DNA-based progeny testing and development of commercial ranch EPDs

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Commercial herds using multiple-sire breeding pastures often have no way of identifying the paternity of the calves. DNA markers can be used to assign calves to their individual sires based on the inheritance of markers. Sires pass on only one of the two marker alleles that they carry for each gene. If a calf does not have a marker allele in common with a sire at a particular gene, then that sire is excluded as being the parent of that calf.

Paternity "identification" involves examining each calf's genotype at multiple different gene loci and excluding as potential sires those bulls that do not share common alleles with the calf. Because paternity identification is a process of excluding potential sires on the basis of their genotype, it is therefore important that DNA from all possible sires be included in paternity tests. While parents can be excluded using this process, results cannot be used to "prove" parentage. Parentage testing identifies individuals that, due to a specific combination of marker alleles, could qualify as a parent for a particular offspring.

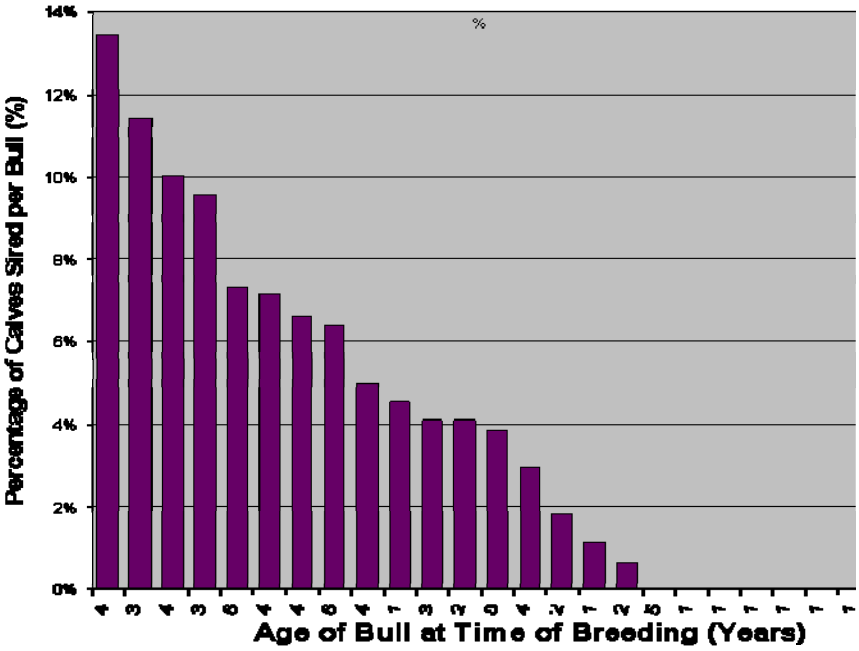
Example: How does parentage assignment work?

	Bull A	**Bull B**	**Bull C**	**Bull D**
Genotype	A/A, C/C	A/T, C/G	T/T, G/G	T/T, C/C

- A calf with the genotype "A/T, C/G" could have received one allele from any of these bulls and so none of these bulls can be excluded as the possible sire. Additional markers would need to be used to uniquely assign one of the bulls as the sire of the calf.
- A calf with genotype "A/A, C/C" could not have been sired by Bulls C or D, but could have been sired by either Bull A or B
- A calf with genotype "T/T, G/G" could have been sired by Bull B or C.

Paternity testing is complicated by genetic relationships between the bulls. If bulls are closely related then they are more likely to carry the same marker alleles. Consequently, it will be more difficult to definitively make paternity assignments on closely related bulls in a multiple-sire breeding pasture. Forming multiple-sire groups for each pasture from unrelated animals, i.e. putting full-brothers in with different groups of cows, will help to minimize this problem. If there is only one potential sire for a calf (e.g. an A.I. calf), then paternity can be "assigned" by confirming that the calf's genotype shares a marker allele in common with the alleged sire at all of the genetic loci that are tested. Although microsatellites have typically been the marker of choice for paternity analysis, the use of SNP markers is becoming more common for a number of reasons including their abundance, high potential for automation, low genotyping error rates, and ease of standardization between laboratories.

Uses of parentage testing include identifying the sire(s) of outstanding or poorly performing calves and ascertaining whether one particular bull is routinely siring progeny that require calving assistance. To identify the sire(s) of a select group of calves (e.g. calves that are pulled or top 10% of carcass quality animals) the costs of DNA analysis are minimized by sampling and DNA testing the herd bulls and only a targeted subsample of the calves. More extensive sampling of the entire calf crop can allow for a determination of the proportion of the calf crop attributable to each bull in the herd. It is generally assumed that each bull contributes equally to the calf crop. However, studies have shown that some bulls sire more than their "fair share" of the progeny, while other bulls sire none of the progeny (see graph).



Matching individual sires with the performance records of their entire calf crop also provides the data required to develop within-herd EPDs for herd sires. The use of progeny testing to develop within-herd EPDs for herd sires on economically-relevant traits has the potential to generate value by improving the response to selection for targeted traits. It is important that DNA samples be collected from all potential sires. It is also important to try to keep young sires and mature bulls in separate breeding pastures.

Missing sires can occur for a variety of reasons (neighboring bulls jumping the fence, precocious bull calves, or inadvertent omission of sire(s) from sample collection). Missing sire DNA samples when using DNA marker-based parentage for genetic evaluation decreases the rate of genetic gain. The frequency of sire misassignment can be minimized by using a powerful marker panel; or by simple management practices that include: dividing large herds into smaller multiple-sire breeding groups with fewer sires while maintaining the same bull:female ratio; genotyping all potential bulls before breeding; sorting bulls into sire groups with divergent genotypes; keeping young bulls in separate breeding groups; and minimizing relatedness among bulls. Sampling bulls for DNA testing as they are put out with cows, rather than at a later time helps to minimize the missing sire samples.

The return on investment that results from such progeny testing has been found to be greatly influenced by the cost of genotyping. New SNP genotyping platforms continue to drive down the cost to generate SNP genotypes, and the future will undoubtedly see the introduction of less expensive genotyping assays using high resolution SNP parentage panels. As with any new technology, the value associated with the parentage information must be estimated to determine if it outweighs the expense of collecting and genotyping the DNA samples.