SIGNATURES OF SELECTION IN THE IBERIAN HONEY BEE: A GENOME WIDE APPROACH USING SINGLE NYLUCOTIDE POLYMORPHISMS (SNPs)

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BACKGROUND

Detection of signatures of selection across genomes and identification of their role in adaptive population divergence is a central issue in evolutionary biology.

The Iberian Peninsula harbours the greatest honey bee genetic diversity and complexity in Europe. The challenge of deciphering the mechanisms underlying such complexity has led to numerous surveys of the Iberian honey bee (IHB). Yet, the evolutionary processes underlying patterns of IHB genetic diversity remain poorly understood.

With the sequencing of the honey bee genome and development of high density SNPs, the IHB genome can now be scrutinized for adaptive divergence. Herein, we show a preliminary exploration of a genome scan to detect signatures of selection on the Iberian honey bee genome.

GENOTYPING

All individuals were genotyped for a panel of 1536 SNP’s with high density SNPs, the IHB genome can now be scrutinized for adaptive divergence. Herein, we show a preliminary exploration of a genome scan to detect signatures of selection on the Iberian honey bee genome.

SNPS SUMMARY

Of the 1536 SNPs, 99 were unscored for every individual. For the remaining 1437 SNPs, 63 were invariable. The minimum allele frequencies (MAF) are shown in the table.

<table>
<thead>
<tr>
<th>SNPS</th>
<th>MAF ≤ 0.005</th>
<th>MAF ≤ 0.01</th>
<th>MAF ≤ 0.02</th>
<th>MAF ≤ 0.05</th>
<th>MAF ≤ 0.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>63</td>
<td>1292</td>
<td>1214</td>
<td>1120</td>
<td>629</td>
<td>352</td>
</tr>
</tbody>
</table>

Candidate loci under selection were identified using a Bayesian likelihood method implemented with the software BayeScan. Simulations were run considering each Iberian transect separately and the total Iberian data set. Simulations were performed including reference populations (right) and monomorphic (0.98 cutoff) loci (top) and removing reference populations (left) and monomorphic loci (down).

FUTURE DIRECTIONS

- Refine simulations with BayeScan.
- Employ other frequentist (e.g. DetSel, Fdist) and haplotype-based methods and landscape genetics tools to alleviate the problem of detecting false positives and excluding positives.
- Identify and interpret the spatial structure generated by loci under selection
- Reveal the molecular basis of the observed adaptive differentiation.

ACKNOWLEDGEMENTS

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