A Century of Conservation Genetics of the African Lion (Panthera leo)

We determined the genetic architecture of both historical (>100 years ago; n=155) and contemporary (2000 to present; n=557) African lion populations across the traditional range states in Africa (Figure 1). Both datasets were analyzed using the same methods allowing for a more direct comparison over time than has previously been employed. The historical lion dataset is DNA isolated from high quality and well-documented museum specimens while the contemporary lion dataset is from modern material and data from several recently published studies. Combining the datasets of historical as well as contemporary populations provides quantitative measures on the extent of change in the genetic diversity of lions over the past 100 years and provides a basis for assessing the genetic health of the African lion.

Methods

Genetic diversity is examined using fourteen microsatellites with primers designed to be closer to the target region and specific to the lion (miniSTRs). Preliminary statistical analyses include determining the number of alleles per locus and calculation of expected heterozygosity (GenALEX), structural analysis (Structure) and determining the most likely number of clusters following the ΔK method (Structure Harvester).

Table 1

<table>
<thead>
<tr>
<th>Overall</th>
<th>Leo006</th>
<th>Leo008</th>
<th>Leo031</th>
<th>Leo045</th>
<th>Leo077</th>
<th>Leo085</th>
<th>Leo098</th>
<th>Leo126</th>
<th>Leo224</th>
<th>Leo230</th>
<th>Leo247</th>
<th>Leo281</th>
<th>Leo391</th>
<th>Leo506</th>
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</thead>
<tbody>
<tr>
<td>%AS</td>
<td>97.5%</td>
<td>98.1%</td>
<td>98.5%</td>
<td>92.5%</td>
<td>100.0%</td>
<td>98.5%</td>
<td>92.5%</td>
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<td>98.5%</td>
<td>92.5%</td>
<td>100.0%</td>
</tr>
<tr>
<td>N</td>
<td>455</td>
<td>476</td>
<td>470</td>
<td>405</td>
<td>410</td>
<td>441</td>
<td>499</td>
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<td>501</td>
<td>504</td>
<td>415</td>
<td>508</td>
<td>464</td>
<td>408</td>
</tr>
<tr>
<td>Na</td>
<td>12</td>
<td>20</td>
<td>8</td>
<td>8</td>
<td>11</td>
<td>9</td>
<td>12</td>
<td>9</td>
<td>16</td>
<td>10</td>
<td>13</td>
<td>10</td>
<td>16</td>
<td>10</td>
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<tr>
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<td>0.84</td>
<td>0.75</td>
<td>0.40</td>
<td>0.39</td>
<td>0.75</td>
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<td>0.82</td>
<td>0.82</td>
<td>0.72</td>
<td>0.74</td>
</tr>
</tbody>
</table>

Figure 1

All samples are categorized into 6 conventionally recognized regions:
- North
- West
- Central
- East
- Southeast
- Southern

Additional sample categories:
- India (African Lion – Panthera leo persico)
- Unknown (Historical Only – Data Provide, No Location)

Figure 2

The historical and modern populations both have high levels of overall genetic diversity (Table 1). They also exhibit similar trends in population structure (Figure 2). Heterozygosity by region (Figure 3) supports observations from recent studies of a precipitous decline in population size occurring in West and Central Africa.

Further analysis will include the addition of mtDNA haplotypes. A phylogeographic analysis will be performed along with estimation of effective population size (Ne) and calculation of genetic differentiation between regions (Fst).