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Methodological aspects of the mapping of disease resistance loci in livestock

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4.1. Introduction

The most commonly used methods for QTL mapping assume that the phenotype of interest is normally distributed. When dealing with disease resistance traits, which in most of the cases do not satisfy this requirement (as observed in the Chapter 3), these methods could be not appropriate. To obtain the maximum power to detect QTL, the phenotype could be **mathematically transformed** to satisfy the normality assumption, or **non-parametric methods** could be used. Both strategies should be evaluated.

Different methods exist for the comparison of statistical tests. Although the accuracy of the estimates is of great importance, the most important parameter for practitioners is the ability of a test to evidence true significant results, *i.e.* the **statistical power**. This statistical power is defined as the probability of rejecting the null hypothesis when it is false. To identify the statistical tests giving the best results, it is therefore relevant to compare them according to their statistical power. For this purpose, simulations will be carried out in the methodological part of this thesis (Chapters 5 and 6).

In addition to the application of a mathematical transformation to non-normally distributed traits (Chapters 5 and 6), another way of increasing the power of QTL detection tests is to increase the reliability of the phenotypic measurements performed on animals. This can be done by reducing the environmental noises in order to have measurements approaching at best the genetic values of animals. One way of doing this is to use **aggregates** of repeated measurements. This approach will be evaluated in the context of repeated measurements of resistance traits (Chapter 7).

As simulations are only mimicking the reality, the comparison between classical and non-parametric QTL mapping methods will be completed by the **analysis of real data sets** with both methodologies (Chapters 8 and 9).

4.2. Objectives of this thesis

Based on the demonstrated genetic basis of disease resistance in livestock animals, on the current status of the QTL mapping methodology, and on the statistical properties of some disease resistance traits used in livestock species, the objectives of the present thesis are:

- (1) the development of an algorithm for the simulation of non-normally distributed traits based on observed distributions rather than on theoretical distributions (Chapter 5).
- (2) the analysis of the robustness (statistical power) of current classical methods when used with phenotypes that do not satisfy the normality assumption (Chapter 5).
- (3) the assessment of the impact of mathematical transformations on the power of QTL detection tests (Chapters 5 and 6).
- (4) the comparison, in terms of power of QTL detection, of the non-parametric interval mapping method with classical methods such as least-squares or maximum likelihood-based methods (Chapter 5 and 6).
- (5) the extension of the non-parametric method developed for half-sib populations to the analysis of resistance traits with peculiar statistical properties (Chapter 6)
- (6) the assessment of the impact of using aggregates of multiple measurements of the same resistance trait on the power of QTL detection (Chapter 7).
- (7) The application of the improved non-parametric method to resistance data collected from actual experimental designs on chicken and sheep, and the comparison of the results with the results obtained using the most commonly used approach, i.e. the least-squares-based method (Chapters 8 and 9).