

## Genetics mechanisms of resistance and response to tick infestation in Hereford cattle: a global view

Daniela D Moré; EMBRAPA Southeast Livestock, São Carlos, SP, Brazil  
Wilson M. Junior; EMBRAPA Southeast Livestock, São Carlos, SP, Brazil  
Maurício A. Mudadu; EMBRAPA Southeast Livestock, São Carlos, SP, Brazil  
Adhemar Z. Neto; EMBRAPA Agriculture Informatics, Campinas, SP, Brazil  
Claudia C. G. Gomes; EMBRAPA South Animal Husbandry and Sheep, Bagé, RS, Brazil  
Adriana M. G. Ibelli; EMBRAPA Swine and Poultry, Concórdia, SC, Brazil  
Vitor Catoia; EMBRAPA Southeast Livestock, São Carlos, SP, Brazil  
Fernando F. Cardoso; EMBRAPA South Animal Husbandry and Sheep, Bagé, RS, Brazil  
Luciana C. A. Regitano; EMBRAPA Southeast Livestock, São Carlos, SP, Brazil  
**Corresponding author e-mail:** luciana.regitano@embrapa.br

### Abstract:

**Introduction.** Ticks are haematophagous parasite of domestic and wild animals and potential vector of many diseases. Many efforts have been done to control this parasite in livestock once that they impair substantially the animal production. Unfortunately, tick control has been done by the use of acaricides that contaminate the environment and animal products, and also induce tick resistance. Researching on alternatives of control have indicated that genetic resistance of the host is the best choice against this parasite. Additionally, the development of new generation technologies to analysis genomic data and the sequencing of the bovine genome bring the unique opportunity to perform genomic association studies (GWAS) and marked assisted selection (MAS) in animal breeding. **Objectives.** In this way, the present study aims to analyze the bovine skin transcriptome before and after tick infestation between resistant and susceptible cattle, to identify genes differentially expressed (DE), SNPs in transcribed (QTLs) and regulatory (eQTLs) regions, alternative transcription sites and imprinted genes to draw a map of the skin transcriptome in response to tick infestation. Additionally, the data obtained will be integrated with previously results from a GWAS performed with the same animals to search for candidate genes, perform pathways analysis and draw metabolic maps. **Methods.** For this, skin from 39 Hereford bovines presenting contrasting phenotypes, e.g. the 20 most and the 19 less infested bovines, among 900 animals, were biopsied before and after tick infestation and the total RNA was extracted using Trizol<sup>®</sup> reagent (Life Technologies). The samples were submitted to library preparation using TruSeq Sample Preparation Kit<sup>®</sup> (Illumina) following the manufacture's recommendations and submitted to sequencing (RNA-Seq) in Illumina platform using HiSeq1500 system. High-throughput bioinformatic tools will be used to perform the analysis. **Conclusion.** The differences observed in the genetic mechanisms against tick infestation in Hereford cattle certainly will contribute to the genomic selection of this trait and improve the animal production in a sustainable way. **Acknowledgements** EMBRAPA Southeast Livestock, EMBRAPA South Animal Husbandry and Sheep, EMBRAPA Agriculture Informatics and FAPESP