

REPORT ON SHORT TERM FELLOWSHIP 2008 (INCO)

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Quantitative Trait Loci are the chromosomal regions which underlie the continuous variation of the complex traits. Search for QTL is often a difficult task, and statistical methods are used for both the detection and location. A whole genome scan of specific QTL starts with a dense linkage map of polymorphic molecular markers. The mating design involves Experimental Crosses between phenotypically divergent breeds in pigs and poultry because generation interval is short and number of offspring is moderate to high. Such experimental crosses are expensive and time consuming to develop for cattle and sheep. A more common approach is to exploit the large paternal half-sib families. Daughter design (DD) and Grand daughter design (GDD) are very commonly employed. A sample from the progeny population is then genotyped for the markers and phenotyped for the trait of interest. The simplest analysis that follows defines the null hypothesis of no linkage between each marker and a putative QTL in terms of recombination fraction between the two loci. Then, the power of detecting a QTL is, 1-Type II error. There are a number of factors that affect the power of QTL detection, but from a design point of view the marker density and the sample size are the most important. The issue is, therefore, one of relative costs of producing larger families vs more markers. Conventional methods for the detection of quantitative trait loci (QTLs) are based on a comparison of single QTL models with a model assuming no QTL. For instance in the interval mapping method (LANDER and BOTSTEIN 1989) the likelihood for a single putative QTL is assessed at each location on the genome. However, QTLs located elsewhere on the genome can have an interfering effect. As a consequence, the power of detection may be compromised, and the estimates of locations and effects of QTLs may be biased (LANDER and BOTSTEIN 1989; KNAPP 1991). Even non existing so-called .ghost. QTLs may appear (HALEY and NOTT 1992; MARTINEZ and CURNOW 1992). Therefore, it is obvious that multiple QTLs could be mapped more efficiently and more accurately by using multiple QTL models instead of the single QTL models used in interval mapping. Multiple linear regression methods can be combined with conventional interval mapping, by fitting one QTL at a time in a given interval and simultaneously using (part of) the markers as cofactors to eliminate the effects of additional QTLs.

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