Genotypes imputation as a supporting method in pedigree control in Polish Holstein-Friesian cattle

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Objectives
Utilize microsatellite (MS) and single nucleotide polymorphism (SNP) information to predict MS genotypes through imputation methods from selected SNP panels for parentage testing in cattle.

Material and Methods
- MS and SNP genotypes from 321 Polish Holstein-Friesian bulls, the same bulls were utilize in training and validation dataset
- 11 MS markers recommended by ICAR/ISAG for parental control testing
- SNP genotypes obtained from Illumina Bovine50SNP
- each MS were flanked by 10 or 20 markers (Figure 1)
- three models of genotypes missingness: without 50% of MS (ms), without of 100% of MS (no.ms), without 50% of MS and 50% of SNP markers (snp.ms) in validation dataset
- multiallelic imputation software: PHASE (Stephens et al., 2001) and BEAGLE (Browning and Browning, 2009).

Results
Figure 2
Heatmaps of imputation accuracy between the reference and validation datasets presented across 11 chromosomes for different software, windows size and model of data missingness.

Conclusions
The PHASE imputation for multiallelic markers is more accurate, however the approach works only for chromosomes on which markers were in stronger LD blocks. It is recommended to use higher density SNP panels, for example SNPs from microarray Illumina BovineHD.