Improving the performance of crossbred animals using genomics

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In pig and poultry breeding programs, animals from genetically distinct purebred lines are mated to produce crossbred animals, which provide food products to consumers. The purebred lines usually differ in the traits that they are selected for. Dam lines may be selected for female fertility traits, whereas sire lines may be selected for growth or egg production traits, and feed efficiency. The breeders then benefit from breed complementarity in the crossbreds, meaning that the crossbred animals combine the desirable traits that the purebred lines were selected for. Another benefit of crossbreeding is heterosis, which refers to the better average performance of crossbreds compared to the average performance of their parental lines. The aim of crossbred breeding programs is to improve the performance of crossbred animals by selecting genetically superior individuals in the purebred lines to become parents of the next generation. When these selection decisions are based on performance of the purebreds, improvement in crossbred performance follows from a correlated response. This strategy may be suboptimal because the genetic correlation between purebred and crossbred performance () is usually lower than 1. It may therefore be beneficial to make selection decisions based on information on crossbred performance instead of purebred performance. This used to be a challenging task, because purebred animals cannot be tested directly for crossbred performance. Now, with the developments in genomics, it has become possible to estimate breeding values for crossbred performance for purebred animals, by training the genomic prediction model with crossbred instead of purebred data. The benefit of training on crossbred data partly depends on the value of , which may differ across species, breeds and traits. In this thesis, I studied the genetics of crossbreeding, with a focus on genomic prediction for crossbred performance. One of the aims was to investigate the benefit of using crossbred instead of purebred data for prediction accuracy. I used data from purebred and crossbred broilers, and analysed two traits that had different . The results suggest that when is lower than ~0.8, prediction accuracy can be improved by training the model with crossbred instead of purebred data. Based on the results in my thesis, I conclude that genetic models that best resemble genetic reality do not necessarily result in the best predictions.