Genomic regions associated with somatic cell score in dairy cattle

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The EU project RobustMilk combines unique data from research dairy herds located in four European countries. The dataset contains detailed recordings on somatic cell score (SCS), with up to 50 SCS test-days per cow per lactation. Variation in SCS can be due to genetic and environmental factors. The aim of the present study was to identify regions on the genome that contribute to genetic variation in lactation-average SCS (LASCS) and the standard deviation of SCS (SCS-SD). The standard deviation of SCS aims to capture temporary increases in SCS associated with infection. First lactation SCS records and DNA of 1,484 cows were analysed. Cows were genotyped for 50,000 markers. Each individual marker was tested for its detection of variation in LASCS or SCS-SD. One marker on chromosome (BTA) 18 detected variation in both LASCS and SCS-SD. One marker on BTA4 detected variation in LASCS, and one marker on BTA6 detected variation in SCS-SD. The present study identified genomic regions on BTA4, BTA6 and BTA18 contributing to genetic variation in LASCS and SCS-SD. More knowledge on genetic control of LASCS and SCS-SD may not only enable more accurate breeding value estimations that allow farmers and the dairy industry to reassess their selection decisions, but also helps to find genes for mastitis resistance which is relevant for understanding the genetic mechanisms leading to mastitis.