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**0172 The identification of a putative mutation for SLICK hair coat in Senepol cattle.**

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The slick hair coat (SLICK) is a dominantly inherited trait typically associated with tropically adapted, Criollo-derived cattle breeds. The trait is of interest relative to climate change, due to its association with improved thermo-tolerance and subsequent increased productivity. The goal of this work was to identify the mutation underlying the *SLICK* locus, which was previously mapped to a 4 cM region on chromosome (Chr) 20. To refine this map position, BovineHD genotypes were generated from a sampling ( $N = 195$  animals) of Senepol, Carora, Romosinuano, three additional slick-haired cross-bred lineages and a group of non-slick ancestral breeds. Genome-wide association analysis narrowed the *SLICK* locus to a 0.8Mb (37.7-38.5 Mbp UMD 3.1) consensus region, which contains *SKP2* and *SPEF2* as possible candidate genes. Three specific haplotype patterns were identified in slick individuals, all with zero frequency in non-slick individuals. In an attempt to identify candidate causative mutations in this region, whole genome re-sequencing was completed for one Romosinuano and five Senepol animals. SNP discovery and annotation analyses revealed a putative causative polymorphism within *prolactin receptor* (*PRLR*), which would truncate an encoded domain involved in JAK/STAT5 signaling. Validation testing of this SNP and 37 others was done across a DNA panel ( $N = 466$ ) that included representation from five *SLICK* and seven non-*SLICK* breeds. The results

strongly suggest the frameshift mutation in *PRLR* is the causative mutation underlying *SLICK* in Senepol and some Romosinuano cattle. However, no associations between this SNP and *SLICK* animals from Limonero and Carora breeds were found. This information along with accompanying population structure information supports potentially two independent *SLICK* mutations, one common to Senepol and Romosinuano and another in Limonero and Carora.

**Key Words:** slick hair coat, cattle, prolactin receptor

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**0173 Genomic selection of Nili-Ravi buffalo.** M. Moaenud-Din<sup>\*1</sup>, G. Bilal<sup>1</sup>, and M. S. Khan<sup>2</sup>, <sup>1</sup>PMAS-Arid Agriculture University, Rawalpindi, Pakistan, <sup>2</sup>University of Agriculture, Faisalabad, Pakistan.

Among three well-documented breeds of buffalo dairy breeds in Pakistan, Nili-Ravi is the best milk producer owing to its characteristic of disease and parasitic resistance, and a better convertor of roughages into useful products than cattle. A selection program to enhance the genetic potential for milk production of Nili-Ravi using progeny testing program is going on. Traditional progeny testing program has made a remarkable improvement in the genetic potential of dairy cattle in the developed world. However, this program faces severe implementation issues in buffalo improvement due to limitation of resources and basic infrastructure. Simulated studies have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement. The current study intends to explore the application of genomic selection in a typical buffalo breeding perspective using Nili-Ravi in Pakistan as an example. The assumed size of the training population for genomic selection was 15,860 present with BRI, Pattoki. Our calculations indicated that genomic selection can reduce the generation intervals in the male to male selection pathway from 9.5 yr down to 3.3 yr. It can result in almost 2 times increase in response to selection compared to that in a progeny testing program. Furthermore, it reduced the costs of proving bulls by 88%. The present study suggests the initiation of the program of genomic selection for Nili-Ravi in Pakistan and may serve as an example for other developing countries. The findings of the current study may encourage researchers and policymakers to use genomic selection for improvement in the productivity of dairy cattle of developing countries.

**Key Words:** developing country, genomic selection, Nili-Ravi buffalo