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GENETICS OF COMPLEX TRAITS IN LIVESTOCK AND HUMANS

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Complex or quantitative traits are important in evolution (*e.g.* clutch size in birds), medicine (*e.g.* hypertension) and agriculture (*e.g.* yield of crops). The availability of assays for 100,000s of single nucleotide polymorphisms (SNPs) has revolutionised our understanding of the genetics of these traits. Genome wide association studies (GWAS) based on SNP assays have increased our knowledge of the genetic architecture of complex traits, mapped causal variants and been used to predict the genetic value of individuals for complex traits. The best analysis of GWAS fits all SNPs simultaneously assuming that the effect of SNPs on the trait are random effects. Genetic variation in a typical complex trait is due to thousands of polymorphisms, most of which have a very small effect on the trait. Very large sample sizes (*e.g.* 100,000 people or animals) are needed because the effect sizes are so small. Most of the causal variants are non-coding and their allele frequency is biased slightly to low minor allele frequencies indicating weak selection has operated on these polymorphisms. The causal variants can be mapped to within approximately 50 kb but the linkage disequilibrium between variants makes it difficult to identify the causal variant. Despite this, the genetic value of individuals can be predicted with good accuracy especially in populations of low effective population size such as breeds of livestock. This prediction, known as genomic selection, is now the basis for most livestock breeding programs.