

**P0132****Imputation of Microsatellite Alleles from Dense SNP Genotypes for Parentage Verification Across Multiple *Bos taurus* and *Bos indicus* breeds**

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Room: Grand Exhibit Hall

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Microsatellite markers (MS) have traditionally been used for parental verification and are still the international standard in spite of their higher cost, error rate, and turnaround time compared with Single Nucleotide Polymorphisms (SNP)-based assays. Despite domestic and international demands from the livestock and research communities, no viable means currently exist to verify parentage for any individual unless all familial connections were analyzed using the same DNA marker type (MS or SNP). We have previously devised an effective and inexpensive method to impute MS alleles from SNP haplotypes within and potentially across breeds. This method was verified at >98% accuracy for imputing the MS alleles for 12 markers of ISAG recommended parentage panel using SNP genotypes from 479 dairy animals across 4 dairy cattle breeds (Brown Swiss, Guernsey, Holstein, and Jersey). Some MS-haplotype association held true across these phylogenetically diverse breeds, implying that some combinations were present before modern breed formations and have been preserved across breeds. To expand the utility of this imputation >8,000 animals with MS and SNP data from 45 breeds (*Bos taurus* and *indicus*) were used in this study to identify haplotypes that can be used across bovine breeds to impute MS genotypes. While MS are currently the international standard for parentage verification of exported semen, this work represents a tool to quickly migrate towards SNP based verification in 1 generation for any domesticated bovine breed. Finally, these imputation methods can be integrated into any livestock species that desires to move from MS- to SNP- based parental verification.

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Meeting Information

When:

January 11 - 16, 2013

Where:

San Diego, CA
