GEM 3

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Signature of selection around the myostatin locus in Piedmontese cattle typed by a 54,000 SNP panel

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Breeds have been isolated and selected for different traits since many generations. This left selection signatures that could be detected in chromosomal regions harbouring the targeted genes. Today, genome scan technologies could allow to pinpoint these regions.

As proof of principle, here we report the evidence of a selection signature around the myostatin gene known to have been target of recent selection in Piedmontese breed.

Methods

DNA was extracted from blood or semen using Macherey & Nagel kit and its integrity was checked on agarose gel. DNA solutions have been dried, resuspended and quantified using Picogreen in a fluorescence plate reader. Fluorescence measures were used to program a robotic station to prepare samples aliquotes of 20 µl DNA at a concentration of 50ng/µl. SNP typing by the Illumina 54k chip was outsourced to Geneseek, USA. SNP calls were accurate to more than 99.8%.

Samples

228 Marchigiana male beef (MR)
used as null hypothesis

379 Piedmontese tested bulls (PD)

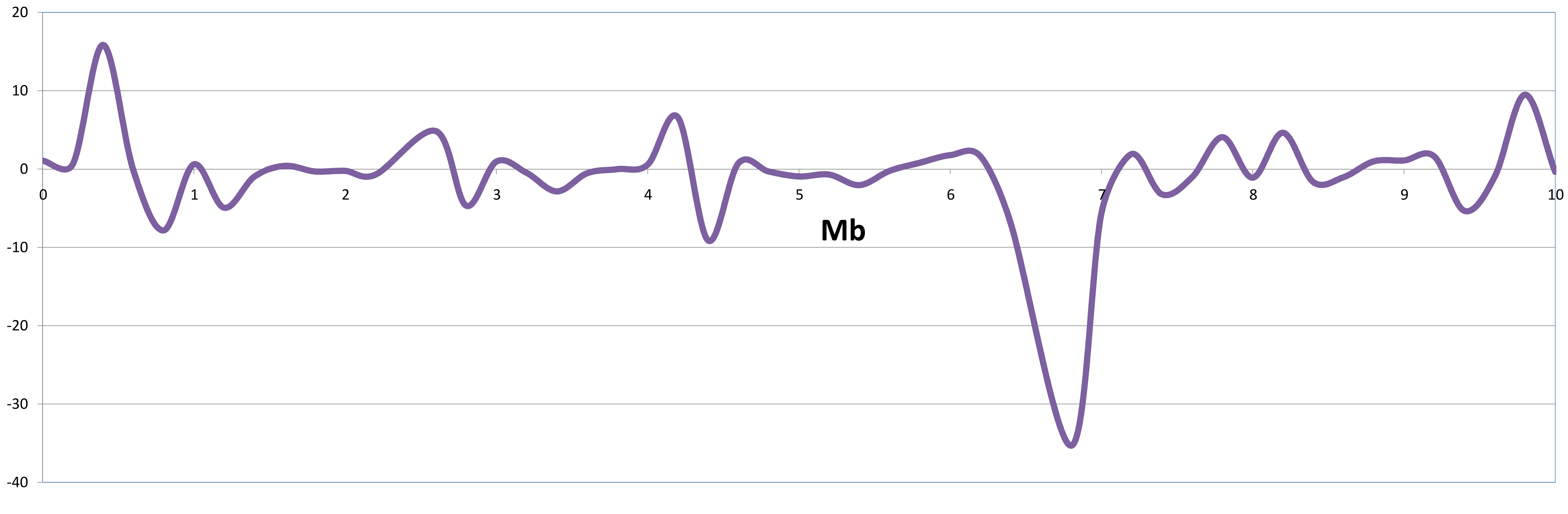
Population Statistics

Population inbreeding coefficient was calculated as

$$F = (H_{exp} - H_{obs}) / H_{exp}$$

Where H_{exp} and H_{obs} are the expected and observed heterozygosities, respectively. Ratio of F_{PD} versus F_{MR} is shown in the figure below. F values were averaged at 200kb intervals.

Marchigiana versus Piedmontese relative inbreeding (BTA 2)



Results and discussion

A strong signal in chromosome 2, around the location of the myostatin gene, can be detected in Piedmontese (selected for this gene to exploit double muscling phenotype) against Marchigiana (not selected for this gene). Further analyses extended to whole genome could reveal other chromosomal regions under selection, helping in focusing the research of causative genes within narrow DNA stretches amenable to full sequencing.

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