Epigenetic study of methylation changes in rat astrocytes caused by cellular phone exposure

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Background

There are many ways that gene expression is controlled in eukaryotes, but methylation of DNA is a common epigenetic signaling tool used to control gene expression. DNA methylation occurs at the cytosine bases of eukaryotic DNA.¹

![Figure 1: Shows the difference between methylated and unmethylated cytosines.](image)

The methylation of these sequences can lead to changes in the expression of genes, such as tumor suppressor genes in cancer cells.¹

![Figure 2: Shows the early effects of methylation on tumorigenesis and the development of cancer.](image)

In this study, the environmental factor is the device that is used daily by individuals in today’s society, cellular phones. Cell phones emit radiofrequency energy, a form of non-ionizing electromagnetic radiation, which can be absorbed by tissues closest to where the phone is held.² The amount of radiofrequency energy a cell phone user is exposed to depends on the technology of the phone.²

Research objective

The objective is to identify and analyze genes that are modified as a result of exposure to radiation from cellular phones and are associated with the disease development.

Methodology

Cell culture:

Rat astrocyte cells are maintained in DMEM growth media supplemented with 20% heat-inactivated FBS (v/v), 2 mM glutamine and 5 mL of antibiotic solution (streptomycin and penicillin) and incubated at 37°C and 5% CO₂. Growth media is changed every other day. Cell culture is grown until 80-85% confluency and then plated according to the protocol.

Time-dependent exposure:

Two controls were used as reference for the exposures. Control 1 consisted of 2 plates being placed in an incubator at 37°C and 5% CO₂ for 6 hours. Control 2 consisted of 2 plates being placed in the water bath warmed at 37°C for 6 hours.

Once the number of cell culture plates are confluent and cell count is sufficient, two plates are used to perform the time-dependent exposure. The two plates are placed into a water bath warmed at 37°C. A cellular phone is placed on top of the plate and put on call mode for 6 hours. The cell phone was on call mode with a frequency of 1700/2100 MHz. After 24 hrs, the cells were harvested.

DNA extraction:

Harvested cells were thawed and the DNA was extracted. The concentration of DNA and the 260/280 ratio was measured and recorded

Results

<table>
<thead>
<tr>
<th>Sample</th>
<th>DNA Concentration (ng/μl)</th>
<th>260/280 ratio</th>
<th>Volume (μl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control 1</td>
<td>1370.5</td>
<td>1.46</td>
<td>15.0</td>
</tr>
<tr>
<td>Control 1</td>
<td>1207.4</td>
<td>1.57</td>
<td>15.0</td>
</tr>
<tr>
<td>Control 2</td>
<td>1358.3</td>
<td>1.65</td>
<td>15.0</td>
</tr>
<tr>
<td>Control 2</td>
<td>1184.1</td>
<td>1.63</td>
<td>15.0</td>
</tr>
<tr>
<td>Exposure</td>
<td>1266.5</td>
<td>1.55</td>
<td>15.0</td>
</tr>
<tr>
<td>Exposure</td>
<td>1342.6</td>
<td>1.53</td>
<td>15.0</td>
</tr>
</tbody>
</table>

Note: Control 1 are plates placed in the incubator at 37°C and 5% CO₂; Control 2 are plates placed in the water bath at 37°C.

Future work

With the DNA concentrations recorded, the DNA samples will be methylated, bisulfite converted and bisulfite-methylated amplified. With the amplified DNA, the PCR protocol will be performed. Finally, DNA samples will be analyzed and referenced to the house-keeping gene to identify any differences.

Acknowledgement

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References: