Results: Individual CNAs and somatic mutations may predict poor survival in rituximab treated patients with DLBCL by univariate analysis

This dataset of 59 DLBCL patients includes comprehensive molecular, COO, and clinical information. The median length of follow-up was 68 months (~5.7 years). Of this dataset, 17 were of the GC phenotype and 22 were of the ABC phenotype by IHC. Upon analysis, 37 CNAs and 73 genes with somatic mutations were identified. By univariate analysis, both R-PI and COO were not significantly associated with survival in patients treated with a rituximab based regimen. However, 3 CNAs (loss 1p10.35, 10q25.31 and loss 6q11.1-q27) and 4 somatic mutations (PM1, APC, P53, and KMT2D) demonstrated potentially significant (p<0.10) effect that may be associated with overall survival. CNAs and somatic mutations associated with survival and COO are presented in tables 1 and 2.

<table>
<thead>
<tr>
<th>Alteration</th>
<th>Hazard ratio</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loss of 10q25.31</td>
<td>0.38997</td>
<td>0.07141</td>
</tr>
<tr>
<td>Loss of 7q11.1</td>
<td>4.09349</td>
<td>0.07698</td>
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<tr>
<td>Gain of 10q25.3</td>
<td>0.57113</td>
<td>0.00191</td>
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<tr>
<td>Gain of 10q25.31</td>
<td>0.57486</td>
<td>0.00191</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Alteration</th>
<th>Associated with</th>
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</thead>
<tbody>
<tr>
<td>APC</td>
<td>0.90013</td>
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<tr>
<td>P53</td>
<td>0.57486</td>
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<tr>
<td>KMT2D</td>
<td>0.02492</td>
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</tbody>
</table>

Conclusions: Systematic analysis of DLBCLs using multiple immunohistochemical and molecular methods identified potential mutational and copy number biomarkers that may be predictive of survival in patients treated with a rituximab based regimen for DLBCL, as shown by univariate analysis. Multivariate analysis and data from additional cases will reveal whether these biomarkers can predict survival in patients independently of prognostic biomarkers currently in routine use (e.g. COO by Hans algorithm and R-PI).