

**Present and future of genomic selection at the commercial level***I. Misztal**University of Georgia, Athens, GA 30605, USA; [ignacy@uga.edu](mailto:ignacy@uga.edu)*

Experiences with genomic selection (GS) in the last couple years were interesting and somewhat unexpected. GS seems to be successful in dairy in populations with large number of genotyped high-accuracy bulls. Successes in smaller populations or with low-accuracy animals genotyped are smaller or none. Improvement in accuracies in some species (e.g. sheep) despite large number of genotypes is limited. Improvement of accuracies may be high for one group of animals and low for other groups. Adding external genotypes is not always helpful. The experiences suggest that: (1) LD for most traits is small; (2) gains with GS are mostly to better relationships; (3) gains from genotyping low-accuracy animals are small; (4) old genotypes are less useful; (5) genotypes from other populations are less useful and from other breeds are likely not useful. Current hope in GS is placed on detecting causative SNP in full-genome sequencing, however, the success of such scheme is based on strong assumptions that substitution effects of these SNP are constant, and epistasis across line/breeds/generations is negligible. As genotyping costs decrease, eventually millions of animals may be genotyped. Using more genotypes for predictions directly will greatly increase costs at low marginal gains (or even losses). Also emphasis on GS reduces attention to model refinement and correctly modelling environmental changes. Future GS needs to be simple, account for line and breed differences, and cannot limit modelling flexibility. It requires a breakthrough like the Henderson's algorithm to create  $A^{-1}$ , which changed the animal model evaluation from tough to simple.