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J. Van Milgen[1] and M.H. Pinard-Van Der Laan[2]
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Panel discussion with stakeholders and interaction with participants on the opportunities and difficulties of multidisciplinary and multiactor research.

Development of and Imputation with a SNP map derived from the latest reference genome sequence

X. Yu[1], J.C. McEwan[2], J.H. Jakobsen[3] and T.H.E. Meuwissen[1]
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SNP chips of different densities are often used together on farm animals for economic reasons. The missing genotypes on the low-density (LD) chips can be imputed with genotype results of high-density (HD) chips and a linkage map of HD loci. Genome references and SNP chips are under continuous development. This may introduce several problems. For example, different chips may be based on different versions of the reference sequence. The SNP names can come from different naming systems. There are also typically many duplicated loci, because of SNP types and importance. Any one of these problems can increase imputation errors. One solution for these problems is to derive a SNP map from the most up-to-date reference sequence. The probes that come with the manifest of a chip-design can be used to position the SNPs on this map. Each of these probes is 50 base pairs (bp) in length, and can uniquely define a mutation position. Because the ends of the probes may also be the SNP, one bp was trimmed from both ends of a probe. All possible 48-bp sequences of a chromosome were then indexed by their positions and sorted in alphabet order. This can speed up the search procedure thousands of times, for sequential searches were converted to binary ones. This method was tested on data from Norwegian White Sheep genotyped with an 8k LD chip and a 600k HD chip. Random animals who were genotyped with the HD chip were masked at the missing loci on the LD chip. Only autosome loci were considered. Using the provided 600k linkage map, the correct allelic imputation rate was only 85%. Using the map derived from the sheep genome reference version 3.1.91, the imputation rate increased to 92%. When the number of animals with known HD genotypes increased from 120 to 617, the imputation rate increased to 94%, indicating the accuracy improvement was mainly from the new map. In conclusion, using a SNP map derived from the latest reference can greatly increase imputation rate. The described binary search algorithm makes such map construction feasible with limited computation costs.