Summary

The breeding process aims to obtain new genotypes with traits improved over the parental forms. Parameters related to the additive effect of genes, as well as their interactions (such as the additive × additive interaction effect and the additive × additive × additive interaction effect), can influence decisions on the suitability of breeding material for this purpose. Understanding the genetic architecture of complex traits is a major challenge in the post-genomic era, especially for quantitative trait locus (QTL) effects, QTL×QTL interactions and QTL×QTL×QTL interactions.

The presented dissertation aimed to compare methods of estimating the higher rank interactions of genes determining quantitative traits based on phenotypic observations and molecular markers. Two estimation methods were presented: the phenotypic method and the genotypic method. The genotypic method used unweighted multiple regression and weighted multiple regression in two variants of parameters selection. The presented methods for estimating the total interaction effect of *aaa* were compared analytically, numerically and in simulation.

The study material consisted of four data sets consisting of: 150 barley doubled haploid lines tested in sixteen environments; 145 barley doubled haploid lines tested in nine environments; 252 maize inbred lines tested in two environments; and 94 wheat doubled haploid lines tested in one environment. In the simulation study, 84 experimental situations were analyzed.

All of the methods presented proved to be useful statistical tools for QTL characterization and estimation of the *aaa* interaction. Compared to the phenotypic method, weighted multiple regression yielded the most accurate estimates among the genotypic methods. In simulation studies, weighted regression also produced results closest to the true value. The results presented in the papers discussed above are the first reports on the use of analytical, numerical and simulation methods for estimating *aaa* interactions of QTL×QTL×QTL effects.

Keywords: higher-order genetic interactions, quantitative trait locus, Monte Carlo simulation study, regression analysis, molecular markers

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