

BREEDING AND GENETICS

Copy number variation of PRAME gene across dairy breeds

Wednesday, July 11

2:15 PM - 2:30 PM

Author(s)

TS

Tatiane Seleguim Chud

Centre for Genetic Improvement of Livestock, Dept of Animal Biosciences,
University of Guelph.

DB

Derek Bickhart

Dairy Forage Research Center, USDA-ARS

JC

John Cole

Animal Genomics and Improvement Laboratory, USDA-ARS

FB

Fernando Baldi Rey

São Paulo State University (Unesp), School of Agricultural and Veterinarian
Science (FCAV), Jaboticabal, Brazil

Md

Marcos Vinícius da Silva

Embrapa Dairy Cattle
Juiz de Fora

DM

Danísio Munari

Universidade Estadual Paulista (Unesp) , Faculdade de Ciências Agrárias e
Veterinárias, Departamento de Ciências Exatas

The *PRAME* gene plays an important role on reproduction function in cattle and that gene almost present in high copy number in the mammalian genome. Copy number variation (CNV) states have been used in population genetics studies to identify population divergences due to alterations in copy number regions or genes and to identify their impact on economic interest traits, including reproductive traits. The aim of this study was to identify the copy number differences of the *PRAME* gene within the Gir, Holstein, and Girolando breeds. We analyzed two whole genome sequencing datasets from Girolando bulls, 13 from Gir and five from Holstein. A read depth method was performed using the

CNVnator software to detect the CNVs in each sample. To identify the population differentiation among the breeds, the Vst statistic was used. The Vst value (0.77) for the *PRAME* gene (BTA17:51252501-51660000) indicated a high level of population differentiation among the breeds. The average of the copy number on the *PRAME* region for the Gir bulls was 14.51 per animal, whereas Girolando and Holstein animals did not exhibit copy number variation in this specific region. Our findings suggested that the *PRAME* region is copy number variable only in the indicine lineage. This study identified positive selection on the *PRAME* gene in Gir cattle that may have originated from the domestication process.