility to receive BRCA1/2 screening following genetic counseling. Mothers who received risk estimate results derived from their screening for BRCA1/2 mutations were counted as belonging to the *tested* group. Mothers who underwent genetic counseling but who were not eligible for BRCA1/2 screening were counted as belonging to the *not-eligible* group.

Daughters were also separated into groups according to their mothers' eligibility to receive BRCA1/2 screening following genetic counseling. Daughters of mothers who received risk estimate results derived from their screening for BRCA1/2 mutations were counted as belonging to the *tested* group. Daughters of mothers who underwent genetic counseling but who were not eligible for BRCA1/2 screening were counted as belonging to the *not-eligible* group.

Measures

Fear representation. As described by Witte (1992), fear is conceptually defined as a negatively toned emotion that is stimulated by a threat that is perceived to be significant and personally relevant. Expressions of fear can appear as physiologic arousal (e.g., heart beating

faster), self-report (e.g., “I feel scared”), or through overt acts that demonstrate fear (e.g., facial expressions). Russell and Barrett, (1999) note that, at a conceptual level, fear is different than anxiety or worry. Whereas fear is more immediate and intense, worry, in contrast, is typically carried out over time. Additionally, the affect attached to fear is stronger than for worry (McCaul & Goetz, nd). As described by Champion et al. (2004) breast cancer fear is “the emotional and physiologic response to the threat of breast cancer (and) is conceptually different from the cognitive processing . . . when responding to perceived threat to breast cancer” (p. 754).

Fear representation in this study was measured using Champion et al.’s (2004) Breast Cancer Fear Scale-Revised (BCFS-R; Appendix D). The BCFS-R is an 8-item scale that measures fear by using a Likert-type rating scale with a scoring range of 1 (strongly disagree) to 5 (strongly agree; Champion et al., 2004). The scale was developed specifically for assessment of the perceived fear of breast cancer. The instrument has been tested for reliability and validity and obtained a Cronbach alpha coefficient scale of .91 (Champion et al., 2004) with a test re-test reliability of $r = .71$. Sample items include, “The thought of cancer scares me,” “When I think about cancer, I get upset,” “When I think about cancer, I get jittery,” and “When I think about cancer, I get depressed.” Higher scores on the scale indicate higher breast cancer fear. Of note, the scale queries about breast cancer in general and does not specifically address fear of recurrence of breast cancer. For this study, Cronbach’s alpha coefficient was .91 for the total scale and the measure was used as a global assessment of *fear representation*. Mothers were asked to retrospectively rate feelings they had regarding breast cancer at the time of their genetic counseling for BRCA1/2 mutations.

Maternal psychosocial functioning. Mothers completed a battery of standardized and widely used psychological tests. These measures included (a) the Center for Epidemiologic

Studies Depression Scale (CES-D Scale; Radloff, 1977) as an indicator of depressive symptomatology, (b) the State-Trait Anxiety Inventory (Spielberger, 1983) as a measure of general trait anxiety and situation specific anxiety levels, (c) the Impact of Events Scale, MIES, as a measure of distress associated with genetic counselling, and (d) the Family Assessment Measure – III, dyadic form as a measure of mother-daughter dyadic functioning.

Table 4

Measures of Maternal Psychosocial Functioning

Maternal Dependent Variable	Definition	Measure
Depressive Symptoms	subjective or observed low mood, feelings of guilt, worthlessness, hopelessness, helplessness, change in appetite, sleep disturbances, fatigue or loss of energy	Center for Epidemiological Studies Depression Scale (CES-D; Radloff, 1977)
Anxiety	an unpleasant emotional arousal in face of threatening demands or dangers.	The State-Trait Anxiety Inventory (Spielberger, Gorsuch, Lushene, Vagg, & Jacobs, 1983)
Intrusive Ideation	subjective response to a specific event, in this case, genetic counseling that can involve intrusion, avoidance, and/or hyperarousal.	Impact of Events Scale (Horowitz, 1979)
Dyadic functioning	the relationship quality between pairs and, in this case, is specific to mothers and adolescent daughters.	Dyadic Relationships Scale of the Family Assessment Measure-III (Skinner, Steinhauer & Santa-Barbara, 1983)

Depressive symptoms. Depressive symptoms were defined in this study as experiences of subjective or observed low mood, feelings of guilt, worthlessness, hopelessness, helplessness, change in appetite, sleep disturbances, fatigue or loss of energy (Radloff, 1977). The Center for

Epidemiological Studies Depression Scale (CES-D) was selected as the measure of depressive symptoms in this study and is represented in the analyses by the label depressive symptoms.

The CES-D is a 20-item self-report measure designed to assess depressive symptomatology (Radloff, 1977; Appendix F). It was developed for, and has been used extensively, in the general population as well as with medical populations. The CES-D correlates highly with self-report and clinician ratings of depression, and shows good internal consistency with alpha coefficients of .85 for general populations and .90 for patient populations (Husaini, Neff & Harrington, 1979; Nezu, McClure, Meadows & Ronan, 2000). The CES-D screens for affective features associated with depression, including depressed mood and feelings of helplessness. Each item uses a Likert scale with four response options ranging from 0 (“Rarely or none of the time”) to 3 (“Most or all of the time”), yielding total scores ranging from 0–60. Higher scores on the CES-D indicate more depressive symptoms. A clinical cut-off score of ≥ 16 has been used to identify people who require diagnostic follow-up (Myers and Weissman, 1980). The CES-D has demonstrated high sensitivity, as well as, satisfactory specificity (Verdier-Taillefer et al. 2001; Weissman, Sholomskas, Pottenger, Prusoff & Lock, 1977). With respect to the psychosocial genetics literature, the CES-D has demonstrated acceptable internal consistency (Vadaparampil, Ropka & Stefenak, 2005), and has been administered to patients undergoing genetic counseling for BRCA1/2 mutations in a number of studies with Cronbach coefficient alphas in those samples between .79 and .91 (e.g., Biesecker, et al., 2000; Lerman et al., 1997). In the present study, the CES-D was used as a global measure of depressive symptoms. Cronbach’s alpha coefficient was .79 for the total scale in this study.

Anxiety. Anxiety in the current study was defined as an unpleasant emotional arousal in face of threatening demands or dangers (Spielberger, 1983). The State-Trait Anxiety Inventory-

State scale (Spielberger, Gorsuch, Lushene, Vagg, & Jacobs, 1983) was selected as the measure of anxiety in this study and is represented in the analyses by the label anxiety.

The STAI was developed based on the notion that there are two distinct, but linked, forms of human anxiety: state and trait. State anxiety refers to a transient and conscious emotional response to a specific stressor (i.e. how a person feels at the moment), and is characterized by feelings of tension, apprehension, nervousness and worry, which are likely to fluctuate over time and may vary in intensity (Spielberger 1983). In contrast, trait anxiety refers to relatively stable or enduring individual differences in susceptibility to anxiety (i.e. how a person tends to feel and perceive the world in general). The STAI consists of two separate 20-item scales measuring each form of anxiety. The STAI-State asks respondents to indicate how they feel “right now, at this moment” using a four-point frequency scale ranging from “Not at all” (1) to “Very much so” (5). For example: “I feel calm”.

In the context of the psychosocial genetics literature, the STAI has been used extensively in studies of BRCA1/2 screeners (e.g., Brain et al. 2002; Cull et al. 1999; Julian-Reynier et al. 1999; Watson et al. 1999) and has demonstrated excellent internal consistency estimates (Vadaparampil et al. 2005). The STAI correlates highly with self-report and clinician ratings of anxiety, and shows good internal consistency, with alpha coefficients of .95 in community populations. This measure has been used in other studies assessing the psychosocial impact of genetic testing for BRCA1 and BRCA2 gene mutations and Cronbach’s coefficient alpha for those samples were between .79 and .85 (Biesecker, et al., 2000; Lerman et al., 1996). In the context of the current study, the measure was used as a global indicator of state anxiety, with higher scores indicating more symptoms of anxiety. Cronbach’s alpha coefficient was .96 for the total scale in this study.

Intrusive ideation. Intrusive ideation was defined in this study as a subjective response to a specific event, in this case, genetic counselling, that could involve intrusion, avoidance, and/or hyperarousal (Horowitz, 1979). The Impact of Events Scale (IES; Horowitz, 1979; Appendix F) was selected as the measure of intrusive ideation related to genetic counseling and is represented in the analyses by the label intrusive ideation.

The IES is a 15-item self-report measure designed to assess subjective distress in relation to a specific stressor (Horowitz et al. 1979). The IES has been applied in the context of psychosocial genetics research because susceptibility to disease may be construed as a traumatic stressor (e.g., Kasparian Wakefield & Meiser, 2007). For the purposes of this study, participants were asked to reflect on their genetic counseling experience and rate their current level of distress associated with that genetic counseling experience. Participants rated items on the scale according to the frequency of intrusive and avoidant cognitions and behaviours during the past 7 days using a four-point frequency scale: “Not at all” (0), “Rarely” (1), “Sometimes” (3), and “Often” (5). In genetic counseling research, the IES has also been used to assess disease-specific distress amongst BRCA1/2 screeners (e.g., Kash, Holland, Halper & Miller, 1992; Lerman et al. 1995; Lloyd et al. 1996; McCaul et al. 1998; Valdimarsdottir et al. 1995; Watson et al. 1999; Zakowski et al. 1997). This scale has been identified as reliable measure in samples of women undergoing BRCA1/2 testing with Cronbach’s alpha levels for internal consistency assessed at .84 to .91 and test-retest reliability evaluated at $r = .86$ (Thewes et al., 2001). More recently, the Impact of Events Scale used to study stress related to genetic screening (e.g., Broadstock, Michie & Marteau, 2000; Sundin & Horowitz, 2002). Higher scores on the measure indicate greater distress. For the purposes of this study the IES was used as a global indicator of intrusive ideation associated with genetic counseling. Cronbach’s alpha coefficient for this study was .94.

Dyadic functioning. Dyadic functioning is defined as the relationship quality between pairs and, in this case, is specific to mothers and adolescent daughters. Dyadic functioning in this study was measured using the Dyadic Relationships Scale of the Family Assessment Measure-III (FAM-III; Skinner, Steinhauer & Santa-Barbara, 1983). The FAM-III Dyadic scale (Mother Version) was selected as a global indicator of mothers' perception of the relationship quality with their daughters and is represented in the analyses by the label dyadic functioning.

The FAM-III is a self-report instrument that provides quantitative indices of family strengths and weaknesses. Items are arranged on a 4-point Likert scale ranging from "Strongly Agree" to "Strongly Disagree." The FAM-III was developed based on a Process Model of family therapy and the basic concepts assessed include: task accomplishment, role performance, communication, affective expression, involvement, control, and values and norms. The FAM consists of three components: (a) *General Scale*, which focuses on the family as a system; (b) *Dyadic Relationships Scale*, which examines relationships between specific pairs; and (c) a *Self-Report* scale which assesses an individual's perception of functioning in the family. Higher scores in any of the 6 areas of functioning indicate greater disturbance in those areas. Internal consistency reliability estimates for adult completion of the dyadic scale were .95 and the scale is able to distinguish between clinical and non-clinical families (Skinner, Steinhauer & Santa-Barbara, 1983). Given the important role of functional outcomes in the measure of psychosocial distress, as well as previous literature documenting the impact of communication and affective expression in breast cancer and BRCA1/2 families (e.g., Lapointe et al., 2011; Tercyak et al., 2012), the FAM-III Dyadic scale (Mother Version) was selected as a global indicator of relationship quality of mothers and adolescent daughters in this study and is represented by the label dyadic functioning in the analyses. Cronbach's alpha coefficient for the current study was .92.

Daughters' psychosocial functioning. Daughters completed a battery of standardized and widely used psychological tests. These measures included (a) the Children's Depression Inventory (Kovacs, 1992; CDI) as an indicator of depressive symptomatology; (b) Multidimensional Anxiety Scale for Children (March, 1997; MASC) as a measure anxiety; (c) Piers-Harris Children's Self-Concept Scale, Second Edition (Piers-Harris, 1984 and (d) the Family Assessment Measure – III (daughter version), dyadic form as a measure of mother-daughter dyadic functioning.

Table 5

Measures of Daughters' Psychosocial Functioning

Daughter Dependent Variable	Definition	Measure
Daughters' depressive symptoms	feelings of negative self esteem, lack of motivation or inability to complete tasks, interpersonal difficulties, as well as irritability or anger	Children's Depression Inventory (Kovacs, 1992)
Daughters' anxiety	signs of distress that extend across three domains: cognitive (i.e., anxious thoughts and worries), emotional (i.e., fearful feelings and physical sensations associated with fear), and behavioural (e.g., avoidance, reactive behaviours, maladaptive coping	Multidimensional Anxiety Scale for Children (March, 1997)
Self-concept	both evaluative and descriptive, an accumulative judgment of self. Judgments of the self are interpersonal (i.e., taken on from others) as well as intrapersonal (i.e., unique to the individual).	Piers-Harris-2 (Piers, Harris, 1984)
Daughters' dyadic functioning	the relationship quality between pairs and, in this case, is specific to mothers and adolescent daughters.	Dyadic Relationships Scale of the Family Assessment Measure-III (Skinner, Steinhauer & Santa-Barbara, 1983)

Daughters' depressive symptoms. Depressive symptoms in youth are defined as feelings of negative self esteem, lack of motivation or inability to complete tasks, interpersonal difficulties, as well as irritability or anger and were measured in the current study using the Children's Depression Inventory (Kovacs, 1992; CDI). These symptoms are represented in the analyses by the label daughters' depressive symptoms.

The CDI is a 27-item self-report measure designed to assess depressive symptomatology in school-aged children and adolescents. The measure takes approximately 15 minutes to complete and has excellent readability statistics (Kazdin & Petti, 1982). Each item consists of three sentences that describe a range from non-distressed to severe and clinically significant symptoms; the child chooses the sentence that best describes him or her over the past 2 weeks. Responses are scored on a 0 – 2 choice scale; 0 = the absence of a symptom, 1 = the mild form of a symptom 2 = the severe form of that symptom. The CDI has been found to have good internal consistency, to distinguish children with general emotional distress, and to correspond well with self-report measures of self-concept (e.g., Saylor, Finch, Spirito, & Bennett, 1984). In addition to a total score, the CDI also yields scores for each of the five factors: Negative Mood, Interpersonal Problems, Ineffectiveness, Anhedonia, and Negative Self Esteem. Internal consistency for the total score of the CDI amongst community samples is excellent (Cronbach's alpha = .87; Kovacs, 1985). Test-retest reliability is adequate ($r = .75$; Siterenios & Stein, 2004). For the current study, the total scale score was used as a global assessment of daughters' depressive symptoms. Cronbach's alpha coefficient for this study was .86.

Daughters' anxiety. Anxiety symptoms are described as signs of distress that extend across three domains: cognitive (i.e., anxious thoughts and worries), emotional (i.e., fearful feelings and physical sensations associated with fear), and behavioural (e.g., avoidance, reactive behaviours,

maladaptive coping; March, 1997). Daughters' anxiety was measured in the current study using March's (1997) Multidimensional Anxiety Scale for Children (MASC) and is represented in the analyses by the label daughters' anxiety.

The MASC is a 39 item self-report measure designed to assess anxious symptomatology in children and adolescents from 8-19 years of age (March et al., 1997). The MASC has four main factors: Physical Symptoms, Social Anxiety, Harm Avoidance, and Separation Anxiety. Items are rated on a four point Likert-style format with response options of 0 for "Never True About Me," 1 for "Rarely True About Me," 2 for "Sometimes True About Me" and 3 for "Often True About Me." Higher scores indicate increasing emotional problems. The measure takes approximately 15 minutes to complete and, with a grade 4 reading level, has excellent readability statistics (Chall & Dale, 1995). Internal reliability of the MASC total score is .90. Although many studies of children of breast cancer patients have used the Revised-Children's Manifest Anxiety Scale (R-CMAS; Reynolds & Richmond, 1985) to measure anxiety symptoms, this measure has demonstrated convergence with the CDI (March et al., 1997). The MASC was selected for use in this study because while it displays good convergent validity with the R-CMAS ($r = 0.633, p < .01$) and the main factors of the MASC demonstrate divergent validity with the CDI. Discriminant validity of the MASC is excellent with sensitivity rates of 90% and specificity levels of 84% (Muris et al., 2002). In a previous study that assessed the impact of breast cancer on youth, internal reliability for the MASC was .88 (Brown et al., 2007). The total scale score of the MASC was used as a global assessment of daughters' anxiety symptoms. Cronbach's alpha coefficient for this sample was .86.

Self-concept. Self-concept is both evaluative and descriptive and is defined in this study as an accumulative judgment of self that is both interpersonal (i.e., taken on from others) as well as intrapersonal (i.e., unique to the individual; Piers, Harris & Harzberg, 2002). Self-concept is

represented in the analyses by the label self-concept.

As described by Esplen et al. (2009), the “centrality of a person’s self-concept in maintaining . . . psychosocial well-being has been well recognized” (p. 1216). For example, studies of BRCA1/2 counselees have demonstrated that lower self-concept is associated with increased psychosocial distress and vulnerability (e.g., den Heijer et al., 2011; Esplen et al., 2011). Although research indicating that adolescence represents a critical time in the development of self-concept (e.g., Sabastian, Burnett & Blakemore, 2008), this variable has not been well-studied in offspring of high-risk breast cancer families (e.g., Krattenmacher et al., 2012). Daughters’ self-concept was measured in the current study using Piers & Harris’ (1984) Piers-Harris Children's Self-Concept Scale, Second Edition (Piers-Harris 2).

The Piers-Harris-2 is a 60 item self-report measure designed to assess the psychological health and self-esteem of children and adolescents from 7-18 years. The measure takes approximately 15 minutes to complete and, with a grade 2 reading level, has excellent readability statistics (Piers, Harris & Harzberg, 2002). The Piers-Harris has six main factors: Physical Appearance and Attributes, Intellectual and School Status, Happiness and Satisfaction, Freedom From Anxiety, Behavioural Adjustment, and Popularity. Items responses are “yes” or “no” and higher scores indicate better self-concept. With respect to psychometric properties, test–retest reliabilities for the subscales have ranged from .62 to .96, internal consistency estimates have ranged from .89 to .93, and moderate to strong correlations have been reported between the Piers-Harris and other self-concept scales (Piers & Harris, 1984). The Piers-Harris is inversely correlated with the CDI ($r = -0.64$ $p < .01$; Saylor et al., 1984). Although the Piers-Harris has commonly been used in studies with chronically ill children, self-concept has not been well-studied in children who have chronically ill parents affected by breast cancer (Krattenmacher et al., 2012) or in BRCA1/2

populations. In the current study, this scale was used as a global measure of self-concept. Cronbach's alpha coefficient for this in the current study was .83. Of note, interpretation of the Piers-Harris -2 differs from the other measures included in this battery with respect to directionality. More specifically, higher scores on the Piers-Harris are indicative of higher self-concept whereas lower scores reflect lower self-concept ratings.

Daughters' dyadic functioning. Dyadic functioning is defined as the relationship quality Between pairs and, in this case, is specific to daughters and mothers. Dyadic functioning in this study was measured using the Dyadic Relationships Scale of the Family Assessment Measure-III (FAM-III; Skinner, Steinhauer & Santa-Barbara, 1983). The FAM-III Dyadic scale (Daughter Version) was selected as a global indicator of daughters' perceptions of relationship quality with their mothers and is represented in the analyses by the label daughter dyadic functioning.

Skinner, Steinhauer & Santa-Barbara's (1983) The Family Assessment Measure-III (FAM-III) is a self-report instrument that provides quantitative indices of family strengths and weaknesses. Items are arranged on a 4-point Likert scale ranging from "Strongly Agree" to "Strongly Disagree". The FAM-III was developed based on a Process Model of family therapy and the basic concepts assessed include: task accomplishment, role performance, communication, affective expression, involvement, control, and values and norms. The FAM consists of three components: (a) *General Scale*, which focuses on the family as a system; (b) *Dyadic Relationships Scale*, which examines relationships between specific pairs; and (c) a *Self-Report* (i.e., an individual's perception of his or her functioning in the family). Higher scores in any of the 6 areas of functioning indicate greater disturbance in those areas. For the purposes of this study, only the *Dyadic Relationships Scale* (i.e., daughters' ratings of their dyadic mother-daughter relationships) was used to assess disturbance in these areas. Internal consistency reliability estimates for adult

completion of the dyadic scale were .95 and the scale is able to distinguish between clinical and non-clinical families (Skinner, Stein & Santa-Barbara, 1983). Cronbach's alpha coefficient for the current study was .93.

Results

Power Analysis

Power calculations for maternal analyses. Prior to regression analyses, Tabachnick and Fidell's (2001) guidelines to evaluate the power of analyses were consulted. Using their formula of $N > 50 + 8m$ (where m = number of independent variables), a suggested N of 74 was recommended [i.e., for testing regression with 3 predictor variables, $N = 50 + 8(3)$]. Sample size calculations were cross-checked using G*Power statistical software (Faul, Erdfelder, Lang, & Buchner, 2007). Given that our previous research on high-risk breast cancer families, specifically mother-daughter dyads, have revealed medium effect sizes (e.g., Korneluk & Cappelli, 2001) an estimated effect size of .15 was considered appropriate for this study. In order to achieve adequate power of .80 with an alpha level of .05 and a medium effect size of 0.15, using three predictor measures and multiple regression as the mode of analysis, the necessary total sample size for the present study was calculated to be 76 (Faul et al., 2007). This result was consistent with recommendations based on Cohen's work (1992) that to achieve a medium effect size, 76 participants would be required. As a result, calculation of power was deemed adequate with a total number of participants in this study at $N = 77$.

Power calculations for daughter analyses. Prior to regression analyses, Tabachnick and Fidell's (2001) guidelines to evaluate the power of analyses were consulted. Using their formula of $N > 50 + 8m$ (where m = number of independent variables), the suggested $N = 82$ [for testing regression with 4 predictor variables, $N = 50 + 8(4)$] was below the 99 participants in this study.

Sample size calculations were cross-checked using G*Power statistical software (Faul et al., 2007). Given that our previous research on high risk breast cancer families, including mother-daughter dyads, have revealed medium effect sizes (e.g., Korneluck & Cappelli et al., 2001) an estimated effect size of .15 was considered appropriate for this study. In order to achieve adequate power of .80 with an alpha level of .05 and a medium effect size of 0.15, using four predictor measures and multiple regression as the mode of analysis, the necessary total sample size for the present study was calculated to be $N = 85$ (Faul et al., 2007). This result was consistent with recommendations based on Cohen's work (1992) that to achieve a medium effect size, 84 participants would be required. As a result, calculation of power was deemed adequate.

Assumptions

Prior to planned analyses, study variables were examined for accuracy of data values, missing data, normality of distribution, and assumptions of multivariate analysis. Analyses were performed using SPSS REGRESSION and SPSS EXPLORE for evaluation of assumptions.

Maternal data. All data points were within specified ranges for their respective variables and measures. Valid individual values and score combinations were also observed. Linearity and homoscedasticity checks of study variables revealed three non-normally distributed variables. Examination of variable distributions found that depressive symptoms (as measured by CES-D), anxiety (as measured by the STAI) and intrusive ideation (i.e., distress associated with genetic counseling, as measured by the IES) were positively skewed and kurtotic. These results were not unexpected given the nature of this study and the fact that such variables are not typically normally distributed within a non-clinical sample. Given the degree and direction of the skew and kurtoses, linear transformations (i.e., LG10 transformations) were computed for the variables depressive symptoms and anxiety as recommended by Tabachnick & Fidell (2007). Following this, the

normality of these distributions was improved significantly; therefore, these transformations were included in analyses. Given that significance values were consistent between transformed and untransformed analyses, regression tables and graphs within the body of the manuscript present only the untransformed values for mothers' depressive symptoms and anxiety. However, the transformed analyses have been included in Appendix J. Due to the natural floor of the IES scale in this sample, transformations were not successful in producing normality; therefore, the intrusive ideation variable was retained in its untransformed state and appropriate cautions are provided.

Missing Values Analyses (MVA) were conducted. The number of missing values on dependent variables was low, ranging from 0% to 1.2%. The depressive symptoms total scale score (as measure by the CES-D; 1.2%) was missing for one participant. A missing data point was estimated and imputed for the total score for one participant on the CES-D using expectation minimization (EM) method. Data were also evaluated for evidence of multivariate outliers using Tabachnick and Fidell's (2007) guidelines to determine critical chi-square values for comparison and Mahalanobis distance. With three independent variables ($df=3$) and a critical χ^2 value of 16.266, $p = .001$, several outliers were identified. Prior to transformations, six univariate and two multivariate outliers were identified for depressive symptoms and two univariate outliers were identified for anxiety. However, transformations for these variables eliminated univariate and multivariate outliers and no examined cases exceeded this critical value. One multivariate outlier was identified for intrusive and this case was deleted for regression analyses with intrusive ideation as the dependent variable.

Following standard guidelines, preliminary regression analyses showed no evidence of multicollinearity or singularity (Tabachnik & Fidell, 2001). Bivariate correlations did not exceed $r = .70$, tolerance levels were above .10 for all main study variables, and all study variables'

Variance Inflation Factors (VIFs) were below 10. Casewise diagnostics via standardized residual values did not indicate any dependent variable outliers. For regression models with dependent variables depressive symptoms, anxiety, and dyadic functioning all cases were retained, and the final sample consisted of $N = 77$ participants. For the regression model with dependent variable, intrusive ideation, one case (both a univariate and multivariate outlier) was deleted, and the final sample for that analysis consisted of $N = 76$ participants. Although a significant bivariate correlation for the predictors, risk perception and illness perceptions was 0.70, multicollinearity diagnostics revealed the bivariate correlation did not exceed recommendations provided by Tabachnick & Fidell (2007); additionally, VIF values were less than 10 while tolerance levels were above .10 (Tabachnick & Fidell, 2007). Accordingly, both predictors were retained in the model.

Daughter data. Examination of the data obtained from daughters in the sample revealed that all data points were within specified ranges for their respective variables and measures, and valid individual values and score combinations were observed for all variables. Missing Values Analysis revealed no missing data for the dependent variables. Linearity and homoscedasticity checks of all study variables revealed two non-normally distributed variables. Examination of dependent variable distributions found daughters' depressive symptoms (as measured by the CDI) and daughters' anxiety (as measured by the MASC) were positively skewed and kurtotic. These results were not unexpected given the nature of this study and the fact that such variables are not typically normally distributed within a non-clinical sample. Given the degree and direction of the skew and kurtoses, linear transformation (i.e., LG10 transformations) was computed for daughters' anxiety as recommended by Tabachnick & Fidell (2007). Following this, the normality of this distribution was improved; therefore, this transformation was included in analyses. Given that significance values were consistent between transformed and untransformed analyses, regression

tables and graphs within the body of the manuscript present only the untransformed values for daughters' anxiety. However, the transformed analyses have been included in Appendix J.

Transformations were not successful in producing normality for daughters' depression symptoms. This dependent variable was retained for analyses but interpretation of the results is made with caution given the non-normality of the distribution.

Data were also evaluated for evidence of multivariate outliers using Tabachnick and Fidell's (2007) guidelines to determine critical chi-square values for comparison and Mahalanobis distance. With three independent variables ($df = 4$) and a critical χ^2 value of 18.47, $p = .001$, five univariate and multivariate outliers were identified for daughters' anxiety. However, following transformation, these outliers were eliminated and no examined cases exceeded the critical value. Following standard guidelines, preliminary regression analyses showed no evidence of multicollinearity or singularity (Tabachnik & Fidell, 2001). Bivariate correlations did not exceed $r = .70$, tolerance levels were above .10 for all main study variables, and all study variables' Variance Inflation Factors (VIFs) were below 10. Casewise diagnostics via standardized residual values did not indicate any dependent variable outliers. All cases were retained, and the final sample consisted of $N = 99$ participants.

Dummy Coding

Due to the fact that two of the independent variables were categorical in nature, dummy coding was performed. Women's (i.e., mothers') illness representation was a binary variable and coded accordingly (with *unaffected* participants coded as 0 and *affected* participants coded as 1). Additionally, mothers' risk representation was dummy coded into two groups (with *not eligible* for BRCA1/2 screening participants coded as 0 and *tested* participants coded as 1).

Descriptive Analyses

Maternal data. Means, standard deviations, ranges, and internal consistency estimates of major continuous study variables are presented in Table 6.

Daughter data. Means, standard deviations, ranges, and internal consistency estimates of major continuous study variables are presented in Table 7. Consistent with the research investigating the impact of breast cancer on daughters' psychosocial functioning (e.g., Compas, Worsham, Ey & Howell, 1996; Faulkner & Davey, 2002; Grabiak et al., 2007; Visser et al., 2004), a minority of daughters in this study presented with clinically significant scores on measures of anxiety (N = 14; 14.14%), depression (N = 7; 7.07%), self-concept (N = 10; 10.10%) and mother-daughter dyadic functioning (N = 15; 15.15%).

Table 6

Psychometric Properties of Maternal Study Variables

Variable	<i>M</i>	<i>SD</i>	Cronbach's α	Range Statistic
1. Fear Representation (i.e., Breast Cancer Fear)	24.75	6.26	0.91	34.00
2. Depressive Symptoms	10.00	10.84	0.79	50.00
3. Anxiety	35.54	11.56	0.96	49.00
4. Intrusive Ideation ^a	1.09	1.35	0.94	6.75
5. Dyadic Functioning (T-Scores)	56.23	9.54	0.92	46.00

^a*n* = 76. All other variables *n* = 77.

Table 7

Psychometric Properties of Study Variables (Daughters)

Variable	<i>M</i>	<i>SD</i>	Cronbach's α	Range Statistic
1. Fear Representation (i.e., Breast Cancer Fear)	24.75	6.26	0.91	34.00
2. Daughters' Depressive Symptoms (T-Score)	46.69	11.24	0.86	52.00
3. Daughters' Anxiety (T-Score)	53.62	11.03	0.86	52.00
4. Daughters' Self-Concept (T-Score)	52.53	12.16	0.83	60.00
5. Daughters Dyadic Functioning (T-Score)	54.00	9.00	0.93	41.00

Correlational Analyses

Maternal correlational analyses. Intercorrelations among major study variables are presented in Table 8. Significant positive correlations were reported between mothers' fear representations and mothers' (a) depressive symptoms, (b) anxiety, and (c) intrusive ideation related to genetic screening. Fear representation was not associated with illness representation or risk representation. However, illness and risk perception were significantly correlated (and met but did not exceed $r = .70$). Risk representation was significantly correlated with intrusive ideation while illness representation was correlated with both intrusive ideation ($p < .01$) and depressive symptoms ($p < .05$). Bivariate correlations were also reported between dependent variables including depressive symptoms and anxiety ($p < .01$) as well as depressive symptoms and intrusive ideation ($p < .01$). No correlations were observed between mothers' reports of their mother-daughter dyadic functioning and all other study variables.

Table 8

Correlations Among Maternal Variables (Untransformed Scores)

Variable	1	2	3	4	5	6
1. Fear Representation (i.e., Breast Cancer Fear)	-					
2. Risk Representation (i.e., BRCA Eligibility)	-.01	-				
3. Illness Representation (i.e., Breast Cancer History)	-.02	.70**	-			
4. Depressive Symptoms	.34*	.17	.28*	-		
5. Anxiety	.49*	-.01	.12	.77**	-	
6. Intrusive Ideation	.44**	.27*	.36**	.46**	.55**	
7. Dyadic Functioning	-.03	-.07	.05	.10	.12	.12

Note: Statistically significant correlation coefficients are in boldface.

* $p < .05$, ** $p < .01$

Daughter correlational analyses. Intercorrelations among major study variables are presented in Table 9. Significant correlations were reported between mothers' fear representations and daughters' (a) anxiety as well as (b) self concept, in the expected directions. Mothers' illness representation was significantly correlated with daughters' depressive symptoms and lower self-concept. Bivariate correlations were also reported between dependent variables. More specifically, daughters' depressive symptoms were significantly associated with daughters' (a) anxiety ($p < .05$), (b) self-concept ($p < .01$), and (c) daughters' dyadic functioning ratings ($p < .01$). In addition, daughters' anxiety was significantly associated with daughters' (a) self-concept ($p < .01$) and (b) dyadic functioning ratings ($p < .01$). Finally, significant correlations were reported between

daughters' self-concept ($p < .01$) and their reports of their dyadic functioning with their mothers ($p < .01$).

Table 9

Correlations Among Variables (Untransformed Scores)

Variable	1	2	3	4	5	6
1. Fear Representation (i.e., Breast Cancer Fear)	-					
2. Risk Representation (i.e., BRCA Eligibility)	-.02	-				
3. Illness Representation (i.e., Breast Cancer History)	-.06	.63**	-			
4. Daughters' Depressive Symptoms	.20	.07	.22*	-		
5. Daughters' Anxiety	.25*	.03	.06	.45**	-	
6. Self-Concept	-.21*	-.10	-.21*	-.84**	-.52**	-
7. Daughters' Dyadic Functioning	.12	.04	.09	.42**	.29**	-.45**

Note: Statistically significant correlation coefficients are in boldface.

* $p < .05$ ** $p < .01$.

Univariate Analyses

Maternal univariate analyses. Based on the literature, several demographic variables were considered theoretically important including: marital status, age of daughter, patient age, religiosity, education, time since diagnosis, and time since genetic counseling (e.g., Bradbury, et al., 2007; Hamilton et al., 2009; Meiser et al., 2002). Unfortunately, several variables considered theoretically important including education (10.4% missing), time since breast cancer diagnosis (44.4% missing), and time since genetic counseling (26% missing) were missing a large number of cases so these variables were not included in further analyses. Box plot analyses were conducted to

determine visually whether differences existed for available cases based on both time since breast cancer diagnosis and time since genetic counseling. These analyses appear in Appendix H and I of this dissertation and inform the discussion in Chapter 5.

All analyses were conducted at the 95% level of confidence. No significant effects of marital status, religiosity, age of daughter, or patient age were identified on any of the main independent or dependent variables as evaluated via ANOVA and independent samples *t*-tests. Given the lack of significant differences in independent or dependent variables as a function of each of these demographic variables, they were not included in further analyses.

Group differences were also explored via independent samples *t*-tests, first using mothers' breast cancer status as the independent variable. A significant effect of breast cancer status was reported for mothers' self-reported intrusive ideation symptoms (i.e., distress associated with genetic counseling for BRCA1/2; [$t(74) = -3.11, p < 0.01$], such that mothers affected by breast cancer reported significantly higher rates of intrusive ideation symptoms ($M_{Affected} = 1.59, SD = 1.64$) than mothers not affected by breast cancer ($M_{Unaffected} = .63, SD = .90$). No effects of breast cancer status were reported for mothers' self-reported depressive symptoms [$t(75) = -1.84, p = 0.07$], anxiety symptoms [$t(75) = -1.25, p = .22$], dyadic functioning [$t(75) = -.50, p = 0.62$] and mothers' fear representation [$t(75) = .58, p = .56$]. Group differences were then explored via independent samples *t*-tests, for BRCA1/2 eligibility as the independent variable. No significant effects of BRCA1/2 eligibility were observed for mothers' self-reported depressive symptoms [$t(75) = -1.17, p = .24$], anxiety [$t(75) = -.05, p = .96$], dyadic functioning symptoms [$t(75) = .73, p = .47$] or mothers' fear representation [$t(75) = .21, p = .84$]. However, a significant difference was noted between groups on a intrusive ideation measure [$t(74) = -2.29, p < 0.05$], such that women who received BRCA1/2 screening reported more intrusive ideation symptoms ($M_{Tested} = 1.43, SD =$

1.54) as compared to women who did not receive testing following genetic counseling ($M_{Not-Tested} = .72, SD = 1.11$).

Daughter univariate analyses. Based on the literature, several demographic variables were considered theoretically important including: mothers' marital status, age of daughter, patient age, and religiosity (e.g., Bradbury, Dignam & Ibe, 2007; Meiser et al., 2002; Hamilton et al., 2009). Several variables considered theoretically important including: mother's education (10.4% missing), time since diagnosis (44.4% missing), time since genetic counseling (26% missing) were missing a large number of cases so these were not assessed as part of this analysis. All analyses were conducted at the 95% level of confidence. Group differences were explored using ANOVAs and independent *t*-tests, as appropriate. Significant effects of marital status were observed for daughters self-reports of depressive symptoms [$t(97) = -2.69, p < .05$], such that daughters from families where parents were divorced or separated reported more depressive symptoms ($M = 56.00, SD = 17.48$) than daughters whose mothers reported intact marriages ($M = 45.76, SD = 10.10$). Additionally, significant associations were reported between mothers' marital status and daughters' reports of anxiety symptoms [$t(97) = -1.60, p < .05$], such that daughters from families where parents were divorced reported more anxiety symptoms ($M = 58.67, SD = 17.70$) than daughters from intact families ($M = 41.91, SD = 11.42$). No effects were reported for patient age, daughter age, or religiosity, on any of the main independent or dependent variables. Given the significant differences in the dependent variables as a function of mother's marital status, this variable was included in further analyses.

Group differences were also explored via independent samples *t*-tests, first for mothers' breast cancer status as the independent variable. A significant effect of breast cancer status was reported for daughters' self-reported depressive symptoms $t(97) = -2.21, p = 0.03$, such that

daughters of mothers affected by breast cancer reported significantly higher rates of depressive symptoms ($M_{Affected} = 49.16, SD = 11.79$) than daughters of mothers unaffected by breast cancer ($M_{Unaffected} = 44.26, SD = 12.88$). Additionally, a significant effect was also noted for daughters' self-reported self-concept symptoms $t(97) = 2.16, p = .03$, such that daughters of mothers affected by breast cancer reported significantly more difficulties related to self-concept (as indicated by lower self-concept ratings; $M_{Affected} = 51.24, SD = 8.83$) than daughters of mothers unaffected by breast cancer ($M_{Unaffected} = 55.94, SD = 9.81$). No effects of mothers' breast cancer status were reported for daughters' self-reported anxiety symptoms [$t(97) = .26, p = .80$], daughters' reports of dyadic functioning with their mothers [$t(97) = -.87, p = 0.38$] and mothers' fear representation [$t(97) = .58, p = .56$]. Group differences were then explored via independent samples *t*-tests, with BRCA1/2 eligibility as the independent variable. No significant effects of BRCA1/2 eligibility were observed for daughters' self-reported depression [$t(97) = -.65, p = .52$], anxiety [$t(97) = -.15, p = .88$], self-concept [$t(97) = .95, p = .35$], daughters' reports of dyadic functioning symptoms [$t(97) = -.35, p = .73$] or mothers' fear representation [$t(97) = .21, p = .84$].

Maternal Regression Analyses

Regression analyses were driven by the theoretical foundations of the adapted CSM for genetics as described in Chapter 3 of this manuscript. As such, variable entry into the model included risk representation, illness representation and fear representation. In order to accurately assess the contribution of each independent variable to the dependent variable, and in consideration of the possibility of suppression, all theoretically relevant independent variables were retained, including those variables that were not correlated with the dependent variable at the bivariate level. This decision to retain theoretically relevant variables (i.e., risk representation, illness representation and fear representation) was made in an effort to avoid underestimating some of the

parameters which could potentially compromise the predictive power of the model and result in regression equations that are overly sample-specific (Cohen, Cohen, West, & Aiken, 2003; Tabachnick & Fidell, 2007).

Unlike analyses of the dependent variables depressive symptoms, anxiety, and intrusive ideation, where analyses was completed for mothers only, analysis of the dependent variable, dyadic functioning, was derived from the 77 women included in the analyses had a total of 99 daughters. For the standard multiple regression model with the dependent variable maternal dyadic functioning, intrafamilial effects were controlled through random selection of daughter for mothers who had more than one daughter participating in the study (i.e., 77 participating mothers and 99 participating daughters). Generalized estimating equations (GEE) were then applied to confirm that dependence had properly been accounted for. The simpler multiple regression model yielded results that were identical to the model fit with GEE. Accordingly, results of standard multiple regression model are reported for the dependent variable dyadic functioning.

Testing hypotheses 1a-1d. Four standard multiple regressions were conducted to examine hypotheses 1a –1d. Following a theoretically driven approach, according the adapted CSM for genetics (as described in the literature, see Marteau & Weinman, 2006), risk representation, illness representation and fear representation were entered as predictors with the goal of examining the predictive utility of threat representation on psychosocial distress as measured by mothers' scores on measures of (a) depressive symptoms, (b) anxiety, (c) intrusive ideation, and (d) dyadic functioning with daughters.

Depressive symptoms. Hypothesis 1a predicted that total scores on a global measure of depressive symptoms would be predicted by participants' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was

performed, between the untransformed dependent variable, depressive symptoms and risk representation, illness representation and fear representation as the independent variables (see Table 10 for untransformed analyses and Appendix J for transformed analyses). R for regression was significantly different from zero $F(3, 73) = 5.47, p < .01$, with R^2 at .19). The adjusted R^2 of .16 indicated that 16% of the variability in depressive symptoms was predicted by the overall threat representation including risk representation, illness representation, and fear representation.

In order to interpret the relative strength of the individual predictors, bivariate and partial correlations were examined. Bivariate correlations are described above and presented in Table 8. A partial correlation for risk representation and depressive symptoms was non-significant ($r = -.05$). However, partial correlations between: (a) illness representation and depressive symptoms ($r = .24, p < .05$) and (b) fear representation and depressive symptoms ($r = .37, p < .01$) were both significant. These results indicate, that after factoring out the effects of risk representation, illness representation (i.e., history of breast cancer) and fear representation predicted mothers' depressive symptoms. In other words, illness representation and fear representation, as independent variables, contributed significantly to this model ($p < .05, p < .01$, respectively).

Table 10

Standard Multiple Regression Analysis Predicting Depressive symptoms Scores From Risk Representation, Illness Representation, Fear Representation – Untransformed Depressive Symptoms Scores

IV	<i>B</i>	SE <i>B</i>	β	<i>F</i> (3, 73)	<i>R</i> ²
Risk Representation	-1.23	2.89	-.07		
Illness Representation	5.87	2.91	.32*		
Fear Representation	.53	.159	.36**	5.47**	.19**

* $p < .05$, ** $p < .01$.

Anxiety. Hypothesis 1b predicted that total scores on a global measure of anxiety would be predicted by participants' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed between anxiety as the dependent variable and risk representation, illness representation and fear representation as the independent variables (see Table 11 for untransformed values analyses; Appendix J for transformed analyses). *R* for regression was significantly different from zero $F(3, 73) = 9.31, p < .0001$, with R^2 at .28. The adjusted R^2 of .25 indicated that 25% of the variability in anxiety symptoms was predicted by the overall threat representation including risk representation, illness representation and fear representation.

In order to interpret the relative strength of the individual predictors, bivariate and partial correlations were examined. Bivariate correlations are described and presented in Table 8. A partial correlation for risk representation and anxiety ($r = -.16$) was non-significant, a partial correlation for risk representation and illness representation approached significance ($r = .22, p = 0.06$), and a

partial correlation between fear representation and anxiety ($r = .49, p < .0001$) was significant.

These results indicate, that after factoring out the effects of risk representation, and illness representation, fear representation predicted anxiety symptoms. In other words, fear representation, as an independent variable, contributed significantly to this model ($p < .0001$).

Table 11

Standard Multiple Regression Analysis Predicting Anxiety Scores From Risk Representation, Illness Representation, Fear Representation – Untransformed Anxiety Scores

IV	<i>B</i>	SE <i>B</i>	β	<i>F</i> (3, 73)	<i>R</i> ²
Risk Representation	-8.16	5.88	-.20		
Illness Representation	11.20	5.89	.27 ^a		
Fear Representation	1.59	.32	.49 ^{***}	9.31 ^{***}	.28 ^{***}

*** $p < .0001$, ^a = Findings approached significance, $p = .06$

Intrusive ideation. Hypothesis 1c predicted that total scores on a measure of intrusive ideation associated with genetic counseling experience would be predicted by participants' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed between genetic counseling distress as the dependent variable and risk representation, illness representation and fear representation as the independent variables (see Table 12). *R* for regression was significantly different from zero $F(3, 72) = 10.55, p < .0001$, with R^2 at .31. The adjusted R^2 of .28 indicated that 28% of the variability in genetic counseling distress symptoms was predicted by the overall threat representation including risk representation, illness representation, and fear representation.

In order to interpret the relative strength of the individual predictors, bivariate and partial

correlations were examined. Bivariate correlations are described and presented in Table 8. A partial correlation for risk representation and genetic counseling distress ($r = -.24$) was non-significant while a partial correlation for genetic counseling distress and illness representation ($r = -.01$, $p < .06$) approached significance. A partial correlation between fear representation and genetic counseling distress ($r = .03$, $p < .0001$) was significant. These results indicated, that after factoring out the effects of risk representation, and illness representation (i.e., personal history of breast cancer), fear representation predicted distress associated with genetic counseling. In other words, fear representation, as an independent variable, contributed significantly to this model ($p < .0001$). While these results are significant, they should be interpreted with extreme caution due to the non-normal distribution of the dependent variable, intrusive ideation (see Table 12).

Table 12

Standard Multiple Regression Analysis Predicting Intrusive Ideation Scores From Risk Representation, Illness Representation, Fear Representation.

IV	B	SE B	B	F(3, 72)	R ²
Risk Representation	.15	.20	.11		
Illness Representation	.38	.20	.27 ^a		
Fear Representation	.05	.01	.43 ^{***}	10.55 ^{***}	.31 ^{***}

*** $p < .0001$, ^a = Findings approached significance, $p < .06$

Dyadic functioning. Hypothesis 1d predicted that total scores on a measure of mother-daughter dyadic functioning would be predicted by participants' threat representations (i.e., risk representation, illness representation, and fear representation). However, based on the bivariate correlational analyses, it was not expected that a relationship would be observed between threat

representation and dyadic functioning of mothers and daughters (see Table 8). A standard multiple regression was performed to check for suppressor effects between mothers' reports of dyadic functioning with their daughters (controlled for intrafamilial effects) as the dependent variable and risk representation, illness representation and fear representation as the independent variables. As expected, based on the correlational analyses, R for regression was not significantly different from zero, $F(3, 73) = 0.89, p = 0.45$, indicating that, taken together, the overall threat representation including risk representation, illness representation, and fear representation did not predict mother-daughter dyadic functioning (see Table 13).

Table 13

Standard Multiple Regression Analysis Predicting Dyadic Functioning From Risk Representation, Illness Representation, Fear Representation

IV	<i>B</i>	<i>SE B</i>	<i>B</i>	<i>F(3, 73)</i>	<i>R</i> ²
Risk Representation	-4.02	2.69	-.21		
Illness Representation	3.18	2.69	.20		
Fear Representation	-.06	.15	.04	.89	.03

Testing hypotheses 2a-2d. Four hierarchical multiple regressions were conducted to examine hypotheses 2a –2d. Following a theoretically driven approach, according the adapted CSM for genetics (as described in the literature, see Marteau & Weinman, 2006), with the goal of learning more about the unique contribution of fear representation (as articulated in the study rationale) four hierarchical multiple regressions were planned to examine the predictive utility of fear representation on maternal (a) depressive symptoms, (b) anxiety, (c) intrusive ideation (i.e., distress associated with genetic counseling), and (d) dyadic functioning with daughters. More

specifically, the hierarchical regressions aimed to determine if the addition of information regarding one's fear representation improved prediction of psychosocial distress, beyond that afforded by information from illness and risk representations. Following the theoretical framework of CSM, whereby risk and illness representation are theorized to collectively account for cognitive representation of health threats, these variables were entered, together, into the model in step 1 of each regression. Consistent with CSM theory, fear representation, which is theorized to represent the subjective-emotional component of the CSM, was entered into each model on step 2.

Depressive symptoms. Hypothesis 2a stated that fear representation would add to the prediction of women's depressive symptoms after controlling for risk and illness representations. Hierarchical multiple regression was performed to test this hypothesis. Entry of predictors was theoretically driven. In the first step of hierarchical multiple regression, risk representation and illness representation were entered. After step 1, statistical significance was not reported with $R^2 = .06$ (adjusted $R^2 = .03$), $F_{inc}(2, 74) = 2.38, p > .05$. After step 1, 6% of the variance in depressive symptoms was explained. After entry of fear representation at Step 2, the total variance explained by the model as a whole was 19%. $R^2 = .19$ (adjusted $R^2 = .15$), $F_{inc}(3, 73) = 5.47; p < .01$. The introduction of fear representation explained an additional 12% of the variance in depressive symptoms, after controlling for risk representation and illness representation ($\Delta R^2 = .12; F(1, 73) = 10.98; p < .01$). Results are presented for untransformed values (see Table 14) and transformed values (see Appendix J).

Table 14

Hierarchical Multiple Regression Analysis Predicting Depressive symptoms from Risk Representation, Illness Representation, and Fear Representation – Untransformed Depressive symptoms Scores

IV	<i>B</i>	<i>SE B</i>	<i>R</i>	<i>R</i> ²	<i>F</i>	ΔR^2	ΔF	<i>T</i>
Step 1								
Risk Representation	-.02	3.08						
Illness Representation	.27	3.09	.25	.06	2.38	.06	2.38	1.58
Step 2								
Risk Representation	-.07	2.89						
Illness Representation	.32*	2.91						2.02*
Fear Representation	.36**	.16	.47**	.19	5.47*	.12**	10.98**	3.13**

* $p < .05$, ** $p < .01$

Anxiety: Hypothesis 2b stated that fear representation would add to the prediction of women's anxiety symptoms after controlling for risk and illness representations. Hierarchical multiple regression was performed to test this hypothesis. Entry of predictors was theoretically driven. In the first step of hierarchical multiple regression, risk representation and illness representation were entered. After step 1, this model was not statistically significant $R^2 = .04$ (adjusted $R^2 = .02$), $F_{inc}(2, 74) = 1.06$, $p = .351$ and explained only 4% of the variance in anxiety symptoms.

After entry of fear representation at Step 2, the total variance explained by the model as a whole was 28%. $R^2 = .28$ (adjusted $R^2 = .26$), $F_{inc}(3, 73) = 9.34$, $p < .0001$. The introduction of fear representation improved the predictions of anxiety symptoms, after controlling for risk

representation and illness representation, and explained 24% of the variance in anxiety symptoms ($\Delta R^2 = .24$; $F(1, 73) = 24.52$, $p < .0001$). Results are presented for untransformed (see Table 15) maternal scores on a global measure of anxiety. Transformed analyses appear in Appendix J.

Table 15

Hierarchical Multiple Regression Analysis Predicting Anxiety from Risk Representation, Illness Representation, and Fear Representation - Untransformed Anxiety Scores

IV	β	SEB	R	R^2	F	ΔR^2	ΔF	T
Step 1								
Risk Representation	-.20	6.75						
Illness Representation	.26	6.77	.19	.04	1.33	.04	1.33	1.63
Step 2								
Risk Representation	-.20	5.88						
Illness Representation								
Fear Representation	.27 ^a	5.89						1.90 ^a
	.49 ^{***}	.322	.52 ^{***}	.28 ^{***}	9.34 ^{***}	.24 ^{***}	24.52 ^{***}	4.95 ^{***}

^a, Finding approached significance at $p < 0.06$, ^{***} $p < .0001$.

Intrusive ideation. Hypothesis 2c stated that fear representation would add to the prediction of women's intrusive ideation regarding their genetic counseling experiences (i.e., intrusive ideation) after controlling for risk and illness representations. Hierarchical multiple regression was performed to test this hypothesis. Entry of predictors was theoretically driven. In the first step of hierarchical multiple regression, risk representation and illness representation were entered. After step 1, this model was statistically significant $R^2 = .12$ (adjusted $R^2 = .10$), $F_{inc}(2, 73) = 5.04$, $p < .01$ and explained 11% of the variance in intrusive ideation symptoms. After entry of fear representation at Step 2, the total variance explained by the model as a whole was 31%. $R^2 = .31$

(adjusted $R^2 = .28$), $F_{inc}(3, 73) = 10.54, p < .0001$. The introduction of fear representation explained an additional 17% of the variance in intrusive ideation, after controlling for risk representation and illness representation ($\Delta R^2 = .18$; $F(1, 73) = 19.07, p < .0001$). While these results were significant, they should be interpreted with extreme caution due to the non-normal distribution of the dependent variable, intrusive ideation (see Table 16).

Table 16

Hierarchical Multiple Regression Analysis Predicting Intrusive Ideation from Risk Representation, Illness Representation, and Fear Representation

IV	β	SE B	R	R^2	F	ΔR^2	ΔF	T
Step 1								
Risk Representation	.10	.22						
Illness Representation	.27*	.22	.35*	.12*	5.04*	.11*	5.04*	1.70
Step 2								
Risk Representation	.11	.20						
Illness Representation	.27	.20						
Fear Representation	.43**	.01	.55**	.31**	10.54**	.17**	19.07**	4.37**

* $p < .01$, ** $p < .0001$

Dyadic Functioning. Due to the fact that R for regression was not statistically significant in the standard multiple regression model and examinations of dyadic functioning revealed that this variable did not correlate with any of the independent predictor variables, planned hierarchical regression analyses were abandoned.

Daughter Regression Analyses

Regression analyses were driven by the theoretical foundations of the adapted CSM for genetics as described in Chapter 3 of this manuscript. As such, variable entry into the models included risk representation, illness representation and fear representation according to the CSM theory. In order to accurately assess the contribution of each independent variable to the dependent variable, and in consideration of the possibility of suppression, all theoretically relevant independent variables were retained, including those variables that were not correlated with the dependent variable at the bivariate level. This decision to retain theoretically relevant variables (i.e., risk representation, illness representation and fear representation) was made in an effort to avoid underestimating some of the parameters which could potentially compromise the predictive power of the model and result in regression equations that are overly sample-specific (Cohen, Cohen, West, & Aiken, 2003; Tabachnick & Fidell, 2007).

There were a number of cases where two or more family members (i.e., 99 daughters from 77 families) were represented in this sample, suggesting that their responses may be correlated. Analyses of the dependent variables depressive symptoms, anxiety, and self-concept, and daughter dyadic functioning was completed first using standard multiple regression models and then hierarchical multiple regression models. Generalized estimating equations were then applied to confirm that dependence had properly been accounted for. Both the standard and hierarchical regression models for all dependent variables yielded results that were essentially identical to the generalized estimating equations (GEE) models for all dependent variables. Accordingly, results of the standard multiple regressions and hierarchical regressions are reported.

Testing hypotheses 3a-3d. Four standard multiple regressions were conducted to examine

hypotheses 3a–3d. Following a theoretically driven approach, according to the adapted CSM for genetics (as described in the literature, see Marteau & Weinman, 2006), risk representation, illness representation and fear representation were entered as predictors with the goal of examining the predictive utility of maternal threat representation (i.e., risk representation, illness representation and fear representation) on daughters' psychosocial distress as measured by daughters' scores on measures of (a) depressive symptoms, (b) anxiety, (c) self-concept, and (d) dyadic functioning with mothers.

Daughters' depressive symptoms. Hypothesis 3a predicted that daughters' total scores on a global measure of their depressive symptoms would be predicted by mothers' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed, between the dependent variable, daughters' depressive symptoms, and mothers' risk representations, illness representations and fear representations as the independent variables. R for regression was significantly different from zero $F(3, 95) = 3.83, p < .05$, with R^2 at .11. The adjusted R^2 of .08 indicated that 8% of the variability in depressive symptoms was predicted by the overall model.

In order to interpret the relative strength of the individual predictors, bivariate and partial correlations were examined. Bivariate correlations are described above and presented in Table 9. Partial correlations for (a) mothers' illness representations and daughters' depressive symptoms ($r = .22, p = .01$), and (b) mothers' fear representation and daughters' depressive symptoms ($r = .22, p < .05$) were both significant. These results indicated that, after factoring out the effects of risk representation, illness representation and fear representation predicted daughters' depressive symptoms. In other words, these variables contributed significantly to this model. Given the positive skew of this variable, however, these results are to be interpreted with a degree of caution

(see Table 17)

Table 17

Standard Multiple Regression Analysis Predicting Depression Scores From Risk Representation, Illness Representation, Fear Representation– Depression Scores

IV	<i>B</i>	SE <i>B</i>	<i>B</i>	<i>F</i> (3, 95)	<i>R</i> ²
Risk Representation	-4.01	3.03	-.12		
Illness Representation	7.98	3.03	.29**		
Fear Representation	.38*	.17	.21*	3.83*	.11*

* $p < .05$. ** $p < .01$.

Daughters' anxiety. Hypothesis 3b predicted that daughters' total scores on a global measure of anxiety would be predicted by mothers' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed, between the dependent variable, daughters' anxiety symptoms, and mothers' risk representation, illness representation and fear representation as the independent variables (see Table 18 for untransformed scores, transformed values analyses are found in Appendix J). *R* for regression was significantly different from zero $F(3, 95) = 2.35, p < .05$, with R^2 at .06. The adjusted R^2 of .03 indicated that 3% of the variability in depressive symptoms was predicted by the overall model.

In order to interpret the relative strength of the individual predictors, bivariate and partial correlations were examined. Bivariate correlations are described above and presented in Table 9. A significant partial correlation for mothers' fear representation and daughters' anxiety symptoms ($r = .24, p < .05$) was significant. These results indicated that, after factoring out the effects of risk and illness representation, fear representation predicted anxiety symptoms in daughters. In other

words, this was the only variable that contributed significantly to this model (see Table 18).

Table 18

Standard Multiple Regression Analysis Predicting Daughters' Anxiety Scores From Risk Representation, Illness Representation, Fear Representation – Untransformed Anxiety Scores

IV	B	SE B	B	F(3, 95)	R ²
Risk Representation	-.68	3.4	-.03		
Illness Representation	2.19	3.4	.09		
Fear Representation	.49	.19	.26*	2.35	.06

* $p < .05$.

Self-concept. Hypothesis 3c predicted that daughters' total scores on a global measure of self-concept would be predicted by mothers' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed, between the dependent variable, self-concept, and mothers' risk representation, illness representation and fear representation as the independent variables. R for regression was significantly different from zero $F(3, 95) = 3.57, p < .05$, with R^2 at .10. The adjusted R^2 of .07 indicated that 7% of the variability in self-concept was predicted by the overall model (see Table 19).

In order to interpret the relative strength of the individual predictors, bivariate and partial correlations were examined. Bivariate correlations are described above and presented in Table 9. Partial correlations for (a) mothers' illness representation and daughters' self-concept ($r = -.23, p < .05$), and (b) mothers' fear representation and daughters' self-concept ($r = -.23, p < .05$) were significant. These results indicated that, after factoring out the effects of risk representation, illness representation and fear representation predicted increased difficulties with self-concept among

daughters. In other words, these variables contributed significantly to this model.

Table 19

Standard Multiple Regression Analysis Predicting Self-Concept From Risk Representation, Illness Representation, Fear Representation

IV	<i>B</i>	SE <i>B</i>	<i>B</i>	<i>F</i> (3, 95)	<i>R</i> ²
Risk Representation	2.49	2.99	.113		
Illness Representation	-6.7	2.99	-.31*		
Fear Representation	-.38	.17	-.22*	3.57*	.10*

* $p < .05$.

Daughter dyadic functioning. Hypothesis 3d predicted that total scores on a measure of daughters' ratings of dyadic functioning would be predicted by mothers' threat representations (i.e., risk representation, illness representation, and fear representation). A standard multiple regression was performed between daughters' reports of dyadic functioning with their mothers as the dependent variable and marital status, as well as, risk representation, illness representation and fear representation as the independent variables. *R* for regression was not significantly different from zero $F(3, 95) = .790, p > .05$ indicating that, taken together, the overall threat representation including, risk representation, illness representation, and fear representation, did not predict daughters' ratings of dyadic functioning with their mothers (see Table 20).

Table 20

Standard Multiple Regression Analysis Predicting Dyadic Functioning From Risk Representation, Illness Representation, Fear Representation

IV	<i>B</i>	SE <i>B</i>	<i>B</i>	<i>F</i> (3, 95)	<i>R</i> ²
Risk Representation	-1.00	2.54	-.06		
Illness Representation	2.41	2.69	.14		
Fear Representation	.18	.15	.12	.79	.02

Testing hypotheses 4a-4d. Four hierarchical multiple regressions were conducted to examine hypotheses 4a –4d. Following a theoretically driven approach, according the adapted CSM for genetics (as described in the literature, see Marteau & Weinman, 2006), with the goal of learning more about the unique contribution of fear representation (as articulated in the study rationale) four hierarchical multiple regressions were planned to examine the predictive utility of maternal fear representation on daughters’ (a) depressive symptoms, (b) anxiety, (c) self-concept and (d) dyadic functioning with mothers. More specifically, the hierarchical regressions aimed to determine if addition of information regarding mothers’ fear representation improved prediction of psychosocial distress, beyond that afforded by information from illness and risk representations. In light of the significant effect of marital status noted in the univariate analyses, this variable was entered in step 1 of the regression analyses as a group. Following the theoretical framework of CSM, whereby risk and illness representation are theorized to collectively account for cognitive

representation of health threats, these variables were entered, together, into the model in step 2 of each regression. Consistent with CSM theory, fear representation, which is theorized to represent the subjective-emotional component of the CSM, was entered into each model on step 3.

Daughter Depressive Symptoms. Hypothesis 4a stated that mothers' fear representation would add to the prediction of daughters' depressive symptoms after controlling for risk and illness representations and mothers' marital status. Hierarchical multiple regression was performed to test this hypothesis. Entry of predictors was theoretically driven. In the first step of the hierarchical multiple regression, marital status was entered. After Step 1, 10.4% of the variance in daughters' depression scores was explained ($\Delta R^2 = .043$, $F(1, 97) = 11.26$ $p < .01$). After step 2, with the addition of risk and illness representations, an additional 4.5% ($\Delta R^2 = .045$, $F(3, 95) = 5.53$ $p < .01$) of the variance in daughters' depression symptoms was explained. Following the entry of fear representation at step 3, the introduction of fear representation explained an additional 4.3% of the variance in depression symptoms, after controlling for risk representation and illness representation ($\Delta R^2 = .043$; $F(4, 94) = 5.58$; $p < .001$). In the full model, marital status was the strongest independent predictor of daughters' depressive symptoms, $t(94) = 3.12$, $p < .01$, followed by illness representation, $t(94) = 2.29$, $p < .05$, and fear representation, $t(94) = 2.24$, $p < .05$ (see Table 21).

Table 21

Hierarchical Multiple Regression Analysis Predicting Depression from Risk Representation, Illness Representation, and Fear Representation

IV	β	SE B	R	R ²	F	ΔR^2	ΔF	T
Step 1								
Mothers' Marital Status	.32**	2.28	.32**	.10**	11.26**	.10**	11.26**	3.36**
Step 2								
Mothers' Marital Status	.30**	2.27						3.09**
Risk Representation	-.13	2.98						
Illness Representation	.28*	2.99	.39	.15	5.53**	.045	2.49	2.11*
Step 03								
Mothers' Marital Status	.29**	2.22						3.12**
Risk Representation	-.14	2.92						
Illness Representation	.30	2.93						2.29*
Fear Representation	.21*	.16	.44*	.19*	5.58***	.043*	5.02*	2.24*

* $p < .05$, ** $p < .01$.

Daughters' anxiety. Hypothesis 4b stated that mothers' fear representation would add to the prediction of daughters' anxiety symptoms after controlling for risk and illness representations and mothers' marital status. Entry of predictors was theoretically driven. Hierarchical multiple regression was performed to test this hypothesis. In the first step of the hierarchical multiple regression, marital status was entered. After step 1, 5% of the variance in daughters' anxiety scores was explained ($\Delta R^2 = .05$, $F(1, 97) = 4.09$, $p < .05$). After step 2, the addition of risk and illness

representations, there was no significant additional variance in daughters' anxiety symptoms ($\Delta R^2 = .01$, $F(3, 95) = 2.30$, $p > .05$). Following the entry of fear representation at step 3, an additional 3% of the variance in daughters' anxiety symptoms, after controlling for marital status, risk representation and illness representation was accounted for ($\Delta R^2 = .029$; $F(4, 94) = 2.39$; $p = .06$). In the final model, mothers' marital status was the strongest independent predictor of daughters' anxiety symptoms $t(94) = 2.53$, $p < .05$. Results of the untransformed values analyses are presented in Table 22. The transformed values analyses are included in Appendix J.

Table 22

Hierarchical Multiple Regression Analysis Predicting Anxiety from Mothers' Marital Status, Risk Representation, Illness Representation, and Fear Representation - Untransformed Anxiety Scores

IV	β	SE B	R	R^2	F	ΔR^2	ΔF	T
Step 1								
Mothers' Marital Status	.25*	2.24	.25*	.05*	6.09*	.06*	6.09*	2.47*
Step 2								
Mothers' Marital Status	.26*	2.28						2.57*
Risk Representation	-.12	2.85						
Illness Representation	-.13	2.85	.27	.04	2.30	.01	.45	-.89
Step 03								
Mothers' Marital Status	.26*	2.26						2.53*
Risk Representation	.11	2.83						
Illness Representation	-.11	2.84						
Fear Representation	.16	.16	.31	.06	2.39 ^a	.03	2.53	1.59

^a $p < 0.06$, * $p < .05$.

Self-concept. Hypothesis 4c stated that mothers' fear representation would add to the

prediction of daughters' difficulties related to self-concept, after controlling for risk and illness representations and mothers' marital status. Hierarchical multiple regression was performed to test this hypothesis. Entry of predictors was theoretically driven. In the first step of the hierarchical multiple regression, mothers' marital status was entered. After step 1, 9% of the variance in daughters' self-concept difficulties was explained ($\Delta R^2 = .09$, $F(1, 97) = 9.57$, $p < .01$). After step 2, the addition of risk and illness representations, explained 4% of additional the variance associated with daughters' self-concept symptoms ($\Delta R^2 = .04$, $F(3, 95) = 4.61$ $p > .05$). Following the entry of fear representation at step 3, an additional 5% of the variance in daughters' self-concept symptoms, after controlling for marital status, risk representation and illness representation ($\Delta R^2 = .048$; $F(4, 94) = 4.99$, $p < .001$). In the final model, mothers' marital status was the strongest independent predictor of daughters' self-concept symptoms, $t(94) = -2.90$, $p < .01$, followed by mothers' fear representation, $t(94) = 2.34$, $p < .05$. Additionally, mothers' illness representation approached significance as a predictor in the final model $t(94) = -1.91$, $p < 0.06$ (see Table 23).

Table 23

Hierarchical Multiple Regression Analysis Predicting Daughters' Self-Concept from Mothers' Marital Status, Risk Representation, Illness Representation, and Fear Representation – Self-Concept Scores

IV	β	SE B	R	R ²	F	ΔR^2	ΔF	T
Step 1								
Mothers' Marital Status	-.30**	-6.98	.30**	.08**	9.58**	.09**	9.58**	-3.09**
Step 2								
Mothers' Marital Status	-.28**	2.25						-2.87**
Risk Representation	.06	2.96						
Illness Representation	-.23	2.97	.36	.13	4.61**	.04	2.03	-1.79
Step 03								
Mothers' Marital Status	-.28**	2.20						2.53*
Risk Representation	.07	2.90						
Illness Representation	-.25 ^a	2.91						-1.91 ^a
Fear Representation	-.22*	.16	.42*	.18**	4.99***	.05*	5.48*	-2.34*

^a $p < .06$, * $p < .05$, ** $p < .01$

Daughters' dyadic-functioning. Hypothesis 4d stated that mothers' fear representation would add to the prediction of daughters' reports of mother-daughter dyadic dysfunction, after controlling for risk and illness representations and mothers' marital status. Hierarchical multiple regression was performed to test this hypothesis. In the first step of the hierarchical multiple regression, mothers' marital status was entered. After step 1, 9% of the variance in daughters' reports of dyadic functioning difficulties was explained ($\Delta R^2 = .09$, $F(1, 97) = 8.63$, $p < .01$).

After step 2, the addition of risk and illness representations, explained no additional variance associated with daughters' reports of dyadic functioning was explained ($\Delta R^2 = .00$, $F(3, 95) = 2.95$, $p < .05$). Following the entry of fear representation at step 3, an additional 1.5% of the variance in daughters' reports of dyadic functioning, after controlling for marital status, risk representation and illness representation ($\Delta R^2 = .02$; $F(4, 94) = 2.58$, $p < .05$). In the final model, mothers' marital status was the lone independent predictor of daughters' reported dyadic functioning with mothers, $t(94) = 2.79$, $p < .01$ (see Table 24).

Table 24

Hierarchical Multiple Regression Analysis Predicting Daughters' Reports of Dyadic Functioning with their Mothers' from Mothers' Marital Status, Risk Representation, Illness Representation, and Fear Representation

IV	β	SE B	R	R^2	F	ΔR^2	ΔF	t
Step 1								
Mothers' Marital Status	.29**	3.02	.29**	.08**	8.63**	.08**	8.63**	2.93**
Step 2								
Mothers' Marital Status	.29**	3.12						2.81**
Risk Representation	-.02	2.50						
Illness Representation	.05	2.51	.29	.09	2.95*	.00	.18	.32
Step 03								
Mothers' Marital Status	.28**	3.12						2.79**
Risk Representation	.01	2.49						
Illness Representation	.06	2.51						
Fear Representation	.12	.14	.32	.10	2.58*	.01	1.45	1.20

* $p < .05$, ** $p < .01$.

Chapter 5

Discussion

The primary purpose of this dissertation was to examine the impact of threat representations on the psychosocial functioning of BRCA1/2 counselees and their adolescent daughters. The secondary goal was to investigate the impact of fear representation over and above illness and risk representation on the psychosocial functioning of BRCA1/2 counselees and their adolescent daughters. The present dissertation applied Marteau and Weinman's (2006) common sense model (CSM), adapted for genetics, as a guiding, explanatory framework to better understand the impact of threat representation on psychosocial functioning of BRCA1/2 counselees and their adolescent daughters. *Threat representation*, as articulated by the CSM, is a key factor in predicting psychosocial adaptation, coping and appraisal in response to a health threat (e.g., Cameron, 2003; Marteau & Weinman, 2006). More specifically, researchers were interested in two central aspects of threat representation, the cognitive processes (i.e., risk and illness representation) and the subjective-emotional processes (i.e., fear representation).

Although the correlational design of this study does not yield definitive causal relationships between threat and fear representation and psychosocial outcomes for mothers and daughters, *a priori* hypotheses based on the CSM framework and existing literature in the domains of psychosocial genetic and oncology allowed the correlational results to be framed in the context of existing knowledge in these areas.

Mothers and adolescent daughters were selected as a group of study for two reasons: First, the investigation of the impact of genetic counseling on the elementary family represents a

significant gap in the literature and, second, this decision was informed by literature examining psychosocial adaptation of families to breast cancer, some of which has suggested that adolescent daughters may be more vulnerable to experiencing psychosocial distress secondary to maternal breast cancer (e.g., Krattenmacher et al., 2012; Compas et al., 1996; Compas et al., 1994).

Theoretically Driven Predictors

Based on the CSM framework, predictors were selected according to the theoretical model. Interestingly, in this study, fear representation was not correlated with either risk representation or illness representation. As noted by Cameron (2003), in the development of the adapted CSM for genetics, risk representation and fear representation were not strongly correlated ($r = .29$). The background theoretical and empirical literature that underpins CSM suggests that fear representation often influences behaviours independently of the influence of risk representation (e.g., Cameron, 2003). However, as noted by Marteau & Weinman, inclusion of both subjective-emotional information (i.e., fear representation) and objective-cognitive information (i.e., risk and illness representations) is essential within the framework of the CSM since they both play a role in identifying the determinants of protective behaviour health behaviours. As such, fear representation was retained as a predictor in the study model despite its lack of correlation with illness representation and risk representation. Fear representation was also retained as an independent variable on the basis of research that has demonstrated that fear is often associated with avoidance behaviours (e.g., Clark, 2004). Understanding the associations between fear representation and psychosocial functioning has important implications with

respect to the development of interventions and protocols to support BRCA1/2 counselees and their adolescent daughters in terms of preventative health behaviours.

Maternal Psychosocial Functioning

Maternal depressive symptoms and anxiety

As predicted in hypotheses 1a and 1b, total threat representation, including risk representation, illness representation and fear representation, together, were found to add to the prediction of mothers' self-reported levels of depressive symptoms and anxiety. Additionally, consistent with hypotheses 2a and 2b, when risk representation and illness representation (i.e., objective-cognitive information) were controlled for, through the hierarchical regression modeling, fear representation (i.e., subjective-emotional information) continued to emerge as a significant predictor of mothers' self-reported depressive symptoms and anxiety. Illness representation was a significant predictor of BRCA1/2 counselees' depressive symptoms and an association between illness representation and BRCA1/2 self-reported anxiety approached significance in the hierarchical model. However, results of this study revealed that risk representation did not add to the predictions of BRCA1/2 counselees' depressive symptoms or anxiety.

Risk representation. While studies assessing the impact of BRCA carrier status on depressive symptoms are not directly comparable to the operationalization of risk representation (i.e., eligibility for BRCA1/2 screening) in this study, they do provide a foundation to help contextualize the current findings. With respect to the null finding in the relationship between risk representation and depressive symptoms identified in this study, this result is consistent with

the broader literature that has reported on depressive symptoms in response to BRCA1/2 screening. More specifically, the empirical evidence indicates that BRCA1/2 carrier status (i.e., risk representation) is associated with short-term elevations in depressive symptoms but long-term effects of BRCA1/2 counsees' self-reported symptoms of depressive mood have not been identified (Arver et al., 2004; Bennett et al., 2008; Bowen et al., 2004; Cull et al., 1998; Lobb et al., 2004; Mikkelsen et al., 2009; Reichelt et al., 2008; Watson et al., 1998). Further, although short-term increases in depressive symptoms have been observed in the year after receipt of results, these typically dissipate within one to two years of testing (e.g., Graves et al. 2012; Smith et al., 2008; van Dijk et al., 2006). In fact, Domchek et al., (2010) compared BRCA1/2 carriers and age-matched general population controls and found no differences in depressive symptoms at 1 year post-testing.

Although missing data in the current study prohibited the use of "time since genetic counseling" as a control variable, box-plots were run for available cases using "time since genetic counseling" as a dichotomous variable. These graphs demonstrated that means and ranges for two groups (i.e., "genetic counseling 2 years ago or less" and "genetic counseling more than two years") were similar (see Appendix H). The available cases indicate that only a small number ($N = 6$) of BRCA1/2 counsees in this sample had participated in genetic counseling within the last year and that, most had been seen for genetic counseling in previous years ($M_{time} = 3.21$ years).

The current study is one of a limited number of studies to examine the impact of screening eligibility on depressive symptoms in BRCA1/2 counsees. Findings from one of the

only other known studies to assess eligibility for BRCA1/2 screening and associations with psychosocial functioning indicated that depressive symptom scores, as measured by the Beck Depression Inventory, at 4 months post-screening were significantly lower for BRCA1/2 non-carriers as compared to both BRCA1/2 carriers and women who were not eligible for screening (Meiser et al., 2012). While differences between the groups were observed in that study, it should be noted that scores did not reach the threshold for clinical depression and that these differences were not sustained over time (i.e., at 12 month follow up; Meiser et al., 2002).

One possible explanation for the fact that risk representation was not significant in the current model is that the association between risk perception and time, as described above, was not controlled for and there were limited numbers of participants who had recently participated in BRCA1/2 counseling for determination of eligibility for screening. Additionally, based on results identified above, eligibility may not be a sensitive enough measure to detect differences in depressive symptoms as it does not account for the complex interplay of different type of mutation statuses.

With respect to anxiety, results from the current study are consistent with findings described in the broader literature whereby many of the short-term increases in anxiety reported by BRCA1/2 counselees have not been sustained over time and were subclinical in nature (Hamilton et al., 2009). Once again, the mean time since genetic counseling in the current sample was 3.21 years and this may have impacted study results and our ability to detect anxiety responses in BRCA1/2 counselees as a function of the passage of time (see Appendix H for box plot).

As reported in the broader literature, there are discrepancies in the evaluation of anxiety responses in BRCA1/2 counselees (e.g., Hamilton et al., 2009; Schilch-Baker, 2006). However, several research groups who have investigated the impact of BRCA1/2 mutation status on anxiety have suggested that effects of BRCA1/2 screening on anxiety can be observed when controlling for mutation status (e.g., Low et al., 2008; van Dijk et al., 2006). Due to the fact that risk representation as described in the current study was concentrated on eligibility rather than mutation result, it is possible that eligibility may not have been sensitive enough to detect differences between groups. However, it should be noted that one study investigating the impact of eligibility revealed that women who had family histories of breast cancer, but who had *not* undergone genetic testing were more significantly more anxious and endorsed higher levels of general distress than women who had been identified as BRCA1/2 mutation carriers (Geirdal & Dahl, 2005, 2008). Given these findings, it is recommended that future research in this area include both mutation status and eligibility in assessing risk representation.

Illness representation. Findings from the current study regarding the role of illness representation in prediction of BRCA1/2 counselees' psychosocial functioning were largely consistent with the extant literature indicating that personal history of breast cancer is a vulnerability factor in BRCA1/2 counselees' experience of depressive symptoms. For example, a recent study by Cukier et al. (2013) found that BRCA1/2 screeners with personal histories of cancer, reported significantly higher rates of depressive symptoms on the CES-D [$\beta = .17$, $SE = .28$, $p = .04$]. This finding is especially important in the context of family functioning as the available research on parental cancer has indicated that depressive symptoms and/or negative

affectivity in the parent with cancer has been associated with children's emotional and behavioural problems (e.g., Edwards, Hulbert-Williams & Neal, 2008; Hoke et al., 2001, Lewis & Darby, 2004; Thastum et al., 2009; Watson et al., 2006).

Consistent with the research in this domain (e.g., Esplen et al., 2013), approximately 18% of the current sample endorsed depressive symptoms that were suggestive clinically significant low mood. While women with personal histories of breast cancer reported higher rates of depressive symptoms, the group mean for depressive symptoms endorsed by affected BRCA1/2 counselees was not in this clinically significant range (i.e., $M_{affected} = 12.45$). As such, while illness representation was a significant predictor of depressive symptoms in the current study, the current results do not indicate that affected BRCA1/2 counselees are more likely to endorse clinically meaningful symptoms of depression as compared to unaffected counselees.

With respect to an association between illness representation and BRCA1/2 counselees' anxiety, the background literature has provided support for the relationship between breast cancer and anxiety. In what has become a seminal study, Hughes (1982) investigated the prevalence and incidence of anxiety among breast cancer patients. Results of that study revealed that 91% of participants reported symptoms of anxiety; of these, 25% reported severe anxiety and 66% reported mild to moderate anxiety. Results of more contemporary studies assessing symptoms of anxiety in breast cancer patients indicate that approximately 35% to 40% of women diagnosed with breast cancer before age 50 experience clinically significant anxiety symptoms following diagnosis (Dastan & Buluz, 2011; Burgess et al., 2005). The discrepancies reported in the literature described above may be owing to advances in treatment and medical options as

well as age of study participants. Amongst participants in the current study, approximately 31% of BRCA1/2 counselees endorsed symptoms suggestive of clinically meaningful anxiety. This rate is slightly higher than rates of distress reported in the broader literature on BRCA1/2 counselees (e.g., Esplen et al., 2013). Of note, however, differences between affected and unaffected BRCA1/2 counselees on the measure of anxiety used in this study were non-significant [$t(75) = -1.25, p = .22$]. As such, while illness representation approached significance in the current models predicting anxiety in BRCA1/2 counselees, examination of the data suggest that anxiety responses in this sample are elevated and uncontrolled personal variables may be contributing to the model rather than illness representation, per se.

Fear representation. CSM posits that fear representation plays a central role in determining our subjective understanding as well as the meaning we attach to threat representation (Cameron, 2003). Findings based on the analyses of this group of BRCA1/2 counselees' provide preliminary evidence for the role that fear representation may play in predicting BRCA1/2 counselees' self-reported depressive symptoms and anxiety. These findings converge with Brownlee et al.'s (2001) theory of vulnerability as an important component of the CSM for genetics, suggesting that BRCA1/2 counselees who endorse elevated breast cancer fear are more likely to experience depressive symptoms and anxiety. While these results have provided preliminary evidence for the role of fear representation in the broader framework of the CSM, additional research is needed to help understand the interplay between risk and illness representation and fear representation and whether fear

representation generalizes beyond the high-risk group of women studied as part of this project. Russell and Barrett (1999) note that, at a conceptual level, fear is quite different than anxiety or worry. Whereas fear is more immediate and intense, worry, in contrast, is typically carried out over time. Additionally, the affect attached to fear is stronger than for worry (McCaul & Goetz, nd). While there is some overlap between measurement of fear and other psychosocial functioning variables (e.g., anxiety, depression, intrusive ideation), these conceptual distinctions help to distinguish this predictor from anxiety and depressive symptoms as measured in the current study.

Maternal intrusive ideation

As predicted in hypothesis 1c, total threat representation, including risk representation, illness representation and fear representation, together, were found to add to the prediction of mothers' self-reported ratings of intrusive ideation. Additionally, consistent with hypothesis 2c, when risk representation and illness representation (i.e., objective-cognitive information) were controlled for, through the hierarchical regression modeling, fear representation (i.e., subjective-emotional information) continued to emerge as a significant predictor of mothers' self-reported intrusive ideation and an association between illness representation and BRCA1/2 self-reported intrusive ideation approached significance. However, results of this study revealed that risk representation did not add to the predictions of BRCA1/2 counsees' intrusive ideation. Caution should be applied when interpreting these results as none of the participants in the current sample expressed intrusive ideation that would be considered clinically meaningful and the distribution of the dependent variable was positively skewed and did not improve with transformation.

The current study was designed at a time when the existing evidence regarding the associations between genetic screening and intrusive ideation was understudied (Nelson et al., 2005). The results of the present study contradict evidence published in a recent review examining the impact of BRCA1/2 counseling which indicated that counseling was not associated with any type of trauma response (Nelson et al., 2013). Given the dearth of evidence on this matter that has been published over the course of the last 7 years, results of the current study should be interpreted with caution. Nonetheless, univariate analyses suggest that there are statistically significant differences between affected and unaffected BRCA1/2 counselees in the current sample [$t(74) = -3.11, p < 0.01$] such that BRCA1/2 counselees with personal histories of breast cancer self-reported higher levels of intrusive ideation in response to genetic counseling. Additionally, BRCA1/2 counselees who were eligible for screening self-reported higher levels of intrusive ideation than those who were not tested [$t(74) = -2.29, p < 0.05$]. The subclinical differences in these groups inform the current results and suggest that future research might benefit from more specific measures of counselees' unmet emotional needs following genetic counseling as unmet needs have been shown to impact recalled experiences of BRCA1/2 counseling (Pieterse et al., 2011).

Maternal ratings of dyadic functioning

Contrary to hypothesis 1d, threat representation did not predict mothers' self-reported mother-daughter relationship quality as indicated by a measure of dyadic functioning in the standard multiple regression, nor was it correlated with any of the predictor variables. Planned hierarchical multiple regression of dyadic functioning as a dependent variable was abandoned in

light of the non-significant relationship. This non-significant relationship is important as it suggests that, despite the impact of fear representation on BRCA1/2 counselees' self-reported depressive symptoms, anxiety and intrusive ideation, fear representation did not appear to impact dyadic functioning in mother-daughter relationships. These findings do not support the belief that mother-daughter relationships are disrupted by mothers' threat representation as it relates to hereditary breast cancer and is consistent with the limited literature in this area suggesting that most families cope well with threat representations and associated genetic counseling demands (e.g., Lapointe et al., 2011).

Psychosocial Functioning of Daughters

As noted in the results section of this dissertation, data was fit with GEE models which produced nearly identical results to the standard and hierarchical multiple regressions described in Chapter 4. As such, discussion of the results will focus on the regression analyses. As predicted in hypotheses 3a and 3c, total threat representation, including risk representation, illness representation and fear representation, together, were found to add to the prediction of daughters' self-reported levels of depressive symptoms, anxiety, and self-concept. Additionally, consistent with hypotheses 4a, and 4c, when risk representation and illness representation (i.e., objective-cognitive information) were controlled for, through the hierarchical regression modeling, fear representation (i.e., subjective-emotional information) continued to emerge as a significant predictor of daughters' self-reported depressive symptoms and self-concept.

Additionally, mothers' marital status and illness representation were also significant predictors of daughters' depressive symptoms and associations between mothers' marital status and daughters'

self-concept ratings were significant in the hierarchical models. Contrary to hypotheses 3d and 4b and 4d, results of this study revealed that neither threat representation nor fear representation predicted daughters' ratings of anxiety and dyadic functioning with mothers. Mothers' marital status was the only significant predictor in hierarchical models regressing daughters' ratings of anxiety and dyadic functioning with mothers.

The current research on high-risk breast cancer families with minor children has produced results that are largely consistent with findings described herein in terms of daughters' reports of depressive symptoms. More specifically, as described in several reviews (e.g., Grabiak et al., 2007; Osborn et al., 2007), there is strong and consistent evidence that children's depressive symptoms are related to parents' reports of psychosocial distress. The results of the current study identify associations between mothers' fear representations and daughters' depressive symptoms. These findings are novel and help extend the CSM to explain interpersonal responses to BRCA1/2 counsees' fear representation. Additionally, this study provides preliminary evidence to support proposed theories regarding the impact of parental fear representation (i.e., breast cancer fear) on adolescent daughters' self-concept (e.g., Krattenmacher et al., 2012; Spira & Kennemore, 2000). To date, self-concept has not been well-studied in children who have chronically ill parents affected by breast cancer or within the BRCA1/2 literature (Krattenmacher et al., 2012). This represents an important advancement in the field that aligns with new research on self-concept in BRCA1/2 counsees' self-concept as a measure of vulnerability to psychosocial distress (e.g., Esplen et al., 2009; Esplen et al., 2011). This finding is significant to the extent that it converges with Brownlee et al.'s, (2001) theory of

vulnerability as an important component of the CSM for genetics. Based on these results, the study of self-concept in offspring of BRCA1/2 counselees should be considered in future research.

According to previous research, which suggested that parental distress is associated with functional outcomes and somatic symptoms (e.g., Tercyak et al., 2002; Bradbury, Dignam & Ibe, 2007; Cappelli et al., 2005), we expected that threat representation would also be significantly associated with elevated anxiety symptoms and poorer dyadic functioning. Results of this study do not support our initial predictions. However, it should be noted that marital status emerged a significant predictor of daughters' psychosocial functioning in all hierarchical models. As such, future research should focus on the impact of families as a whole, and, as indicated in this study, the impact of fathers on daughters' psychosocial functioning.

Limitations

Study design. The present study was a single-stage, cross-sectional design. As such, one cannot draw inferences about causal relationships from these correlational analyses. Moreover, this study's data depended on a self-report driven survey design. Accordingly, inferences about correlational and predictive relationships need to be interpreted while keeping in mind the possible impact of common method variance (e.g., Podsakoff, MacKenzie, Lee, & Podsakoff, 2003). While the cross-sectional design does support the findings in the broader literature that *threat representation* and *fear representation* have no adverse clinically severe psychosocial implications, it does not eliminate the possibility of subtle adverse effects, as no pretest comparisons are available. This is significant as research with BRCA1/2 counselees has

demonstrated that when psychosocial distress has been reported in BRCA1/2 counselees, effects are typically subtle and short-term, and only a small minority experience clinically significant levels of distress (e.g., Nelson et al., 2013). Detailed below are several important design and methodological considerations as well as more comprehensive depictions of how these considerations impact the present study. Areas covered include selection bias, sample size, retrospective reports of fear representations, lack of a control group for comparison, and a broader discussion concerning ethical barriers to psychosocial genetics research with vulnerable population, including minors.

Selection Bias. Mothers in the present study were recruited through a genetic counseling program at a tertiary care centre and self-selected whether they wished to participate, as did their offspring. As a result, there may be a level of inherent self-selection bias within the sample itself. The current study sample of mothers and daughters was relatively homogeneous (i.e., Caucasian, identified a religious affiliation and had intact, elementary families). Although sample characteristics are consistent with demographic characteristics of women participating in genetics counseling for BRCA1/2 at the recruitment location (e.g., Cappelli et al., 1999; Cappelli et al., 2005), the homogeneity of this sample may limit generalizability of study findings. Certainly, the research on self-selection in the context of BRCA1/2 screening, has indicated that women who participate in research in this domain are more likely to be recruited from clinical populations, have increased concerns about their risk of breast cancer, are more likely to involve family in the genetic counseling process, and are more likely to identify daughters as a motivator for participation in screening (e.g., Lapointe et al., 2012; Geller, Doksum, Bernhardt, & Metz,

1999). Additionally, the uptake of presymptomatic screening for BRCA1/2 mutations is higher in persons of higher socioeconomic status who have greater knowledge of DNA testing, perceive the benefits of genetic screening as important, and who have more relatives affected by breast cancer, and higher family cohesiveness as well as enhance social resources (e.g., Schlich-Baker et al., 2007; Biesecker et al., 2000).

Despite the concerns relate to selection bias, the response rate in this study was 64.3%, which is generally consistent with response rates from other mail out survey designs of BRCA1/2 counselees. For example, other research studies of BRCA1/2 counselees have generally reported response rates varying between 49% to 80% (e.g., Richter et al., 2013; Cheung, Olson, Yu, Zan & Beattie, 2010). However, the current response rate is slightly higher than typical response rates in mail out survey design research within health and clinical psychological research (i.e., 49.6%; Van Horn, Green & Martinussen, 2009). As such, we cannot eliminate the possibility that selection bias was present in the sample and, therefore, there may be important distinctions between nonparticipating subjects and participants in the current study.

Attempts to control selection bias in the sample were made *a priori* through the use of monetary incentives for daughters (i.e., 35 dollars) as this incentive strategy was identified as a common technique to reduce selection bias and has been applied in previous psychosocial genetics investigations (e.g., Jenkins, Rasmussen, Moore & Honein, 2008; Pal, Rocchi, Garcia, Rivers, Vadaparampil, 2011). However, due to the fact that incentives were reserved for daughters, it may be possible that the effect of incentives in this study was not as impactful as in

other psychosocial genetics research, particularly given the fact that mothers were recruited first and asked to invite participation of their daughters.

The considerations discussed above with respect to sample characteristics underpin the need for important caveats regarding generalizations of this study to a larger pool of high-risk BRCA1/2 families. For example, results of this work may not generalize to men undergoing BRCA1/2 counseling, BRCA1/2 counselees with both daughters and sons, as well as BRCA1/2 counselees from more socio-economically, ethnically, and clinically diverse patient populations. Additional research is required in this area to determine the psychosocial implications of BRCA1/2 counseling and the effect of eligibility for screening in more diverse populations.

Missing data. Files were identified based on specified parameters described in the method section by a professional staff member of the genetics department and data abstraction from medical records was limited to the following variables: history of breast cancer (i.e., personal or family) and BRCA1/2 eligibility (i.e., eligible for screening or ineligible for screening). As such, collection of demographic information relied on participants self reports. Of note, a significant percentage of missing data points (i.e., > 10%) were observed on the following theoretically important variables that would typically act as control variables in analyses using the CSM model. These variables included: education (10.4% missing), time since genetic counseling (26% missing) and time since breast cancer diagnosis (44.4%). As such, these variables were not entered into the model and their control effects are not known.

Review of the data indicated that given the large number of missing cases and the small sample size, imputation was not realistic. As such, visualization was used in a compensatory,

although basic strategy, for data validation of variables that were considered especially theoretically important and where horizon effects were possible. In an effort to capture the impact of both times since genetic counseling and time since breast cancer diagnosis, box plot graphs were constructed and appear in Appendix H. Although this information does assist in the interpretation of some of the study findings as discussed at the forefront of this chapter, it is acknowledged that the missing data itself is a significant limitation of this study and impacts interpretation of results.

Sample size and power of analyses. While the sample size certainly appeared to be adequate to detect moderate effect sizes, the sample size may have had an impact on the power of analyses. A portion of hypothesized differences that were not found could be related to insufficient power. Additionally, the sample size impacted the type and strength of conclusions made the impact of which was likely compounded by the explicit focus on a theoretically driven model. More specifically, while the analytic strategy is parsimonious, it may well be considered simplistic in the broader context of the psychosocial genetics literature, particularly in the presence of missing control variables that are recognized in the CSM model as theoretically important. While visualization techniques (i.e., box plots) were used to help contextualize this matter, this does not fully reconcile the issues of power and interpretations that may be drawn from the data. Additionally, as noted in the extant literature, for the majority of BRCA screeners, BRCA1/2 testing does not impact psychosocial functioning at clinically significant levels (Bennett et al., 2008; Mikkelsen et al., 2009; Reichelt et al., 2008) and anxiety and distress experienced during the course of genetic counseling is not typically sustained over time and is

typically subclinical in nature (Hamilton et al., 2009). As such, the study described herein may have been underpowered and unable to detect more subtle effects of *threat representation* and *fear representation* due to horizon effects.

Measures of psychosocial functioning. Other methodological limitations included the fact that the measures applied in this study were, for the most part, clinical instruments and while all of the questionnaires and surveys selected had good to excellent psychometric properties, the vast majority of mothers and daughters in this study did not meet criteria for clinically significant symptoms. While the modeling performed does yield predictions, these associations are related to the presence of symptoms rather than addressing clinically significant levels of these symptoms. Future research may include other questionnaires that are more sensitive to assessment of psychosocial functioning rather than distress per se.

Of note, while daughter measures in this study were designed to capture psychosocial distress, self-concept and dyadic relationship quality, important omissions include measures of wellness and resiliency in youth as well as health communication within families. With respect to maternal measures, increasingly, self-concept is being recognized as important to psychosocial functioning within the context of the BRCA1/2 literature (e.g., Esplen et al., 2009; Metcalfe et al., 2012). Unfortunately, the BRCA Self Concept scale (Esplen et al., 2009) did not exist when this study was designed but the addition of this tool as a self-concept measure would be important to include in the future. Additionally, maternal satisfaction with genetic counseling and emotional needs of mothers in response to genetic counseling were not assessed in the current study. Based on recent estimates which suggest that approximately one-third of

counseless have some level of unmet need for psychosocial services in relation to genetic counseling (Cappelli et al. 2009; Douma et al. 2010), understanding whether emotional needs are fulfilled in the context of genetic counseling is a crucial step forward in measuring psychosocial adaptation to BRCA1/2 eligibility. This is especially salient given the contemporary literature in this area which has demonstrated that counselees who perceived their needs to be fulfilled in the genetic counseling process, demonstrate significantly higher perceived personal control and the significantly lower their anxiety ratings following counseling (Pieterse et al., 2011). Of note, unmet emotional needs following genetic counseling have also been shown to impact of family functioning (e.g., McDaniel et al. 2006), providing further evidence of the utility of a scale designed to capture these needs.

Retrospective reports. With respect to the issue of measurement, the current study also used retrospective ratings of mothers' *fear representations* (i.e., fear of breast cancer). Accordingly, these ratings are self-reports of mothers' remembered breast cancer fear at the time of their genetic counseling and may be prone to error or bias. Recall bias constitutes a significant threat to internal validity of studies that include self-report data. Recall bias arises when there is intentional or unintentional differential reporting of information and, if this type of bias is sufficient, there is the propensity for it to depart the estimated measure of effect size either toward or away from the null hypotheses (Hassan, 2005). Recall of information in this study was largely dependent on autobiographical memory. Given the evidence suggesting that 20% of critical details of a life event are irretrievable after 1 year and almost 50% are irretrievable after 5 years, recall bias poses a significant threat to the internal validity of this study (Bradburn, Rips,

Shevell, 1987; Green, 2006). Unfortunately, due a large number of missing cases in the data on the self-report variable “time since genetic counseling” (i.e., 26%), time could not be controlled for within the main analyses. In an effort to address this, box plots using time as a control for available cases (i.e., 50 participants) were constructed and appear in Appendix H. Review of these box plots indicated that mean score for maternal *fear representation* for participants who received genetic counseling between 2 and 5 years ago was quite similar to mean *fear representation* of those who received genetic counseling 2 years ago or less.

Despite the consistency in fear representation scores across the two groups, greater variability was noted in the distribution in the group who received genetic counseling between 2 and 5 years ago. This variability may be due to information recall bias or possibly confounding recall bias, owing to other events that have happened since the index genetic counseling session which have the potential to contribute to evaluation of fear of breast cancer (Hassan, 2005). For example, such events may include a diagnosis of breast cancer, health communication with family members, familial difficulties, death or illness (particularly breast cancer) in the elementary or extended family, and/or knowledge of kindred screening results. Importantly, these events were not controlled for in the analyses. Of the confounders noted above, the most relevant for this study and mothers’ ratings of *fear representation* is likely to be maternal breast cancer diagnosis occurring since the time of genetic counseling. Although this confounder was not explicitly controlled for in the current study, efforts were made via study eligibility criteria to address this particular confounder. More specifically, during recruitment, women diagnosed with breast cancer and who were awaiting or undergoing treatment were excluded from participating

in the study because previous research demonstrated that these women differed significantly from women who are who are in partial or full remission (Lerman et al., 1996).

Lack of a control group. While it could be argued that our sample did not include a control group, other studies in this domain have applied eligibility for BRCA1/2 screening among counselees' as an independent variable, thereby creating a control group of ineligible BRCA1/2 counselees (e.g., Meiser et al., 2002). Given the limited study on this group, investigators constructed a study design to specifically assess eligibility as a control measure (along with breast cancer history and fear). Certainly, the study could have been improved by including a control groups of mothers and daughters who have not participated in BRCA1/2 counseling and were not considered high-risk for breast cancer (e.g., no personal or family history) but this was not part of the original study design or the Canadian Institutes of Health Research funded grant. Accordingly, the source funding obtained for this study was intended to be directed toward the study high-risk, vulnerable BRCA1/2 counselees. The inclusion of a control group, however, is an important consideration for future research in this area.

Experimenter Effects. There may have been possible experimenter effects concerning mothers' potentially being prompted to disclose risk status or illness history to daughters as a result of their study participation in the current study. Measures were taken during recruitment to help manage possible effects. More specifically the following steps were taken: (a) during recruitment, the research assistant explained to mothers that investigators would not be disclosing any information related to mothers' illness, risk, or participation in genetic counseling; (b) The recruiter did note, however, that daughters would be informed that they were being asked

to participate as a result of the history of breast cancer in their extended families; (c) mothers were asked to invite participation of their daughters and; (d) Mothers and daughters were asked by the recruiter to complete their questionnaires privately. While efforts were made to reduce possible experimenter effects, it is certainly possible that mothers and daughters discussed the study and that, perhaps, new conversations may have been generated and which are uncontrolled for in the present analyses.

Impact of ethical considerations. Although a prospective study design would have been preferable and is specifically recommended for this type of research (e.g., Meiser et al., 2005; Hamilton et al., 2009), constraints existed which rendered such a design unfeasible in the current setting. Due to the fact that this study was not couched in the standard care and health service delivery of the genetic department at the participating tertiary care centre, the study protocol was subject to more stringent guidelines and restrictions. In particular, abstraction from medical charts was limited and significant limitations were placed around issues of health communication. This was done in an effort to protect the personal health information of participating mothers and daughters. In designing future studies at this centre, an enhanced collaboration with partners in the genetics department as well as prospective study designs are recommended. This recommendation aligns with guideline proposed by Khoury et al. (2011), which specify that integrative approaches to the assessment of the psychosocial impact of BRCA1/2 screening represent an important step in the field of translational genomics.

As described in the literature on minors and psychosocial genetics, many IRBs and REBs take a precautionary approach when considering research protocols involving psychosocial

genetics, particularly when minors are being studied (e.g., Tercyk et al., 2011). In large part, the hesitation to grant ethics approvals for such research projects is informed by some of the extant literature in the field as well as clinical guidelines published by a number of professional agencies that have made particular suppositions about how genetic screening for BRCA1/2 may influence intrapersonal psychosocial functioning of minors as well as their interpersonal relationships. This study was designed and approved at a time when there was less research available documenting the impact of BRCA1/2 disclosure on youth. Additionally, in the interest of protecting high-risk, vulnerable patients, the REB at the participating tertiary care centre approved the study protocol on the basis that mothers' health history, participation in BRCA1/2 counseling, and matters related to BRCA1/2 disclosure would not be directly addressed with mothers or their daughters. Notably, questions pertaining to mothers' breast cancer history as well as daughters' awareness and mothers' disclosure of participation in genetic counseling could not be included in this study. As a result, the research protocol that was followed has limited this study's findings to some degree. However, the results regarding the psychosocial adaptation of youth in this study are quite promising in that psychosocial functioning of this study population is comparable to community populations studied previously by our group (e.g., Cappelli et al., 2001; Cappelli et al., 2005). Importantly, the results of this investigation can be applied in future REB applications as rationale for the broader inclusion of youth as well as questions related to health communication in studies of families undergoing genetic counseling.

Implications, Interventions and Future Directions

Despite the limitations of the present study, this research provides the first conceptually

guided examination of subjective-emotional information as articulated in the adapted CSM for genetics. This study is unique in its use of the CSM (Marteau & Weinman, 2006) as a theoretical framework for comprehending how BRCA1/2 counselees' threat representations and fear representations might affect the psychosocial functioning of patients and their adolescent daughters. This dissertation addressed significant gaps in the conceptualization of the CSM and uniquely added to model development through its specific focus on associations between fear representation (i.e., the subjective-emotional information) and psychosocial functioning. From a theoretical perspective, this view of fear representation (i.e., subjective-emotional information) as an important factor in predicting psychological distress is consistent with recent models of psychological vulnerability that have suggested that understanding the psychological meaning of events is central to predicting psychological outcomes (e.g., as cited in Beausoleil, 2012; Reis et al., 2000). Findings from this study provide preliminary support for the theorized role of subjective-emotional information in predicting BRCA1/2 counselees' psychosocial functioning with respect to depressive symptoms, anxiety and intrusive ideation as well as daughters' depressive symptoms and self-reported self-concept.

By identifying fear representation as an important predictor of mothers' and daughters' psychosocial functioning, this study has provided support for CSM and has the potential to contribute to screening instruments and interventions that are being developed according to this model (e.g., Beyamini, 2009; Wearden & Peters, 2008; McAndrew et al., 2008, Gooding et al., 2006). Further research is required to determine whether findings from this study, regarding the role of fear representation in BRCA1/2 screening, will be replicated in larger, more diverse

populations and whether they will generalize to other AOHDs. Such research may contribute greatly to the health service delivery and practice in the area of genetics by informing assessment and clinical intervention.

Although psychosocial models have long been recognized for their importance in helping to direct patient care in genetic counseling services, standard care in many settings applies a largely biomedical-oriented approach (Cappelli et al. 2009; Pieterse et al., 2011). This approach is problematic when one considers the overall findings of the literature on BRCA1/2 counselees which suggest that, oftentimes, psychological distress in BRCA1/2 counselees occurs at subclinical levels. As a result, distress in this population may only be observable when it reaches a crisis level and results in significant psychosocial impairments (e.g., conflict with family, severe depression). As genetic counseling and screening becomes increasingly accessible, it is important that psychosocial functioning is assessed as a compliment to the genetic counseling process so that emotional reactions which may hamper the integration of risk information and the adoption of preventive measures recommended following genetic counseling can be identified proactively (e.g., Esplen et al., 2013). While screening tools like Multidimensional Impact of Cancer Risk Assessment (Cella et al., 2002) and the Psychological Adaptation to Genetic Information Scale (Read et al., 2005), are helpful in identifying subclinical levels of distress, they are unable to predict psychosocial adaptation in advance of genetic screening. By contrast, the Genetic Psychosocial Risk Instrument (GPRI; Esplen et al., 2013) is designed to proactively identify individuals who are more psychologically vulnerable in order to assist health care providers in anticipating which patients may require additional supports and interventions.

The findings of the current study indicate that, while the majority of mother-daughter dyads cope well following BRCA1/2 counseling, integration of psychosocial or family-based support, may be beneficial for families of BRCA1/2 counsees, particularly those with higher fear representations (Werner-Lin 2008). As such, moving forward in the development of predictive psychosocial screening tools for BRCA1/2 counsees, investigators may wish to consider including items that address fear of breast cancer as part of predictive measures of psychosocial response to BRCA1/2 screening. Additionally, it is imperative that theoretical frameworks, such as the CSM, that are beginning drive assessment and intervention be expanded to integrate families, particularly offspring who may stand to benefit from their parents' risk estimate results (McDaniel et al. 2006).

At present, there are no established evidence-based practices for health professionals to use in providing feedback, recommendations, and interventions to families and to assist parents with the matter of disclosure of genetic risk for hereditary breast cancer to children. Moreover, confusion exists over whether children should be included in the counseling process at all (e.g., Bradbury et al., 2007). However, the available research suggests that parents are discussing their genetic counseling experiences with their children. For instance, it is estimated that between 50% and 63% of mothers share their BRCA1/2 test results with their minor-age children within one month of diagnosis (Tercyak et al 2001b; Tercyak et al., 2009). In general, results of studies assessing health communication of genetic results in families have revealed that family communication regarding BRCA1/2 status was associated with more open patterns of family communication, generally (e.g., Lapointe et al., 2011; Tercyak et al., 2001b; Tercyak et al., 2009,

Patenaude et al., 2012) and younger age in BRCA1/2 counselees (Farely et al., 2013).

Accordingly, the development of intervention tools for parents to support decision-making and family communication regarding BRCA1/2 mutations would be beneficial for providers and families. It is recommended that future studies in this area continue to explore the impact of BRCA1/2 counseling on families with the goal of producing relevant guidelines for communication of BRCA1/2 risk within young families.

While the majority of publicly funded genetics services in Canada are housed in pediatric centres, by and large, training models have focused on delivering health information to adults. Presently, there is a paucity of literature describing the impact of genetic screening on young people as well as an absence of evidence-based theoretical models of genetics practice to draw on specifically for adolescents (e.g., Callard, Williams & Skirton, 2012; Cohen, Stoleman, Walsh, Wasserman & Dolan, 2012). Additionally, research in this area has suggested that many genetic health professionals, are proficient in adult-based counseling theories and techniques but self-report a lack of knowledge regarding the developmental changes that occur during adolescence and specific counseling techniques and skills for working with young people (e.g., Gaff, Lynch & Spencer, 2006). As described by Wade and colleagues (2010) future research in genetics with families will require a knowledge of the web of social influences in the lives of young people. Certainly, additional research is also needed regarding how young people perceive risk information and the manner in which genetic health professionals communicate this information (e.g., Lipkus, 2010). Fortunately, developmental psychologists are uniquely positioned to play a pivotal role redevelopment of training and health service delivery of genetic

risk information as a result of their expertise in human growth throughout the lifespan and family systems. As described by Patenaude (2003), psychologists have unique skills that have been harnessed by other departments (e.g., oncology), to act as members of multidisciplinary teams providing consultation and treatment to “help children and parents cope with the results of genetic testing and may aid in family dissemination of genetic information and related emotional concern . . . when the findings acquire particular saliency because of developmental changes” (p. 135). Psychology, as a discipline, also brings a knowledge of evidence-based practice across the lifespan along with specific skills in program development and evaluation aimed at addressing whether interventions are successful in promoting better psychosocial adaptation amongst families.

Presently, there is limited study regarding adolescent interest in genetic screening for various conditions but two studies in the area of nicotine susceptibility have suggested that between 57% and 62% of adolescents are interested in learning of their genetic risk (Herbert, Walker, Scharff, Abraham, & Tercyak, 2010; Tercyak et al., 2007). Additionally, a study by Harel, Abuelo & Kazura, revealed that approximately 67% of female adolescents were interested in genetic screening for breast cancer (2003). Collating these findings with the evidence that adolescence has been: (a) identified as critical period of carcinogenic vulnerability within the life cycle (e.g. Maruti et al., 2005; Okasha et al., 2003; Warri et al., 2008; Wild et al., 2011) and (b) health and risk behaviours begin to develop during adolescence (e.g., Holmbeck et al., 2002; Mulye et al., 2009), there is a need to expand the study of adolescent perceptions and understanding of genetic risk for breast cancer (particularly in high risk families). As such,

offspring of BRCA1/2 counselees represent a critical group that is necessary to the study of explanatory and change models of health behaviour and development of appropriate interventions. The power of genomic medicine to mobilize preventative health care is perhaps most salient in high-risk groups of young people. Moving forward, it will be necessary to advance genetic services to develop a better understanding of how adolescents utilize personal risk information in the short and long term as they mature, as well as the manner in which genetic information impacts young people psychologically and socially throughout their development. Study of high-risk families represents an initial step toward this goal and improved population health.

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Appendix A: Ministry of Health and Long Term Care CriteriaMOHLTC Hereditary Breast and Ovarian Cancer Genetics Referral Guidelines

Based on Ontario Ministry of Health and Long Term Care guidelines, individuals with a personal or family history of cancer as described below may be eligible to be seen for genetic counselling:

1- Patients who have been diagnosed with cancer:*

- a. Serous ovarian cancer
- b. Breast cancer diagnosed ≤ 35
- c. Both breast and ovarian cancer
- d. Bilateral breast cancer
- e. Male breast cancer
- f. Breast or ovarian cancer + family history of breast or ovarian cancer
- g. Breast or ovarian cancer + Ashkenazi Jewish heritage
- h. Cancer(s) suggestive of a hereditary cancer syndrome
- i. Individuals with a known hereditary cancer syndrome (including mutations in the BRCA1 or BRCA2 genes)

*Patients can be offered urgent appointments if the results of their genetic testing may impact their treatment plan

2- Patients who have not been diagnosed with cancer:

- a. Relatives of individuals with a known hereditary cancer syndrome (this includes relatives with a known BRCA1/2 mutation)
- b. Individuals with a family history of cancer as indicated through the categories above (1a-1h)

Testing for Affected Individuals with Breast or Ovarian Cancer May Be Offered in the Following Cases:*1. At least one case of cancer:*

- a. Ashkenazi Jewish and breast cancer <50 years, or ovarian cancer at any age.
Note: testing limited to ethnic specific mutations, unless other criteria given in this list are met.
- b. Breast cancer <35 years of age.

- c. Male breast cancer.
- d. Invasive serous ovarian cancer at any age.

II. At least 2 cases of cancer on the same side of the family:

- e. Breast cancer <60 years, and a first or second-degree relative with ovarian cancer or male breast cancer.
- f. Breast and ovarian cancer in the same individual, or bilateral breast cancer with the first case <50 years.
- g. Two cases of breast cancer, both <50 years, in first or second-degree relatives.
- h. Two cases of ovarian cancer, any age, in first or second-degree relatives.
- i. Ashkenazi Jewish and breast cancer at any age, and any family history of breast or ovarian cancer. Note: testing limited to ethnic specific mutations, unless other criteria given in this list are met.

At least 3 cases of cancer on the same side of the family:

- j. Three or more cases of breast or ovarian cancer at any age.

2. Testing for Unaffected Individuals (this should be done only if affected individuals are unavailable e.g. deceased)

- a. Relative of individual with known BRCA1 or BRCA2 mutation. Note: specific family mutation only tested.
- b. Ashkenazi Jewish and first or second-degree relative of individual with: breast cancer <50 years, or ovarian cancer at any age, or male breast cancer, or breast cancer at any age, with positive family history of breast or ovarian cancer. Note: testing limited to ethnic specific mutations, unless other criteria are met.
- c. A pedigree strongly suggestive of hereditary breast/ovarian cancer, i.e. risk of carrying a mutation for the individual being tested is >10%.

Retrieved May 03, 2014 from:

<http://www.theprincessmargaret.ca/en/PatientsFamilies/ClinicsAndCentres/FamilialBreastOvarianCancerClinic/Documents/Genetic%20Counselling%20Eligibility%20Criteria.pdf>

Appendix B: Information Letter to Families

Dear Participant Family,

You are receiving this letter because approximately two weeks ago you had a telephone conversation with Claire Goldsmith, a genetics counsellor at the Children's Hospital of Eastern Ontario (CHEO). During that conversation Ms. Goldsmith described a research study that is being conducted at CHEO. This study, titled "The interaction of genetic information and breast cancer in the family: Impact on adolescent daughters' emotional, social, and family functioning" is being held at the Mental Health Research unit of the Children's Hospital of Eastern Ontario (CHEO). This research is being conducted by Dr. Mario Cappelli and is sponsored by the Canadian Institutes of Health Research. If you have any questions about the study at any point you are invited to direct them to a member of the research team or to Dr. Cappelli. He may be reached at (XXXX).

Your family is being invited to join this study because you have been assessed by the genetics clinic at CHEO for the gene alterations associated with breast cancer, you currently have a male partner, and at least one adolescent daughter. The purpose of this study is to better understand the impact on families of genetic counselling. Specifically, we are inviting women who have undergone the genetic testing for the "breast cancer gene" as well as their daughters and husbands to participate in an interview about their experience. We will be asking families a series of questions on family risk, how families cope with genetic information, and any concerns they may have. Women who have been found to carry the breast cancer gene will be compared to others who were found not to carry the gene and others for whom the results were not conclusive. We are asking these types of questions because we suspect that families cope differently with the experience of having a loved one go through genetic counselling. Our hope is that this information will help us understand how families cope with genetic information and if families have specific needs that need to be addressed.

Approximately 150 families will be participating in this study. This study will take about 2 hours of your family's time. All members of your family will be asked to participate in a session at our research facility on the CHEO campus. During this session, mothers, fathers, and daughters will complete a number of questionnaires which will assess how families are cope with risk information, family communication, and any concerns or difficulties they may have. In addition, mothers and daughters will also be asked to participate in a short interview where they will be asked 5 questions about decision making, breast cancer, and coping.

There are some important points for you to consider before you decide to participate and the research team has included the consent forms for participation in the study in this package. These forms give you information about important topics like confidentiality and the protection of you information. At this time, it is important to note that the researchers will not share the results of your genetic screening with any members of your family. Please read through the consent forms and if you have any questions you are encouraged to ask a member of the research team. We encourage you to discuss this study with your family to see if they are also willing to participate.

In approximately one week, a member of the research team will telephone you to find out if you are still interested in participating in the study. During this conversation, the research assistant will also make sure you are still eligible to participate and will confirm that you are currently married to a male partner and have an adolescent daughter living in your home. If you are still interested in participating, the research assistant will arrange an interview time with you and your family. This conversation will be a good opportunity to ask any questions you may have about the study itself. This study has been approved by the CHEO Research Ethics Board. This board is a committee of the hospital that includes individuals from different professional backgrounds. The Board reviews all research that takes place at the hospital. Its goal is to ensure the protection of the rights and welfare of people participating in research. The Board's work is not intended to replace a parent or child's judgment about what decisions and choices are best for them. You may contact the Chair of the Research Ethics Board, for information regarding patient's rights in research studies at (XXXX), although this person cannot provide any health-related information about the study.

Sincerely,

Dr. Mario Cappelli

Appendix C: Mother Consent Form

Dear Participant,

You are being asked to participate in this research study titled “The interaction of genetic information and breast cancer in the family: Impact on adolescent daughters’ emotional, social, and family functioning” along with other members of your family being held at the Mental Health Research unit of the Children’s Hospital of Eastern Ontario (CHEO). This research is being conducted by Dr. Mario Cappelli and is sponsored by the Canadian Institutes of Health Research. If you have any questions about the study at any point you are invited to direct them to a member of the research team or to Dr. Cappelli. He may be reached at (XXXX).

You are being invited to join this study because you have been assessed by the genetics clinic at CHEO for the gene alterations associated with breast cancer. The purpose of this study is to better understand the impact on families of genetic counselling. Specifically, we are inviting women who have undergone the genetic testing for the “breast cancer gene” as well as their daughters and husbands to participate in an interview about their experience. We will be asking families a series of questions on family risk, how families cope with genetic information, and any concerns they may have. Women who have been found to carry the breast cancer gene will be compared to others who were found not to carry the gene and others for whom the results were not conclusive. We are asking these types of questions because we suspect that families cope differently with the experience of having a loved one go through genetic counselling. Our hope is that this information will help us understand how families cope with genetic information and if families have specific needs that need to be addressed. There is a small risk that you may experience some undo anxiety discussing some of these personal matters. In the event that this occurs you may be offered supportive therapeutic services such as psychological counselling by the research team. These services are also available to you at your request.

Approximately 150 families will be participating in this study. This study will take about 2 hours of your time today.

There are some important points for you to consider before you decide to participate. Please read through the following list and if you have any questions you are encouraged to ask a member of the research team.

I understand that:

1. My personal information will be kept strictly confidential except as required or permitted by law.

2. I will not be identified in any publication or presentation of this study.
3. Any personal information about me that leaves the hospital will be coded so that I cannot be identified by name.
4. My decision to participate or not in this study will not affect the care I receive at CHEO.
5. I am free to withdraw from the study at any time and there will be no penalty to me, my child, or any other family member.
6. I will not be charged for any test or research procedure required for this study.
7. There is a small risk of a release of information from my research records. Health and research records have been used against patients and their families. For example, in Canada, insurance companies may deny insurance to patient's with a certain illness or those that have a genetic risk of disease. My hospital medical records cannot, however, be released unless required or permitted by law or if you sign a release of information. The researchers of this study will protect my research records so that my name, address and phone number will be kept private.
8. The researchers will not share your risk estimate result with any members of your family. Your risk estimate refers to the results of your genetic screening for the breast cancer.
9. Researchers will not share information about whether or not you were previously diagnosed with breast cancer with members of your family.
10. At my request, I can receive a copy of the study results at the end of the study.
11. I will be given a copy of this form to take with me.
12. I am not receiving any compensation or reimbursement related to my participation in the study.

The study data will be retained confidentially in a locked filing cabinet in the CHEO Research Institute, for a period of 5 years following the end of the study. At that time, the data will be destroyed. The only personnel who have access to the data are the Principal Investigator and the research study team. This study has been approved by the CHEO Research Ethics Board. This board is a committee of the hospital that includes individuals from different professional backgrounds. The Board reviews all research that takes place at the hospital. Its goal is to ensure the protection of the rights and welfare of people participating in research. The Board's work is not intended to replace a parent or child's judgment about what decisions and choices are best for them. You may contact the Chair of the Research Ethics Board, for information regarding patient's rights in research studies at (XXXX), although this person cannot provide any health-related information about the study.

By signing this form, you are consenting to participate in this study. You may withdraw from the study at any point by telling a member of the research team that you wish to withdraw.

Name (please print)

Signature

Date

Appendix D: Breast Cancer Fear Scale

Please read each statement carefully and rate your agreement based on your own fears about breast cancer *at the time of your genetic counseling for BRCA1/2*.

	Strongly Disagree	Disagree	Neutral	Agree	Strongly Agree
1. The thought of breast cancer scares me.	1	2	3	4	5
2. When I think about breast cancer, I feel nervous	1	2	3	4	5
3. When I think about breast cancer, I get upset	1	2	3	4	5
4. When I think about breast cancer, I get depressed	1	2	3	4	5
5. When I think about breast cancer, I get jittery	1	2	3	4	5
6. When I think about breast cancer, my heart beats faster	1	2	3	4	5
7. When I think about breast cancer, I feel uneasy	1	2	3	4	5
8. When I think about breast cancer, I feel anxious	1	2	3	4	5

**Appendix E: Center for Epidemiologic Studies Depression Scale
(CES-D; Radloff, 1977)**

Below is a list of the ways you might have felt or behaved. Please tell me how often you have felt this way during the past week.

1. I was bothered by things that usually don't bother me.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

2. I did not feel like eating; my appetite was poor.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

3. I felt that I could not shake off the blues even with help from my family or friends.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

4. I felt that I was just as good as other people.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

5. I had trouble keeping my mind on what I was doing.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

6. I felt depressed.

- Rarely or none of the time (Less than 1 day)
- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

7. I felt that everything I did was an effort.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

8. I felt hopeful about the future.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

9. I thought my life had been a failure.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

10. I felt fearful.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

11. My sleep was restless.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

12. I was happy.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

_____ Occasionally or a moderate amount of time (3-4 days)

_____ Most or all of the time (5-7 days)

13. I talked less than usual.

_____ Rarely or none of the time (Less than 1 day)

_____ Some or a little of the time (1-2 days)

- _____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

14. I felt lonely.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

15. People were unfriendly.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

16. I enjoyed life.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

17. I had crying spells.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

18. I felt sad.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

19. I felt that people dislike me.

- _____ Rarely or none of the time (Less than 1 day)
_____ Some or a little of the time (1-2 days)
_____ Occasionally or a moderate amount of time (3-4 days)
_____ Most or all of the time (5-7 days)

20. I could not get "going."

- _____ Rarely or none of the time (Less than 1 day)

- Some or a little of the time (1-2 days)
- Occasionally or a moderate amount of time (3-4 days)
- Most or all of the time (5-7 days)

Appendix F: The Impact of Event Scale (Horowitz, 1979)

Below is a list of difficulties people sometimes have after stressful life events. Please read each item, and then indicate how distressing each difficulty has been for you **DURING THE PAST SEVEN DAYS** with respect to your **GENETIC COUNSELING EXPERIENCE**. How much were you distressed or bothered by these difficulties?

	Not at all	A little bit	Moderately	Quite a bit	Extremely
1. Any reminder brought back feelings about it	0	1	2	3	4
2. I had trouble staying asleep	0	1	2	3	4
3. Other things kept making me think about it	0	1	2	3	4
4. I felt irritable and angry	0	1	2	3	4
5. I avoided letting myself get upset when I thought about it or was reminded of it	0	1	2	3	4
6. I thought about it when I didn't mean to	0	1	2	3	4
7. I felt as if it hadn't happened or wasn't real	0	1	2	3	4
8. I stayed away from reminders about it	0	1	2	3	4
9. Pictures about it popped into my mind	0	1	2	3	4
10. I was jumpy and easily startled	0	1	2	3	4

	Not at all	A little bit	Moderately	Quite a bit	Extremely
11. I tried not to think about it	0	1	2	3	4
12. I was aware that I still had a lot of feelings about it, but I didn't deal with them	0	1	2	3	4
13. My feelings about it were kind of numb	0	1	2	3	4
14. I found myself acting or feeling as though I was back at that time	0	1	2	3	4
15. I had trouble falling asleep	0	1	2	3	4

Appendix G: Child Assent

Dear Participant,

You are being asked to participate in a research study with some other members of your family. This research is being held at the Mental Health Research unit of the Children's Hospital of Eastern Ontario (CHEO). This research is being conducted by Dr. Mario Cappelli and is sponsored by the Canadian Institutes of Health Research. If you have any questions about the study at any point you can talk to a member of the research team or to Dr. Cappelli. Dr. Cappelli isn't here today but you can call him. His number is 613-737-7600 (3311).

You are being asked to join this study to find out more about your thoughts and feelings about breast cancer. The purpose of this study is to find out more about your opinions about breast cancer since there is a history of this illness in your family. This study will help us understand how teenagers like you feel about breast cancer and its impact on them and their families. Knowing your opinions and feelings is important because this will help researchers understand how having a family history of breast cancer might impact kids. In addition, the information you provide will help us learn more about what kinds of information teens have about breast cancer and what information they might like to have.

There is a small risk that you may experience some worries when you are discussing some of this personal information. If this happens you may be offered supportive counseling services by the research team. If you feel upset, worried, or would just like to talk more about your thoughts and feelings about breast cancer, counseling services are available. You can ask the researcher working with you today about these services.

About 150 other families will be participating in this study. This study will take about 2 hours of your time today.

There are some important things for you to think about before you decide to participate. Please read the list below. If you have any questions about the list please feel free to ask the researcher working with you today about it.

I understand that:

1. My personal information will be kept private and will not be shared unless the law says the researchers have to share it.
2. My name and personal information will not appear in this study if the study is published or presented anywhere.
3. Any personal information about me that leaves the hospital will have a special code so that no one can identify me by name.
4. My decision to participate or not in this study will not affect the care I receive at CHEO.
5. The researchers will give me 30 dollars for helping with the study.
6. I am allowed to stop participating in the study at any time and I will still receive the 30 dollars for helping out with the study.
7. If I decide not to participate I will not receive a penalty.
8. If I decide not to participate my parents will not receive any penalties
9. I will not have to pay for any test in this study.
10. If I ask for a copy of the study results, the researchers will give me a copy at the end of the study.
11. I will be given a copy of this form to take with me.

This study has been approved by the CHEO Research Ethics Board. This board is a committee of the hospital that includes individuals from different professional backgrounds. The Board reviews all research that takes place at the hospital. Its goal is to ensure the protection of the rights and welfare of people participating in research. The Board's work is not intended to replace a parent or child's judgment about what decisions and choices are best for them. You may contact the Chair of the Research Ethics Board, for information regarding patient's rights in research studies at (613) 737-7600 (3272), although this person cannot provide any health-related information about the study.

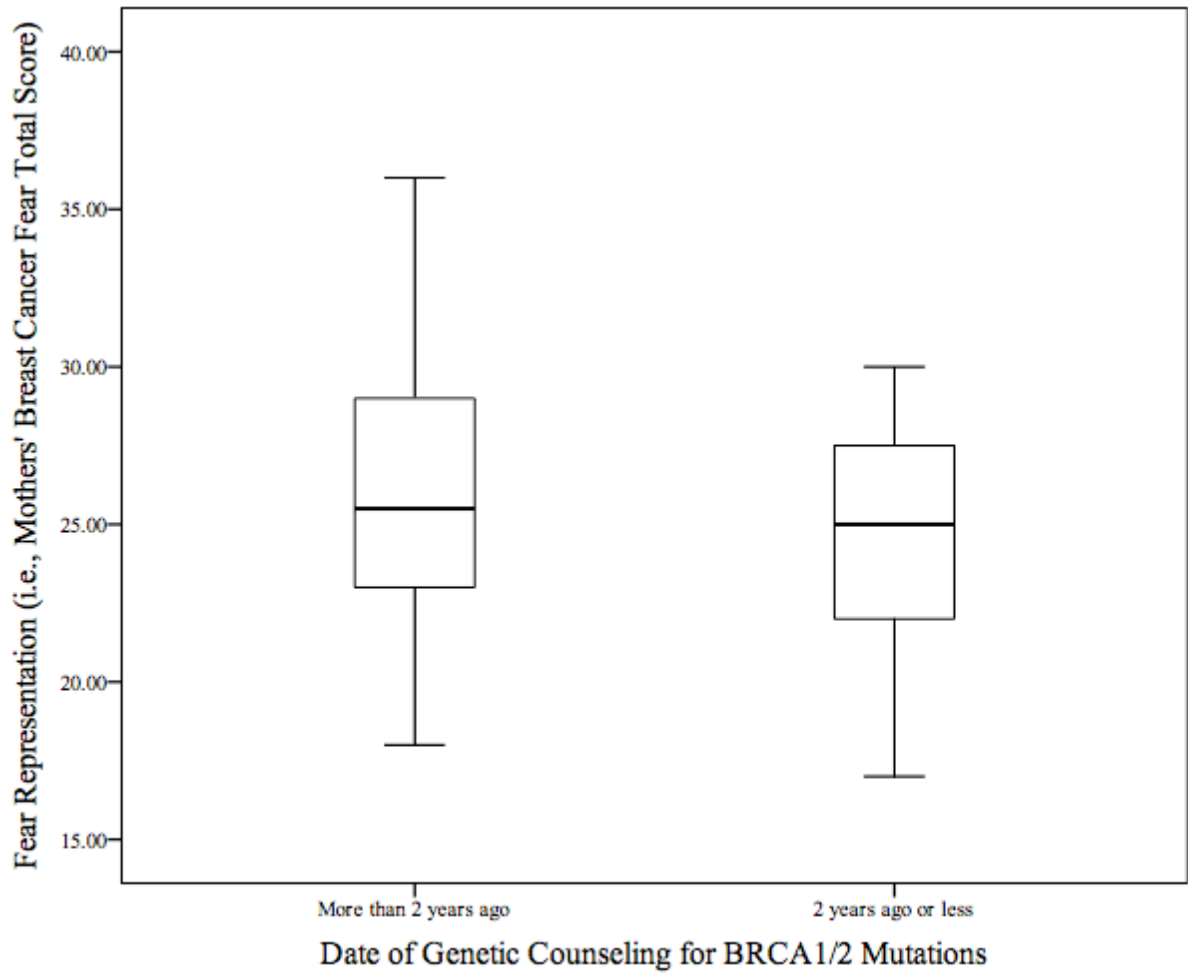
By signing this form, you are agreeing to participate in this study. You may decide to stop participating in the study at any point by telling a member of the research team that you wish to withdraw.

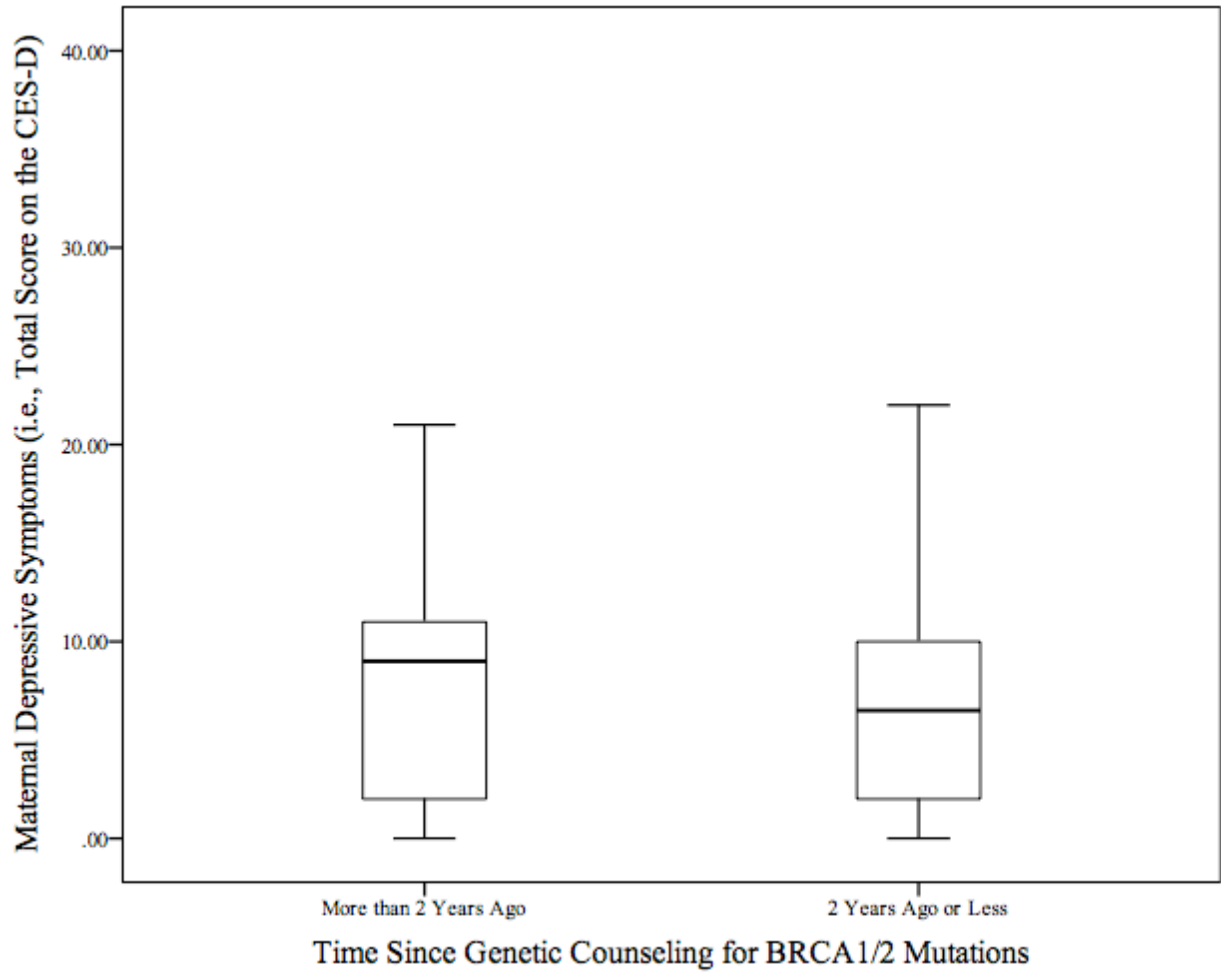
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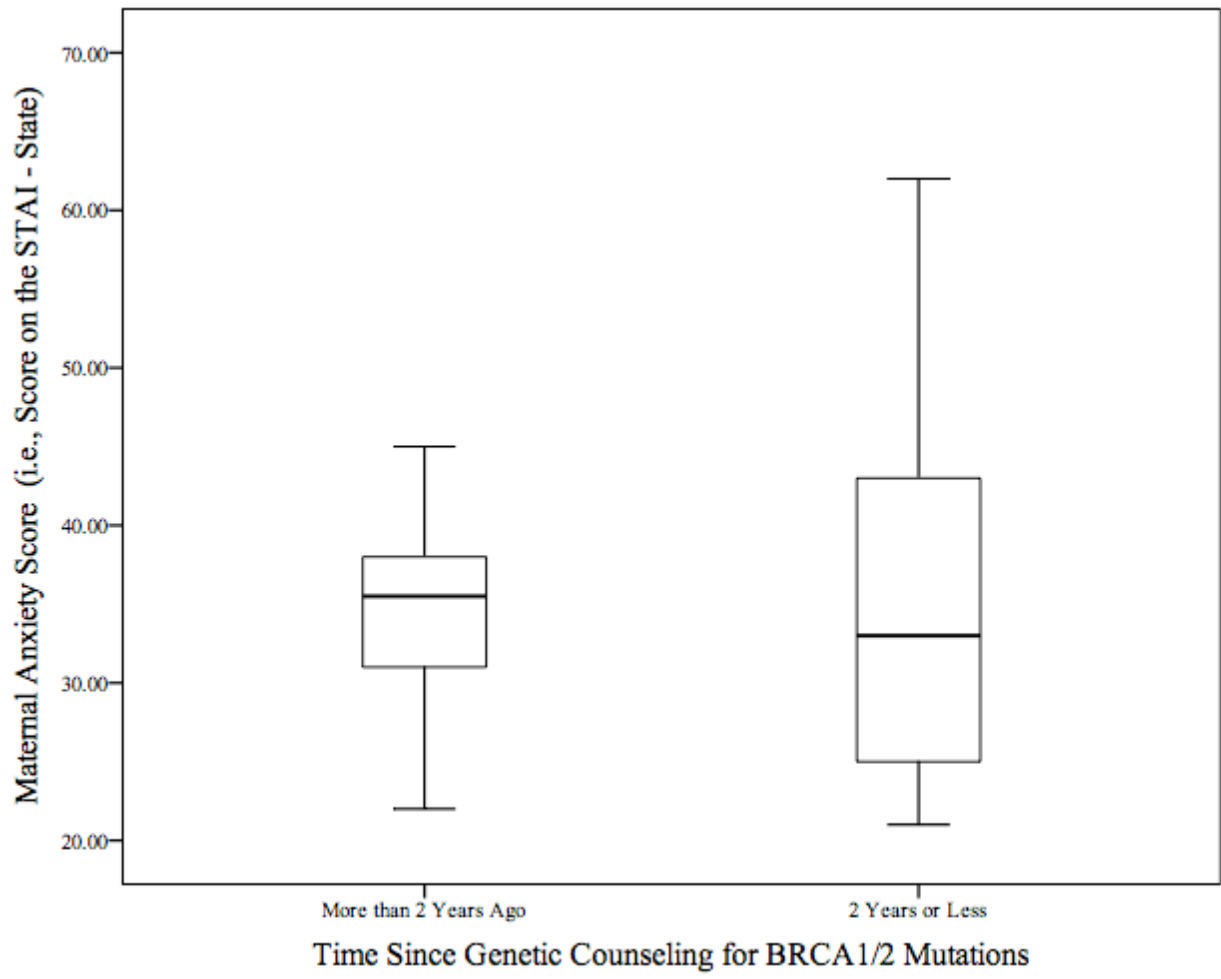
Signature

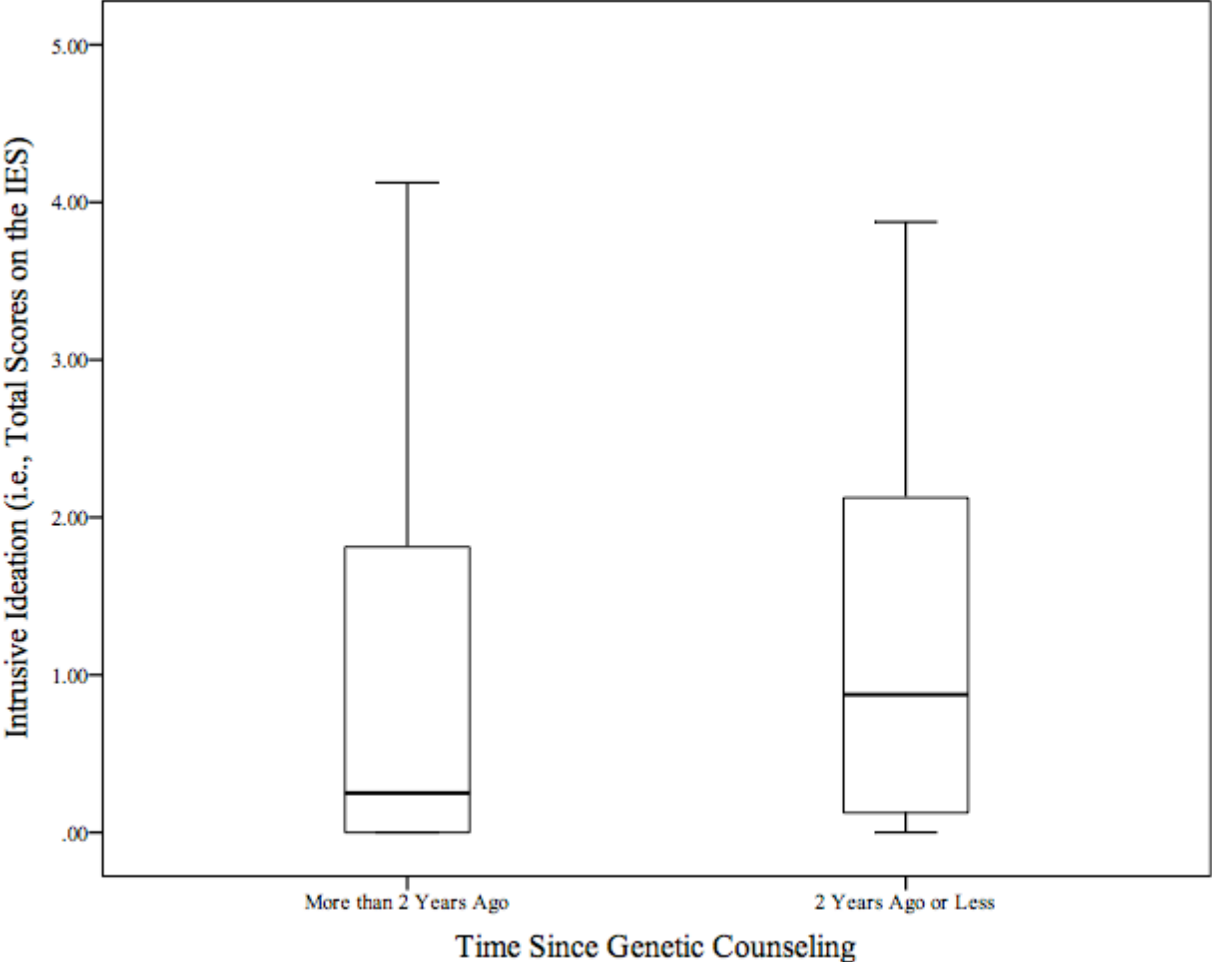
Date

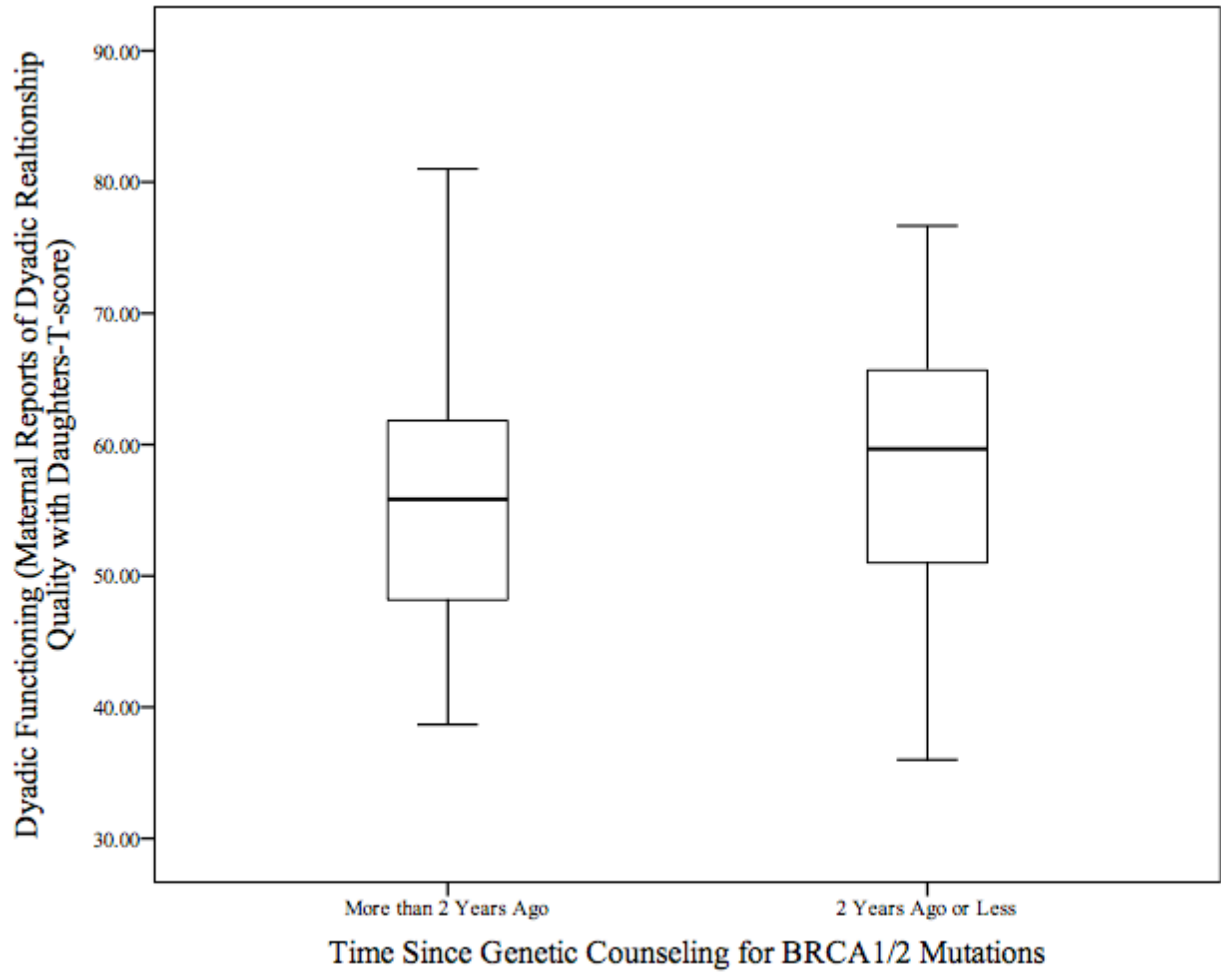
Appendix H: Box Plots For Length of Time Since Genetic Counseling



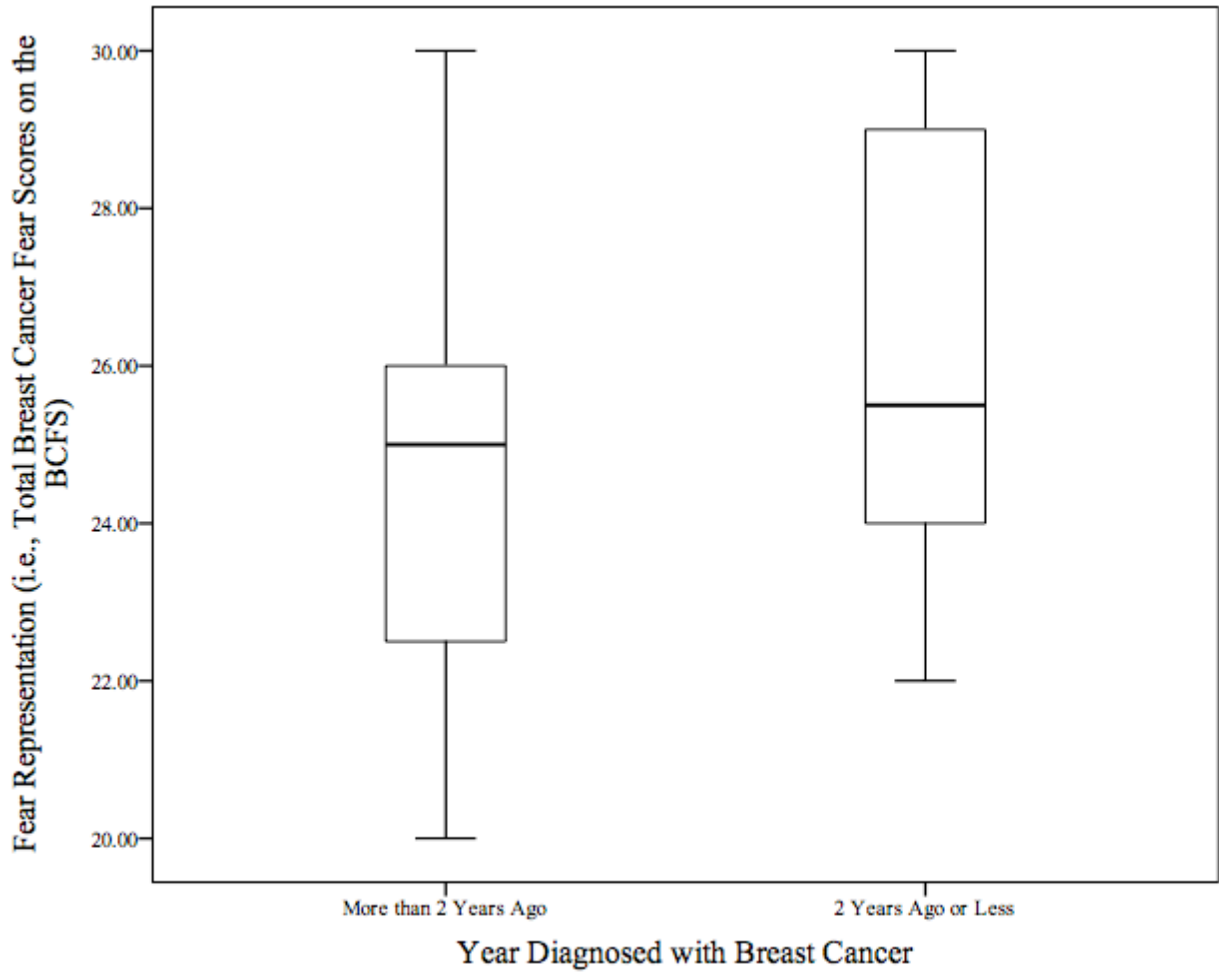


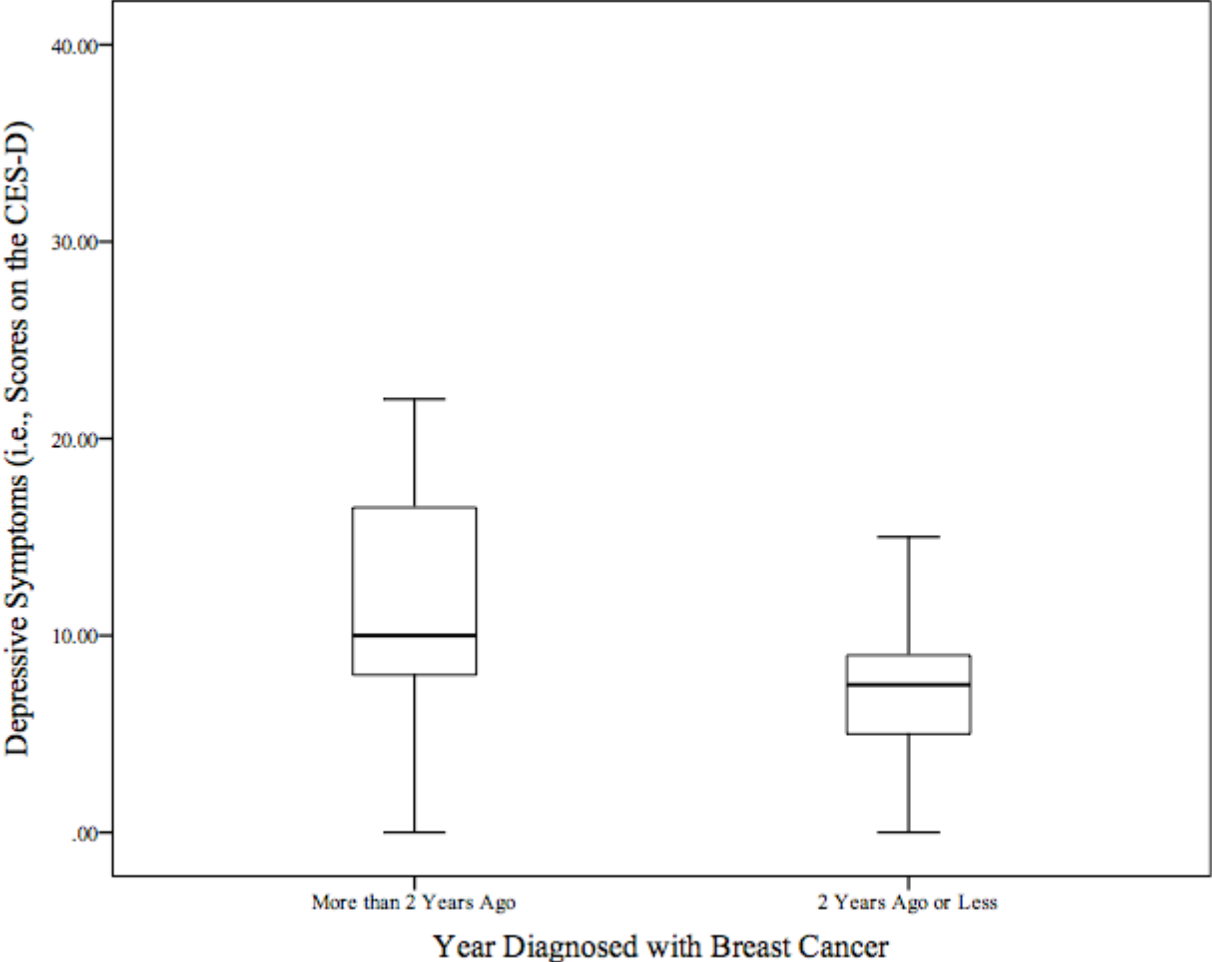


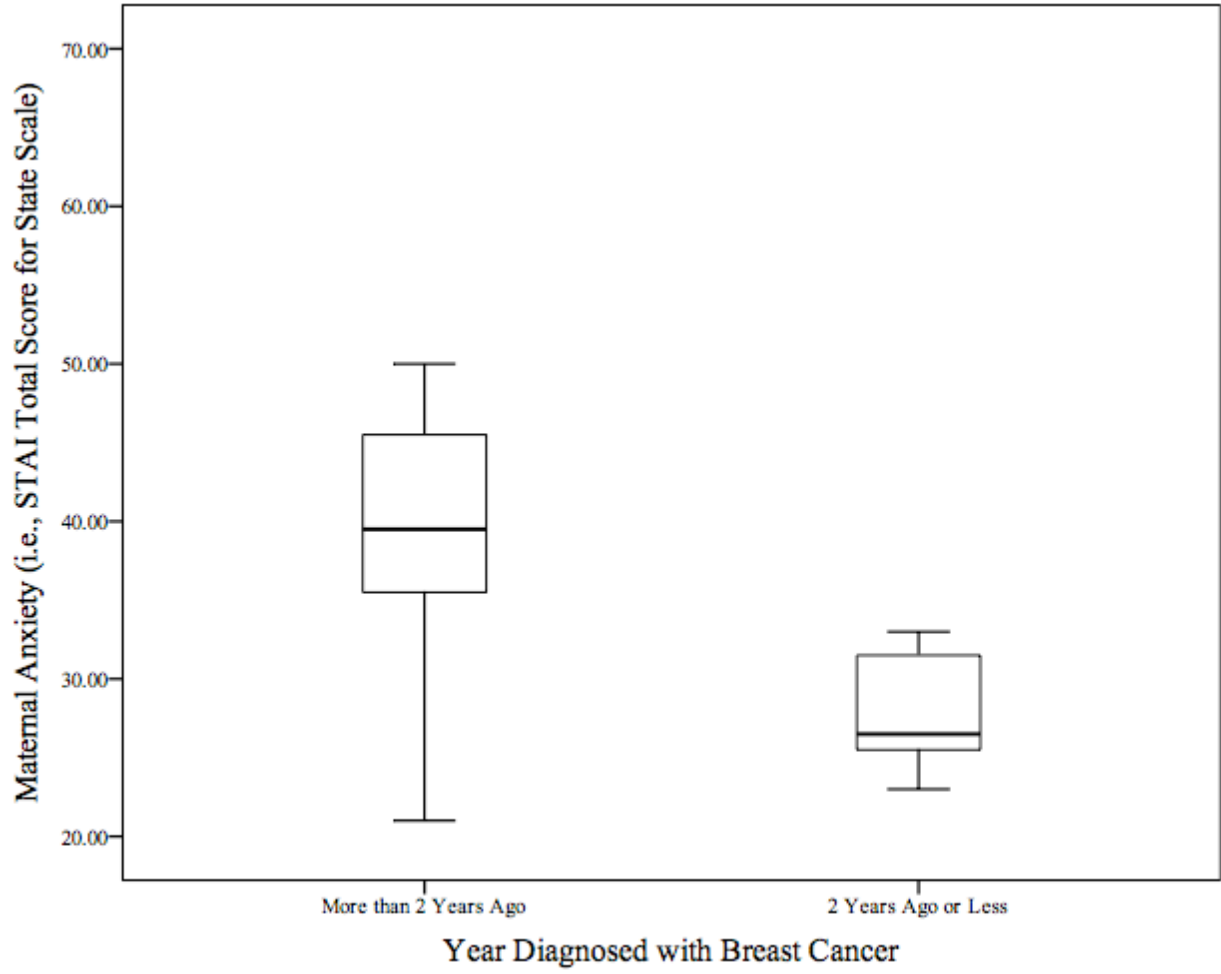


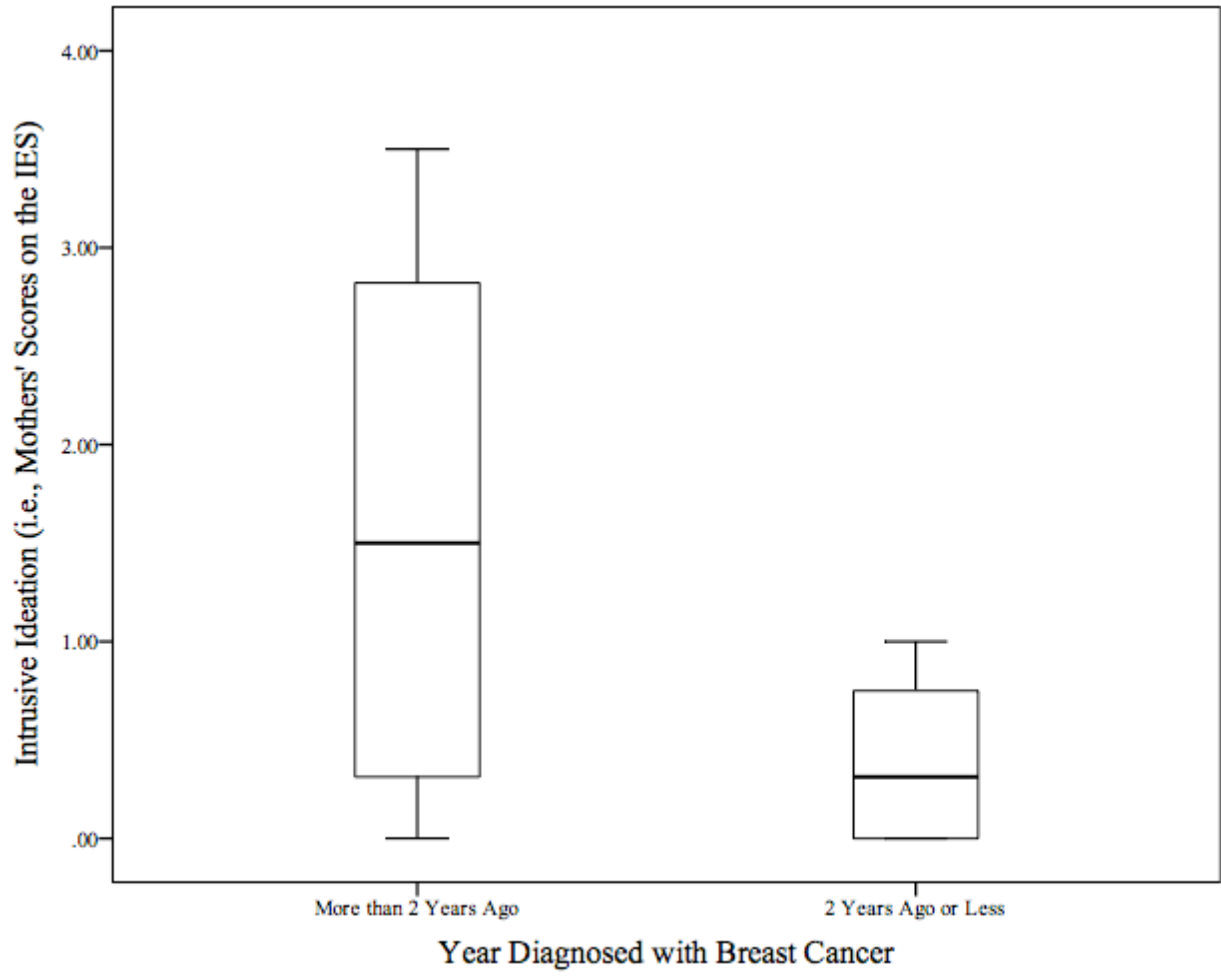


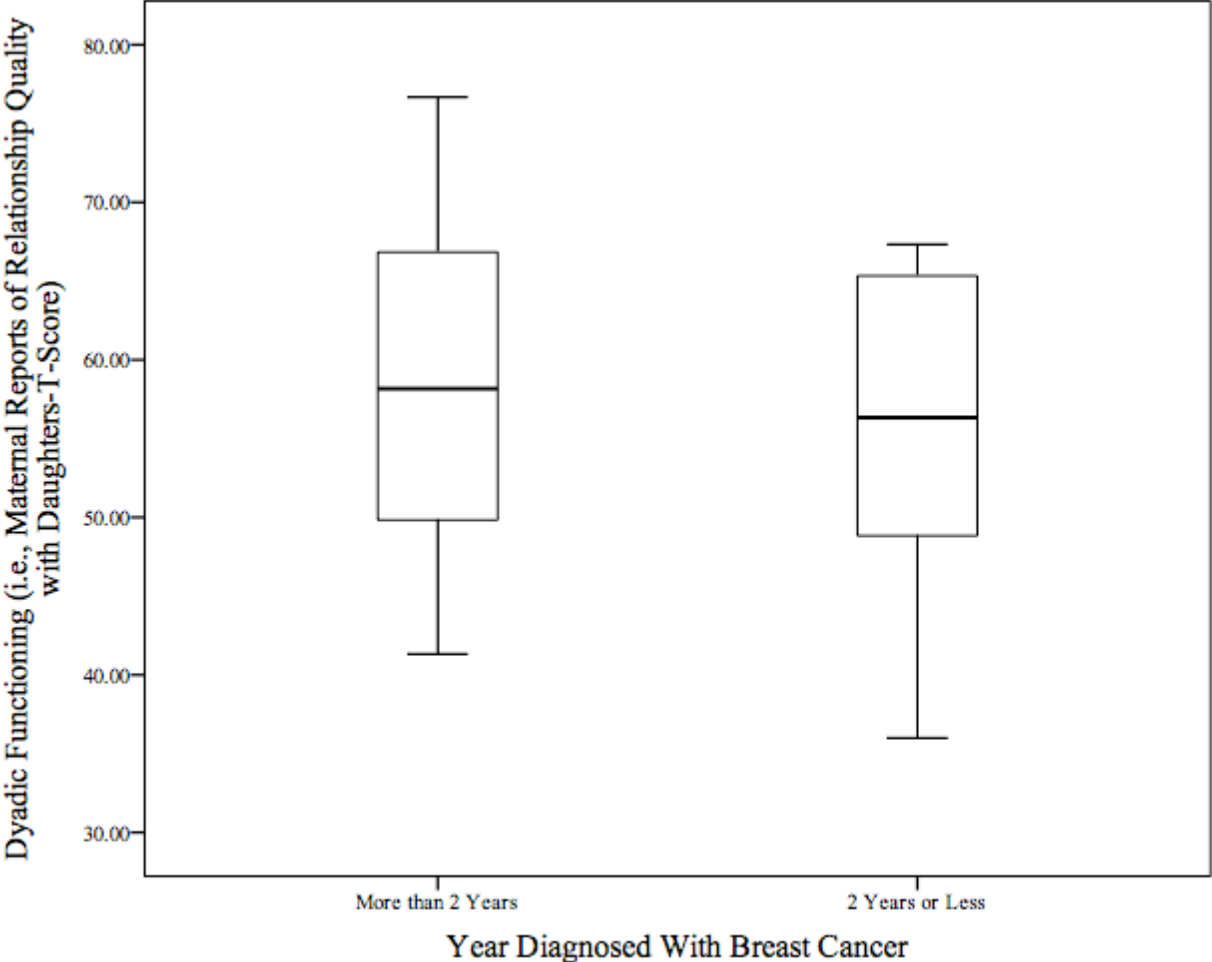
Appendix I: Box Plots for Time Since Breast Cancer Diagnosis











Appendix J: Transformed Analyses

Standard Multiple Regression Analysis Predicting Maternal Depressive Symptoms Scores From Risk Representation, Illness Representation, Fear Representation – Transformed Depressive Symptoms Scores

IV	<i>B</i>	SE <i>B</i>	β	<i>F</i> (3, 73)	<i>R</i> ²
Risk Representation	-.11	.15	-.12		
Illness Representation	.35	.15	.38*		
Fear Representation	.02	.01	.31**	4.94**	.17**

* $p < .05$, ** $p < .01$.

Standard Multiple Regression Analysis Predicting Maternal Anxiety Scores From Risk Representation, Illness Representation, Fear Representation (Breast Cancer Fear) – Transformed Maternal Anxiety Scores

IV	<i>B</i>	SE <i>B</i>	β	<i>F</i> (3, 73)	<i>R</i> ²
Risk Representation	-.05	.034	-.20		
Illness Representation	.06	.034	.24		
Fear Representation	.01	.00	.48***	8.66***	.26***

*** $p < .0001$.

Hierarchical Multiple Regression Analysis Predicting Maternal Depressive Symptoms from Risk Representation, Illness Representation, and Fear Representation – Transformed Depressive Symptoms Scores

IV	β	SE B	R	R ²	F	ΔR^2	ΔF	t
Step 1								
Risk Representation	-.08	.16						
Illness Representation	.33 ^a	.16	.28 ^a	.07 ^a	3.03 ^a	.08 ^a	3.92 ^a	2.00 ^a
Step 2								
Risk Representation	-.12	.15						
Illness Representation	.38 [*]	.15						2.33 [*]
Fear Representation	.31 ^{**}	.01	.41 ^{**}	.17 ^{**}	4.94 ^{**}	.09 ^{**}	8.17 ^{**}	2.86 ^{**}

^a $p < .06$, ^{*} $p < .05$, ^{**} $p < .01$.

Hierarchical Multiple Regression Analysis Predicting Maternal Anxiety from Risk Representation, Illness Representation, and Fear Representation - Transformed Anxiety Scores

IV	β	SEB	R	R ²	F	ΔR^2	ΔF	T
Step 1								
Risk Representation	-.21	.04						
Illness Representation	.23	.04	.17	.03	1.06	.03	1.06	1.41
Step 2								
Risk Representation	-.20	.03						
Illness Representation	.24	.03						
Fear Representation	.48 [*]	.00	.51 [*]	.26 [*]	8.66 [*]	.23 [*]	23.21 [*]	4.81 [*]

^{*} $p < .0001$.

Standard Multiple Regression Analysis Predicting Daughters' Anxiety Scores From Risk Representation, Illness Representation, Fear Representation – Transformed Anxiety Scores

IV	<i>B</i>	SE <i>B</i>	β	<i>F</i> (3, 95)	<i>R</i> ²
Risk Representation	-.01	.03	-.03		
Illness Representation	.02	.03	.09		
Fear Representation	.00	.00	.24*	2.09	.06

* *p* < .05

Hierarchical Multiple Regression Analysis Predicting Daughters' Anxiety from Mothers' Marital Status, Risk Representation, Illness Representation, and Fear Representation - Transformed Anxiety Scores

IV	β	SE <i>B</i>	<i>R</i>	<i>R</i> ²	<i>F</i>	ΔR^2	ΔF	<i>T</i>
Step 1								
Mothers' Marital Status	.22*	2.24	.22*	.05*	4.95*	.05*	4.95*	2.22*
Step 2								
Mothers' Marital Status	.22*	2.28						2.16*
Risk Representation	.02	2.85						
Illness Representation	.03	2.85	.22	.05	1.67	.00	.08	-.89
Step 03								
Mothers' Marital Status	.21*	2.26						2.18*
Risk Representation	.01	2.83						
	.05	2.84						

Illness Representation	.24*	.16	.33*	.11*	2.82*	.06*	5.97*	2.44*
Fear Representation								

* $p < .05$.