PATERNITY ANALYSIS IN LARGE COMMERCIAL CATTLE RANCH SETTINGS USING SNPs - UC DAVIS EXPERIENCES

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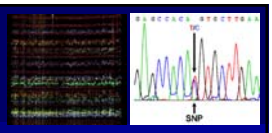
Prather Ranch – Macdoel Northern California

DNA Sample Collection

- Blood collected on FTA cards from **27** herd sires and **624** calves derived from a multiple-sire pasture

Genotyping



- **Genotyping and paternity assignments based on microsatellites (STRs) were done by the UC Davis Veterinary Genetics Laboratory using a panel of 23 cattle markers (P_E=99.9%)**
- **Genotyping based on SNPs were done by a commercial genotyping company using a panel of 28 loci (PE=95.5%)**

A. L. Van Eenennaam, R. L. Weaber, D. J. Drake, M. C. T. Penedo, R. L. Quaas , D. J. Garrick, E. J. Pollak. 2007. DNA-based paternity analysis and genetic evaluation in a large commercial cattle ranch setting. Journal of Animal Science. 85:3159–3169

Results of the paternity analysis

(PE=99.9%)

	23 Microsatellite (STR) panel	
One possible sire	533*	85.4%
More than one sire	4	0.6%
All excluded	76	12.2%
Resubmits	11	1.8%
TOTAL	624	

DNA from more than one animal

* 10 assignments allowed a one locus mismatch

	(PE=99.9%)		(PE=95.5%)	
	23 Microsatellite (STR) panel		28 SNP panel	
One possible sire	533*	85.4%	**175**	**23.3%**
More than one sire	4	0.6%	**420**	**67.3%**
All excluded	76	12.2%	**29**	**4.6%**
Resubmits	11	1.8%	**0**	**0%**
TOTAL	624		**624**	

* 10 assignments allowed a one locus mismatch

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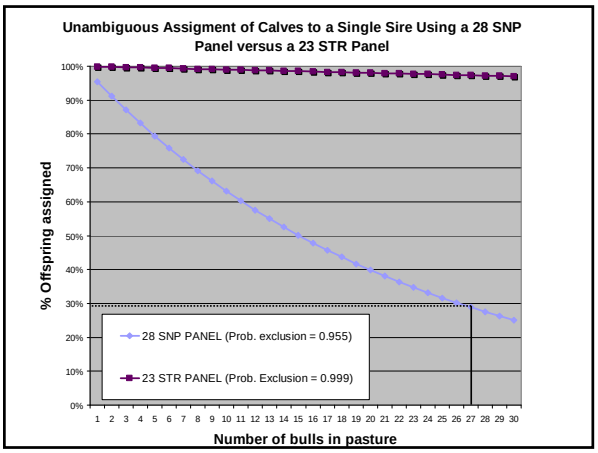

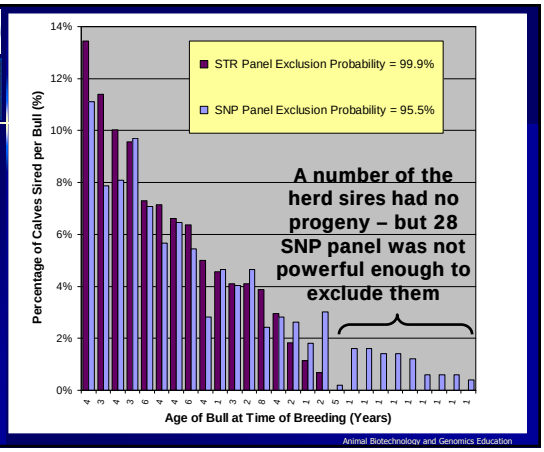

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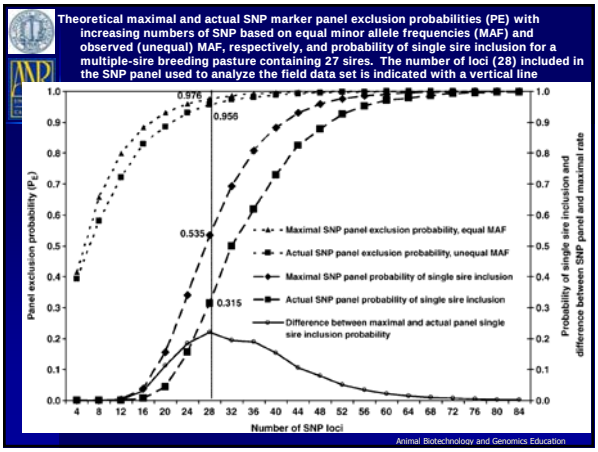

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2006 UCD Sample Collection

- Blood collected on Typifix tags cards from **23** herd sires and **298** calves derived from multiple-sire pastures
- Compared 62 "MARC" parentage loci – average number of loci compared was 53.86 with a range from 6-62; allowed ≤ 1 mismatch
- P_E (assuming equal minor allele frequency) = 0.999746

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2007 UCD Sample Collection

- Blood collected on Typifix tags cards from **28** herd sires and **303** calves derived from multiple-sire pastures
- Compared 99 "MARC" parentage loci – average number of loci compared was 87.04 with a range from 14-99; allowed ≤ 1 mismatch
- P_E (assuming equal minor allele frequency) = 0.999998185

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Results of paternity determinations – 2006, 2007 SNP panels

2006 (62 potential loci, PE=0.99975, number of sires 23)

Sires assigned per calf	Predicted % of calves	Observed % of calves	Observed #
0	0.0	8.00%	24
1	99.4	86.67%	260 (20)
2	0.6	4.67%	14
3	0.0	0.003%	1
4	0.0	0.003%	1
5	0.0	0.00%	0
6+	0.0	0.00%	0
Total:	100	100.00%	300

2007 (99 potential loci, PE=0.99999, number of sires 28)

Sires assigned per calf	Predicted % of calves	Observed % of calves	Observed #
0	0.0	2.6	8
1	99.73	97.03	294 (8)
2	0.27	0.33	1
3	0.0	0.0	0
4	0.0	0.0	0
5	0.0	0.0	0
6+	0.0	0.0	0
	100	100	303

	28 SNP Panel – 27 sires 2005 (PE=95.5%)		62 SNP Panel – 23 sires 2006 (PE=99.975%)		99 SNP Panel – 28 sires 2007 (PE=99.999%)	
One sire assigned	175	23.3%	260	86.7%	294	97.0%
More than one sire	420	67.3%	16	5.3%	1	0.33%
All excluded	29	4.6%	24	8.0%	8	2.6%
TOTAL	624		300		303	

SNPs and parentage using the 50K chip

"The low rate of genotyping errors meant that less than five inconsistencies were usually found when parent-progeny assignment was correct. However, several thousand inconsistencies were usually found when the parent-progeny assignment was incorrect"

Wiggans et al. Genomic Evaluations in the United States and Canada: A collaboration. ICAR 2008

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- Changing SNP panels from year to year without regenotyping all bulls
- Poor call rate – especially problematic when it was a sire (from a panel of 99 SNP loci, the call rate was as low as 5% on occasion)
- Discrepancies between genotypes of bulls genotyped multiple years
- Some sample tracking problems

Implications and considerations regarding SNPs for parentage

It is likely that SNP markers will replace alternatives (i.e. microsatellites) over the next 5 years

- Which SNP panel should be used and how many SNP markers should be included in the panel?
- What should be the number of compared loci cutoff in the case of incomplete genotyping?
- How many exclusions (as a function of number of compared loci) should be allowed to account for genotyping errors – platform dependent?