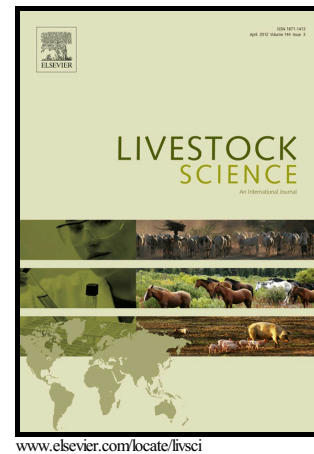


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Genome-Wide Association study for Milk Production in Egyptian Buffalo

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Abstract

With the aim of characterizing the genetic background of Egyptian buffalo and identifying genomic regions and potential causative mutations associated with milk yield, we performed a Genome-Wide Association Study (GWAS) in Egyptian buffalo using Axiom Buffalo Genotyping Array 90K. This study was carried out with 250 buffalo cows using 89,069 daily milk records. After quality control, a total of 42,269 single nucleotide polymorphisms (SNPs) remained for further analysis. Genome-wide analysis was performed in the way of SNP-by-SNP, through regressing the observations of an average daily milk yield deviations on SNP alleles.

¹ 1st and 2nd authors contributed equally to this article.

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