Conclusions

An attempt was made to assign the bovine erythrocyte antigens to their corresponding chromosomes by linkage analysis and to use the bovine blood group systems as additional genetic markers. Therefore, linkage analyses were performed between the genotypes for the blood group systems of the sires from the ADR mapping project and 265 genetic markers covering the bovine genome in regular intervals. Many of the erythrocyte antigens showed significant association to a single chromosome and could definitely be mapped, in which the erythrocyte antigen A (EAA) was assigned to chromosome 15, EAB was assigned to chromosome 12, EAS was located on chromosome 18, EAL could be placed on chromosome 3 and EAS could be assigned to chromosome 21. Calculated Lod-score values were between 11.43 and 107.83.

But for the blood group systems F, J, R' and Z significant associations were detected to microsatellite markers on various chromosomes. As it is shown in humans and in pigs these bovine blood group systems also seem to be influenced by several loci throughout the genome. Therefore, linkage to different loci on the bovine genome provide new knowledge with respect to chromosome mapping of the relevant loci.

Considering the results from mapping the blood group systems a male genetic linkage map was constructed. In total twenty grandsires with 1074 sires were provided from the German cattle population as reference families. Sixteen of these paternal half sib groups are German Holstein families, three are German Simmental families, and one is a Brown Swiss family. From 265 markers included in the linkage map, 248 were microsatellite markers, 5 were bovine blood group systems, 8 SSCP markers and 4 proteins and enzymes. More than 239 000 genotypes from typing the offspring for the respective markers were produced and considered for the construction of the map. On average 478 informative meioses were provided from each marker of the map. The summarised map length over all chromosomes was 3135.1 cM with an average interval size of 13.34 cM. About 17 %, 35.7 % and 79.1 % of the map intervals showed a maximum genetic distance between the adjacent markers of 5 cM, 10 cM and 20 cM, respectively. The number of loci ranged from 2 (pseudoautosomal region of the sex chromosome, BTAY) to 15 (BTA23) with an average of 8.8 markers per chromosome. Comparing the length of the chromosomes shows variation from 49.6 cM for chromosome BTA26 to 190.5 cM for the chromosome BTA1 with a mean of 107.7 cM for all autosomes of the genetic linkage map. The identification of chromosomal discrepancies in locus order and

map intervals was enabled by common usage of many markers within other maps. The map provided sufficient marker density and served as a useful tool for the genomic scan of segregating quantitative trait loci.

The objective within the third chapter was the analysis of the variability of recombination frequency between different breeds of cattle.

Although very little is known of the role, pattern, or regulation of recombination, data from humans and mice indicate that several factors affect recombination. Variation in rates of recombination was found within individuals, between sexes and different ages of the species. But so far, variation in the frequency of recombination at the level of the genome has not been investigated with respect to differences between breeds.

Twenty grandsires consisting of three different breeds with a total of 1074 sons were provided as reference families to construct a male genetic linkage map. Sixteen of these paternal half sib groups represented the German Holstein breed, three were German Simmental famillies, and one was a Brown Swiss family, whereas the number of sires per breed was 872, 170 and 32 respectively. About 265 genetic markers were located on the bovine genome. Two-point recombination rates and their corresponding Lod-score values were determined within each single breed for each adjacent marker. A total of 865 marker-intervals provided estimates of recombination rates for at least two breeds. After a complete genome scan and accounting for multiple tests by applying the false discovery rate 4 marker-intervals representing 3 genomic regions on BTA19, BTA24 and BTA27 showed significant differences in the recombination frequency between the breeds.

The issue of the fourth paper was the use of different measures of average progeny's phenotype as dependent variables in QTL detection. Various studies have suggested daughter yield deviations (DYD) as the unit of measurement, because DYD provide an unregressed measurement of progeny performance, which are independent of all fixed effects and relationships amoung animals and adjusted for the additive genetic values of daughters dams. But DYD's are not available for all traits of interest. De-regressed proofs (DRPF) of estimated breeding values (EBV's) are known to be a measurement of daughter yield deviations accounting for fixed effects in the model, but are not necessarily the same as DYD's. The objective of this study was to examine possible differences between DYD's and DRPF's within the use of QTL detection. Therefore, a whole genome scan was performed using DYD's, DRPF's and EBV's and results were compared with respect to the number of QTL detected. From the results the following facts can be extracted: Performing de-regression of EBV's based on the number of daughters, the heritability of the trait and the additive

relationship matrix of all male animals involved in the ADR grand-daughter design yielded an unit of measurement that was not very different from DYD's. DRPF's provided a similar proportion of QTL detected within this experiment if compared with DYD's. As a further aspect results from a weighted multi-marker regression using DYD's and DRPF's as unit of phenotypic measurement for each trait of interest were compared with an unweighted multi-marker regression by using EBV's. From that, testing a low number of hypotheses yielded similar results. But considering a high number of QTL resulted in a lower proportion of detected QTL if dependent variables are not weighted.