

## **Identifying genes for reproduction traits in dairy cattle**

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The purpose of this study is to identify chromosome regions that have an effect on reproduction traits in dairy cattle and ultimately to be able to identify the specific genes involved. Reproductive problems are the main reason for involuntary culling of dairy cows in Sweden. The cow's ability to reproduce is crucial in milk production and contributes substantially to the economy of the dairy farmer. Poor fertility leads to more inseminations, higher veterinary costs, increased culling rate and higher replacement costs. In addition to being an economic issue, the calving performance is important also in an animal welfare perspective.

Most reproduction traits are complex traits with low heritability, which means that they are regulated by many genes and, to a great extent, by environmental factors. The underlying genes or chromosome segments affecting such complex traits are called quantitative trait loci (QTL). By using traditional methods of selection it has been difficult to improve reproduction traits due to their low heritability. If we can identify QTL responsible for a significant proportion of the genetic variation in these low heritability traits, or detect closely linked genetic markers that are co-inherited with the QTL, the genetic progress could be enhanced by using marker-assisted selection.

The principle in QTL mapping is to search for associations between genetic variation at marker loci and the phenotypic variation for a trait. A significant difference in phenotypes among groups of offspring that inherited alternate marker alleles from their common parent indicates linkage between the markers and a QTL affecting the trait. In this study we have performed a genome scan for QTL affecting the following traits: number of inseminations per service period, number of treatments for reproductive disturbances, interval between calving and first insemination, 56 days non-return rate, heat intensity, stillbirths, and calving ease. Animals from the 10 largest dairy cattle half-sib families in Sweden were used, in total 427 breeding bulls. DNA from each bull was extracted from frozen semen samples (obtained from Svensk Avel) and genotypes for 145 genetic markers distributed over 20 chromosomes were determined. Breeding values (obtained from Svensk Mjölkk) for the traits were used as phenotypic records in the analyses.

In conclusion, we have found that it is possible to identify chromosome regions with effect on fertility and calving traits in dairy cattle. Further work is needed to narrow down the regions before the results can be used in practical breeding.