SNPs for Parentage Testing, Individual Identification, and Traceability

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Basic Objective

Encourage ICAR & ISAG to officially recognize and accept the use of SNP markers for parentage and identification.
Progression of Parentage Technology

On-farm records

Blood typing

STRs

Laboratory

SNPs

Power of SNPs vs. STRs

- Li et al. (2006)
  - 59 SNPs in humans
  - PI, $9.02 \times 10^{-15}$
  - PE in duos, 98.94%
  - PE in trios, 99.92%
  - Same power as 13 STRs used by FBI for forensics
Power of SNPs vs. STRs

- Rohrer et al. (2007)
  - 60 SNPs in pigs
  - Each with MAF > .15
  - PI, $4.6 \times 10^{-23}$ across 4 breeds
  - PE in duos, 95.94% to 99.63%
  - PE in trios, 99.87% to 99.97%
  - Similar power to 10 STRs

- Heaton et al. (2002)
  - 32 SNPs across 18 autosomes in cattle
  - 16 beef breeds + Holstein
  - PI, $2.0 \times 10^{-13}$
  - PE in trios, 99.9%

- Heaton et al. (2007)
  - 121 SNPs in cattle
  - PE in duos, 99.99%
Power of SNPs vs. STRs

- Fisher et al. (submitted 2008)
  - Limited details because paper is not published
  - 40 SNPs with avg MAF = .35
  - Powerful parentage tool when combined with on-farm data
  - 40 SNPs alone were more powerful than typical commercial 14 STR panel

Impact of Mis-ID on Genetic Gain

- 7 to 15% ID error rate
  - Spelman, 2002
  - Visscher et al., 2002
  - Weller et al., 2004
  - Sanders et al., 2006
- 2.5 to 15% decrease in genetic gain
  - Israel and Weller, 2000
  - Banos et al., 2001
  - Spellman, 2002
  - Visscher et al., 2002
Commercial Example

Mis-ID by Dairy Herd Size

Misidentification rate, %

<table>
<thead>
<tr>
<th>Herd size</th>
<th>Misidentification rate, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;100</td>
<td>10</td>
</tr>
<tr>
<td>101-250</td>
<td>15</td>
</tr>
<tr>
<td>251-500</td>
<td>20</td>
</tr>
<tr>
<td>501-1000</td>
<td>25</td>
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<tr>
<td>1001-2000</td>
<td>30</td>
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<tr>
<td>&gt;2000</td>
<td>35</td>
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Daughter Contribution to Proof of a specific bull

<table>
<thead>
<tr>
<th>Qualify status</th>
<th>Number daughters</th>
<th>Milk</th>
<th>Fat</th>
<th>Protein</th>
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<tbody>
<tr>
<td>Yes</td>
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<td>2576</td>
<td>62</td>
<td>66</td>
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<tr>
<td>Not checked</td>
<td>2</td>
<td>2367</td>
<td>62</td>
<td>62</td>
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<td>No</td>
<td>5</td>
<td>2260</td>
<td>51</td>
<td>60</td>
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<tr>
<td>All</td>
<td>21</td>
<td>2481</td>
<td>59</td>
<td>64</td>
</tr>
</tbody>
</table>

SNPs

- are abundant
- are robust in terms of laboratory handling
- are amendable to high throughput
- are low cost
- have a low rate of genotyping errors
- have a relatively stable inheritance
- have a low mutation rate
- are easy to standardize between laboratories
- 50,000+ SNP chip being used worldwide to genotype thousands of influential animals in many breeds