

**P4009 Genomic selection for tick resistance in Braford and Hereford cattle using single-step methodology.** F. F. Cardoso<sup>\*1,2</sup>, C. C. G. Gomes<sup>1</sup>, M. M. Oliveira<sup>1,3</sup>, V. M. Roso<sup>4</sup>, M. L. Piccoli<sup>4</sup>, F. V. Brito<sup>4</sup>, R. H. Higa<sup>5</sup>, S. R. Paiva<sup>2,6</sup>, M. V. G. B. Silva<sup>2,7</sup>, L. C. A. Regitano<sup>2,8</sup>, M. J. Yokoo<sup>1</sup>, A. R. Caetano<sup>2,6</sup>, I. Misztal<sup>9</sup>, and I. Aguilar<sup>10</sup>, <sup>1</sup>Embrapa Southern Region Animal Husbandry, Bage, RS, Brazil, <sup>2</sup>National Counsel of Technological and Scientific Development (CNPq), Brasilia, DF, Brazil, <sup>3</sup>Coordination for the Improvement of Higher Level Personnel (CAPES/PNPD), Brasilia, DF, Brazil, <sup>4</sup>Gensys Associated Consultants, Porto Alegre, RS, Brazil, <sup>5</sup>Embrapa Agriculture Informatics, Campinas, SP, Brazil, <sup>6</sup>Embrapa Genetic Resources & Biotechnology, Brasilia, DF, Brazil, <sup>7</sup>Embrapa Dairy Cattle, Juiz de Fora, MG, Brazil, <sup>8</sup>Embrapa Southeastern Region Animal Husbandry, Sao Carlos, SP, Brazil, <sup>9</sup>University of Georgia, Athens, GA, USA, <sup>10</sup>National Agricultural Research Institute, Canelones, Uruguay.

The *Rhipicephalus microplus* tick is one of the main sources of losses in tropical cattle production, causing decreased performance, hide devaluation, and increased costs with treatments and transmission of infectious agents. The aim of this work was to evaluate the utility of genomic evaluation of Braford and Hereford cattle for genetic resistance to ticks. Repeated tick counts were obtained in 2010 and 2011 from 3,114 Braford and Hereford cattle from 7 herds of the "Delta G Connection" breeding program, totalizing 8,004 records. A sample of 1898 Braford and 262 Hereford animals was genotyped using Illumina BovineSNP50 Beadchip. Averaged and log-transformed records were combined with pedigree and genotypes to carry out single step genomic evaluation using BLUPf90 programs. Heritability of tick counts was estimated to be  $0.42 \pm 0.05$ , with a 75% increase compared with the estimate based on traditional pedigree evaluation ( $0.24 \pm 0.06$ ). Finally, data was split into 8 subsets (7 Braford and 1 Hereford) for a cross-validation study. Correlation between genomic predictions from the cross-validation and from full data analyses were  $0.61 \pm 0.13$  and  $0.47 \pm 0.05$ , respectively for Braford and Hereford animals. These results indicate that genomic selection could be used as a reliable tool to improve genetic progress for resistance to ticks in these breeds and to obtain resistant lines of cattle raised at South America.

**Key Words:** beef cattle, BovineSNP50 Beadchip, *Rhipicephalus microplus*