MAPPING FOR SELECTION SIGNATURES ASSOCIATED TO AGGRESSIVE BEHAVIOR IN CATTLE

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INTRODUCTION

- The Lidia bovine breed has its origins ~500 years ago in the Iberian Peninsula.

- This breed is selected for aggressive behavior to participate in popular festivities as part of the cultural people’s identity.

Different behavior patterns favored a fragmentation of the Spanish racial group into lineages with low population size.
INTRODUCTION

- Lidia breed bovines were brought to Mexico in 1522. To date, the Mexican Lidia population is genetically differentiated from the Spanish lineages.
• Genomic changes produced by selection have been studied, mainly in commercial cattle breeds.

• As a consequence, several hard-sweeps belonging to traditional selected morphological traits have been reported.
OBJECTIVES

• Locate genomic regions associated with agonistic related traits

• A marginal second objective was to identify putative candidate genes mapping within these genomic regions.

Two approaches based on the differences of allele frequencies among populations, were applied.
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MATERIAL

genotypic 50K SNP BeadChip data

- 100 Spanish bovines from the most aggressive lineages.
- 65 Spanish bovines from the less aggressive lineages.
- 45 bovines from the Mexican population
• 65 bovines from the Asturiana de los Valles breed

• 30 bovines from the Morenas Gallegas breed
Selestim

• Genomic regions were built from window of ~10 MB.
• Containing each of the SNP with KLD >99.99%.

BayeScan

• Splits the $F_{ST}$: population-specific component ($\beta$) and locus-specific component ($\alpha$) shared by all the populations.
• Selection is detected when $\alpha$ is significantly different to zero.
• Genomic regions were built from a threshold of 5% FDR, and then SNPs with $\alpha$ values >1.
RESULTS

BTA 3: 119.49 - 119.08 Mb

Average values of Allele selected ($k$)

- RAV
- MG
- Mex
- Spanish (+)
- Spanish (-)

Mb 104 106 108 110 112 114 116 118 120
RESULTS

BTA 8: 14.89 - 27.98 Mbp
## Genes Identified

<table>
<thead>
<tr>
<th>Position (Mbp)</th>
<th>Gene</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>109.29</td>
<td>GRIK3</td>
<td>Learning process</td>
</tr>
<tr>
<td>111.38</td>
<td>DLGAP3</td>
<td>Circadian cycles and neuronal signaling</td>
</tr>
<tr>
<td>110.17</td>
<td>THRAP3</td>
<td>Circadian cycles and behavior</td>
</tr>
<tr>
<td>111.14</td>
<td>SFPQ</td>
<td>Circadian cycles and behavior</td>
</tr>
<tr>
<td>110.78</td>
<td>NCDN</td>
<td>Learning and pigmentation</td>
</tr>
<tr>
<td>111.52</td>
<td>GJB4</td>
<td>Olfactory Neurophysiology</td>
</tr>
<tr>
<td>113.64</td>
<td>SAG</td>
<td>Visual stimulus Neurophysiology</td>
</tr>
</tbody>
</table>

### BTA 3

![Brain image](https://via.placeholder.com/150)

### BTA 8

<table>
<thead>
<tr>
<th>Position (Mbp)</th>
<th>Gene</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>15.68</td>
<td>LINGO2</td>
<td>Neuronal disorders</td>
</tr>
<tr>
<td>17.29</td>
<td>PLAA</td>
<td>Neuro-degenerative diseases</td>
</tr>
</tbody>
</table>
• The difficulty to detect selective sweeps with statistical significance in polygenic traits, in which many loci shift their frequency moderately.

• Expected false positives due to the divergence in allelic frequencies between breeds.

• 50K chip and the sample size of the analysis
CONCLUSIONS

• Two genomic regions associated with agonistic related traits in cattle.

• Direction of selection of both regions differed: The “aggressive” Lidia breed and the “tamed” Asturiana de los Valles and Morenas gallegas breeds.

Thank you for your attention!
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