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2013 REU Poster: Development of SERS-Based Metabolic Profiling Method for Leukemia Cells

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Boston University
Development of SERS-based metabolic profiling method for Leukemia Cells
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INTRODUCTION
Metabolic profiling, or the study of low molecular weight intermediates, as a result of activation of tumorigenesis pathways; has been found to be an important and successful measurement for the pathological state of cells, i.e. leukemia cell. SERS-based method provides us an alternative, ultra-sensitive label-free method to study the cancer cells metabolites. Abnormal metabolite molecules can be identified with comparison to the spectra of non-cancerous cells. The identity of these molecules can be confirmed by comparison with modeling compounds.

PROCEDURE
Using leukemia cells as model, the cells are grown from frozen culture to log phase in vitro before harvesting. Prior to undergo SERS, the cells are washed in a saline solution to avoid interference from possible SERS-active molecule present in the medium. In addition, to identify metabolites the cells secrets as a result of nutrients deprivation the SERS spectra is taken as a function of time. Due to the importance of time viability check of the cells are done at 0 minutes, 60 minutes, 120 minutes, and 180 minutes. The SERS-spectra of the leukemia cells are compared with non-cancerous cells, as well as modeling compounds for the purpose of identification. We hypothesize that the purine metabolism pathway could be responsible for the production of these metabolites, based on the spectra comparison.

<table>
<thead>
<tr>
<th>Time</th>
<th>Average dead</th>
<th>Average alive</th>
<th>Viability %</th>
</tr>
</thead>
<tbody>
<tr>
<td>60 minutes</td>
<td>5</td>
<td>34</td>
<td>84.25</td>
</tr>
<tr>
<td>120 minutes</td>
<td>14</td>
<td>53</td>
<td>78.52</td>
</tr>
<tr>
<td>180 minutes</td>
<td>7.5</td>
<td>15.25</td>
<td>32.97</td>
</tr>
</tbody>
</table>

FUTURE WORK
Future work may involve confirmation of the presence of Hypoxathine and NADH like molecule by using other techniques. In addition, identification of possible molecular target of diagnostic value, and application to other types of cancer cells.

RESULTS

REFERENCES