Design of a Buffalo SNP Panel


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Development of a Buffalo High-Density SNP Assay

Why?
- Genome Selection
- Enhance QTL mapping precision
- Increased accuracy in genetic prediction
- Characterize genetic diversity – subspecies, breeds, etc.

SNP Discovery
- Based on bovine assembly
- A total of 16,675,440 SNP discovered
- Filtered:
  - SNP that did not map uniquely
  - Adjacent SNP – required at least 10 bp on one side of a SNP
  - 5,800,477 SNP remained

Assay Design
- Built from algorithm developed for the BovineHD
- Score is a function of MAF, size of gap being split, and proximity of SNP to center of gap

Data Highlights
- Represents:
  - ~470x coverage
  - 86 animals
  - 8 breeds
  - River & Swamp Buffalo
- SNP Discovery narrowed to
  - 48 animals
  - 4 breeds
  - River Buffalo

Assay Design
- Place 90,000 SNPs!!
- Use the concept of “waves”
  - Prioritization of SNP by starting with the “best” SNP and proceeding through groups of SNPs that are less desirable
  - Criteria included number of oligos needed to query the SNP, design score (expected conversion rate), distance to nearest adjacent SNP (10-30+ bp)
Consideration of Breeds

- Breed weighting
  - Mediterranean – 30%
  - Murrah – 30%
  - Jaffrabadi – 20%
  - Nilli-Ravi – 20%
- Breed-specific gaps and MAF

First Results

- Based on 1036 Mediterranean animals
- Single breed – so polymorphism rate is conservative
  - >67,000 good SNP
  - Still 75% success rate!

Summary

<table>
<thead>
<tr>
<th>SNP Category</th>
<th>SNP Percentage</th>
<th>SNP Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polymorphic High Resolution</td>
<td>74.8%</td>
<td>67330</td>
</tr>
<tr>
<td>VINO</td>
<td>0.1%</td>
<td>83</td>
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<tr>
<td>Missing Homozygote</td>
<td>1.7%</td>
<td>1494</td>
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<tr>
<td>Monomorphic</td>
<td>10.3%</td>
<td>9229</td>
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<td>Low Call Rate</td>
<td>4.1%</td>
<td>3668</td>
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<tr>
<td>Other</td>
<td>9.1%</td>
<td>8184</td>
</tr>
<tr>
<td>Total</td>
<td>100.0%</td>
<td>89988</td>
</tr>
</tbody>
</table>

Conclusions

- The Affymetrix Axiom Buffalo Array is available
- The distribution of SNP and MAF look very promising for a wide range of uses
- The performance of this assay looks very good!