



Genomic characterization of the Montanina cattle

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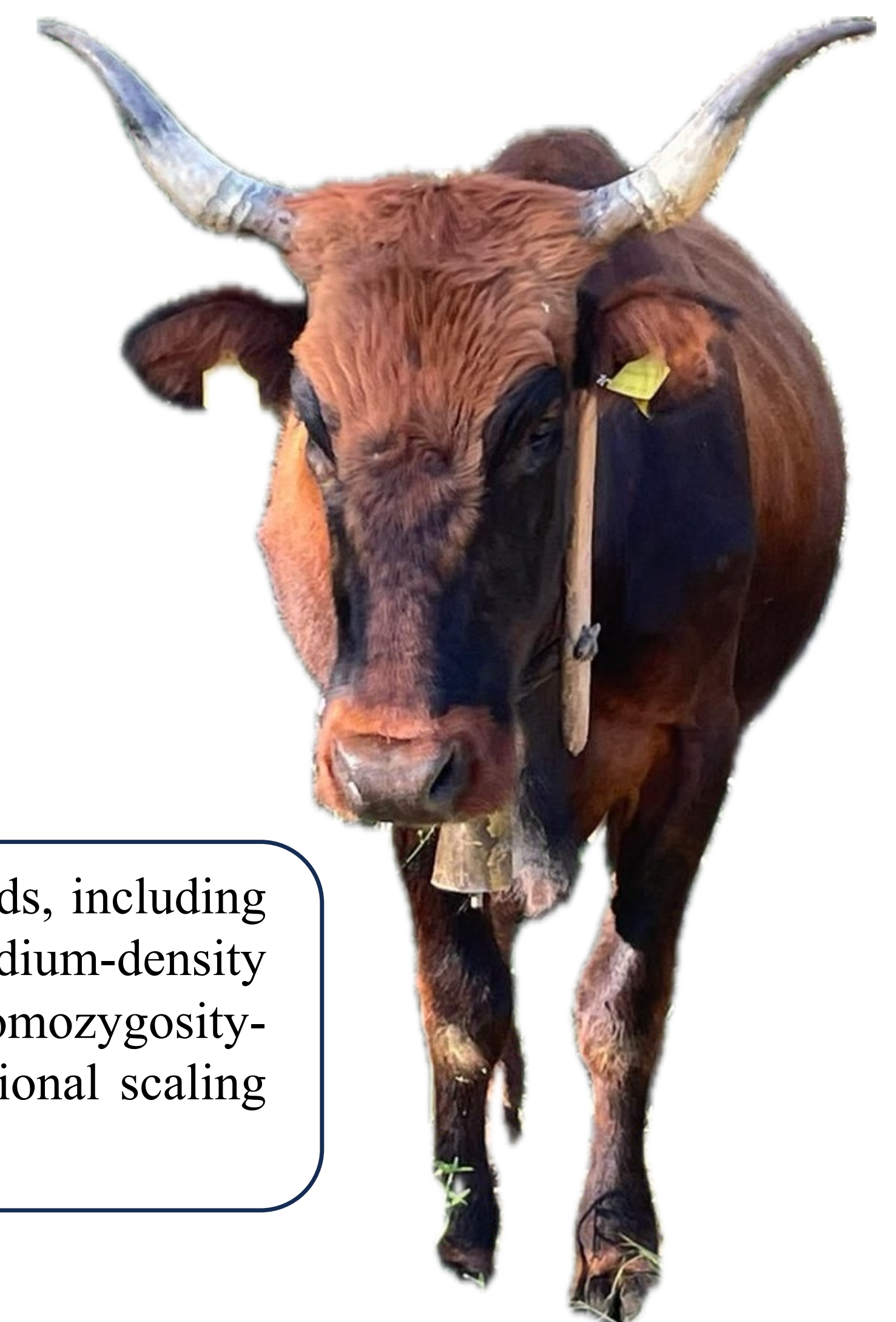
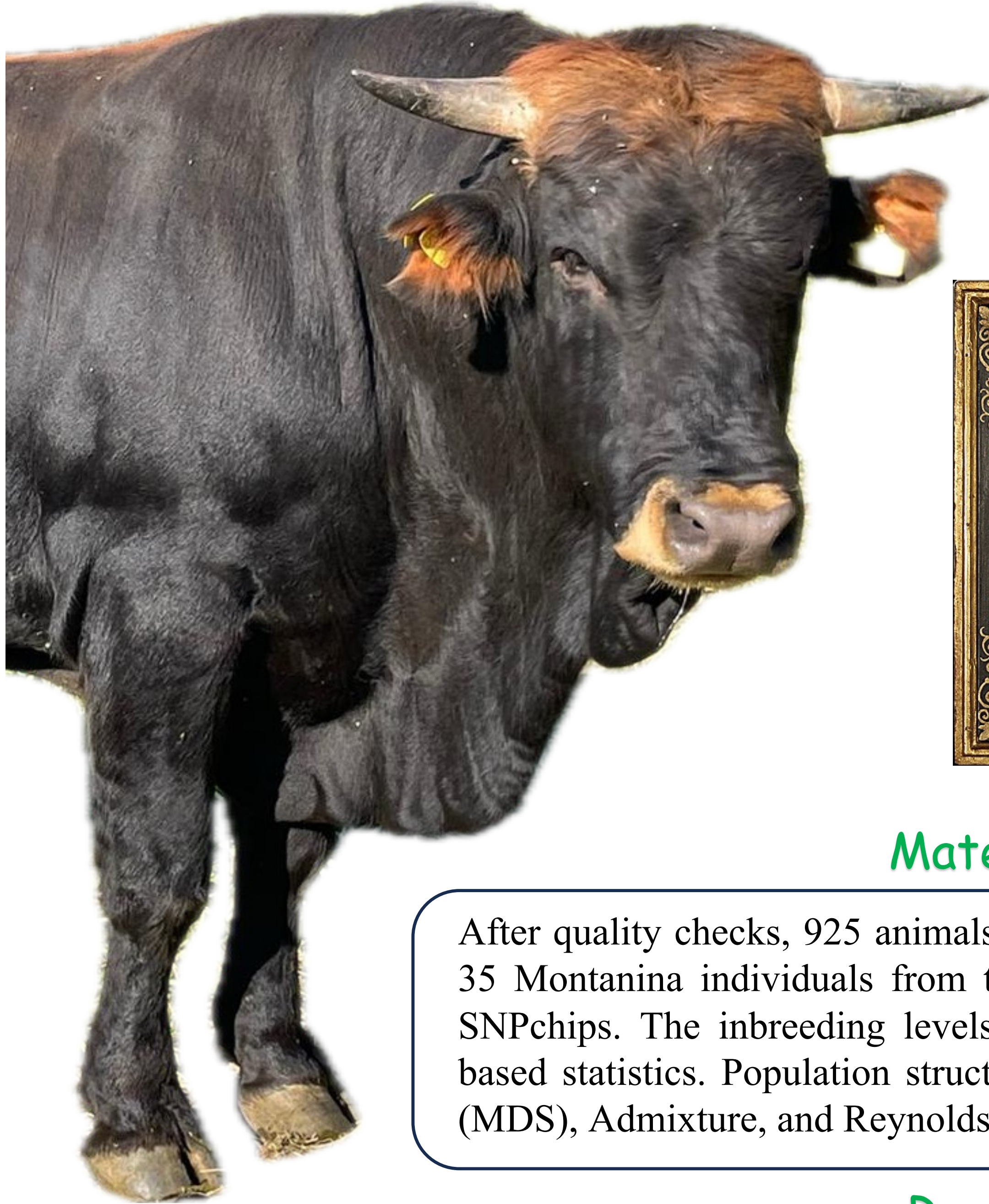
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Introduction and Aim

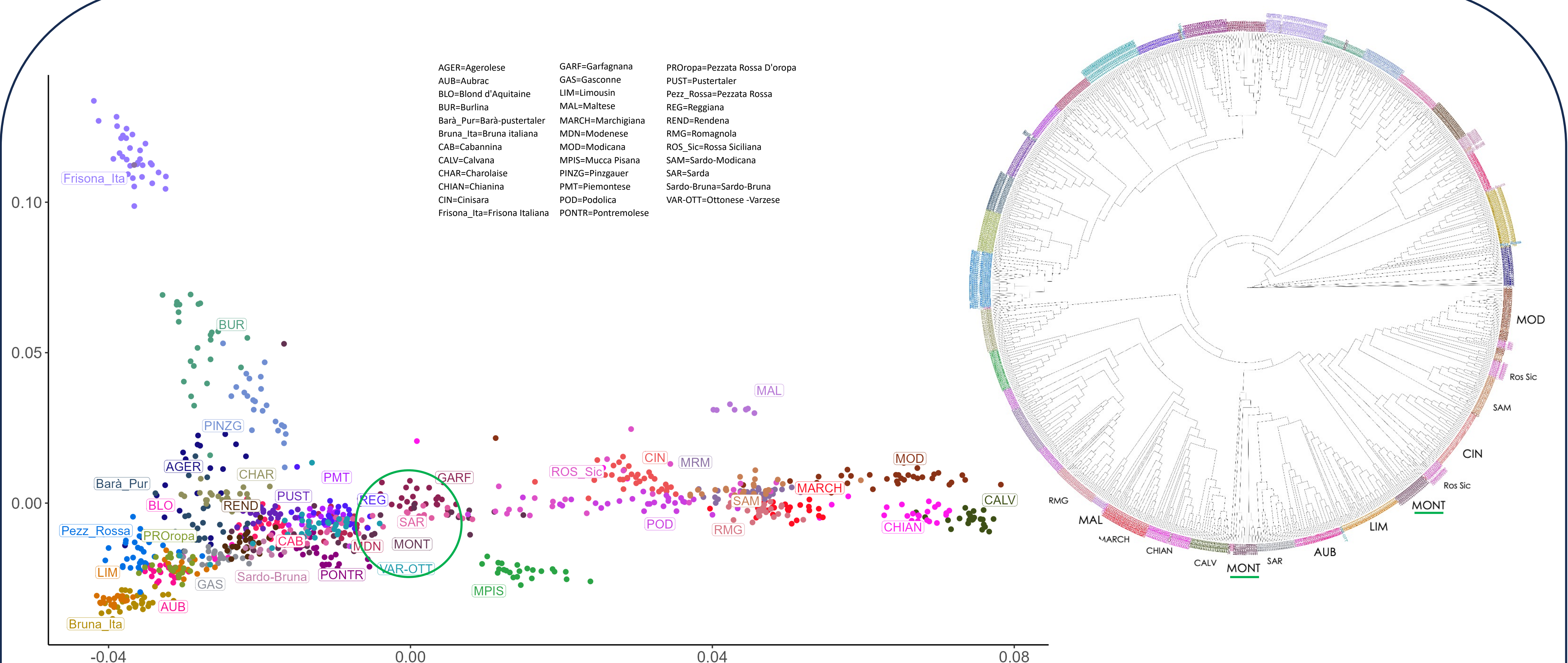
Here we provide the first genomic investigation on Montanina, an indigenous dual-purpose Sicilian (Italy) cattle. Montanina is typically reared under extensive farming systems and well adapted to the harsh mountainous environment they inhabit. However, anecdotal knowledge of crossbreeding with cosmopolitan breeds to improve profitability exists.



Materials and Methods

After quality checks, 925 animals from 37 Italian and French cattle breeds, including 35 Montanina individuals from three farms, were genotyped using medium-density SNPchips. The inbreeding levels were determined through Runs of homozygosity-based statistics. Population structure was analyzed through multidimensional scaling (MDS), Admixture, and Reynolds and identity-by-state (IBS) distances.

Results and Discussion



We recorded low levels of inbreeding comparable among the three Montanina populations (0.013 ± 0.011 ; 0.011 ± 0.006 , 0.024 ± 0.033). Both IBS and MDS positioned Montanina between beef-selected breeds and other Sicilian breeds. By investigating the ancestry components in higher detail, we identified Limousin as the main source of introgression in Montanina. Importantly, we recorded lower levels of introgression in one of the three sampled farms.

Our results reflect the selection history of the breed, including the acknowledged crossbreeding with Limousin bulls, aimed at increasing meat yield. These findings offer crucial insights into the genetic structure, diversity, and history of Montanina, aiming at informed breeding efforts that balance productivity with the preservation of the breed's originality.

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