Hello my name is Cherlynn I will present the poster genes associated with resistance to Anaplasma marginale in Angus

**Background**

In cattle, the rickettsiae Anaplasma marginale, Anaplasma centrale and the protozoa Babesia bovis and Babesia bigemina are the main pathogens that cause Bovine Parasite Sadness (bps) (Vidotto and Marana, 2001, Trindade et al., 2011).

In Brazil, this disease is considered endemic and of high mortality, the symptoms caused by different agents are similar, causing difficulty in differentiating signs and difficult diagnosis because an animal can be affected by more than one endoparasite at the same time (Silva et al., 2021).

Anaplasma marginale is transmitted mainly through feeding on hematophagous insects such as flies, mosquitoes and the Rhipicephalus B. microplus (Vitodo and Marana, 2001, Trindade et al., 2011, Dantas-Torres et al., 2012, De Meneghi et al., 2016, Silva et al., 2021).

Resistance is the ability of the animal to mitigate the pathogen burden. Until now, the understanding of the interaction host versus Anaplasma marginale has not been completely elucidated.

In this work, we estimated a bi-trait model with ss-GBLUP with two parasites: Rhipicephalus B. microplus and Anaplasma marginale. In this poster, we will only discuss the results from Anaplasma marginale.

**Data**

Records of 796 animals naturally exposed to Rhipicephalus B. microplus were collected in 2014 in two farms that contribute to the Brazilian Agricultural Research Corporation (EMBRAPA).

There was two collect of samples, some animals had only on collect. DNA extraction and anaplasmosis quantification was performed as described by Buling et al. (2007) using qPCR techniques using reagents from the SsoFast™ EvaGreen® Supermix kit (Bio-Rad) followed using the CFX™ Real-Time DetectionsSystems equipment from Bio-Rad.

All animals were genotyped with a genotype panel containing one hundred and fifty thousand SNPs. The samples with call rate below 0.90 and SNPs located in the same positions were excluded.

Only SNPs located in autosomal chromosomes with call rate values greater than 0.98, minor allele frequency greater than 0.03, and Hardy-Weinberg values greater than 10-7 were used. After the quality control, seventy-one thousand two hundred and thrity-seven SNPs remained.

The contemporary group were formed by the set: farm, year, season, management group at weaning and collect.

**Method**

The resistant trait was performed, the number of copies of Anaplasma marginale and Rhipicephalus B. microplus was transformed to logarithm base 10 using a single-step GBLUP.

After obtaining the effects and (co)variation parameters, to perform GWAS we choose to analyze the percentage of variance explained by 10 snps adjacent non-overlapping markers.

For the identification of genes, the Ensembl tool (http://www.esembl.org/index.html) was used together with BioMart tool (Kinsella et al., 2011) and having as reference the sequence for Bos taurus species ARS-UCD 1.2 (Geer et al., 2009). Having the gene list available, functional analysis was performed, employing the ClueGo package (Bindea et al., 2009) available for the Cytoscape program (Shannon et al., 2003). For this purpose, we considered the Genes (Go) ontology base for biological and immune system processes; Kappa Score higher than 0.5; overall Network specificity; no minimum cluster size; p values corrected by Boferroni's step down test below the 0.05 significance level were considered significant.

The heritability and repeatability for the level of infection by Anaplasma marginale were 0.0854 and 0.1602, respectively. These estimates are considered significant because their credibility intervals do not encompass zero and were estimated using maximum restricted likelihood with GBLUP.

The chromosomes: 4, 5, 7, 9, 11, 14, 15, 16, 19, 20, and 27 have windows associated with the resistance characteristic explaining 2.84% in total. In the functional analysis, there is no significant path associated with the trait. We had a little size of animals and there is not much power to assure that the significance was achieved. But the paths and genes could be associated with the trait. Most of the paths are related to the T cells (activation, proliferation, regulation, differentiation).

**Key-findings**

The genes that could be associated with the resistance to Anaplasma marginale in Angus females are:

GJA1 : In a study of periodontal infection in mice (Anand et al., 2008) observed that the Cx43 gene plays an important role in the regulation of phagocytes and macrophages, modulating the host immune response to fight infection in vivo and that its regulation has an effect on the survival of the animal after being affected by bacterial infection.

In a study with pigs and Anaplasma phagocytophilum, in real-time RT-PCR and microarray hybridization analysis, the GJA1 gene, together with IL1RAPL1, TCR-alpha and TSP-4 genes, related to immune responses, were upregulated in infected animals, indicating that bacterial infection can be controlled by the host by activating its innate and adaptive immune system (Galindo et al., 2012, Tittarelli, 2021).

In a study with nematodes and Merino sheep, Zhang et al., (2019) also documented the GJA1 gene in the primary infection response in selecting herds resistant to Haemonchus contortus infection. Such studies point to the potential for the GJA1 gene to be a candidate gene in resistance to Anaplasma marginale infection level.

PTPRZ1 : is expressed on B cells and has great importance in the regulation and survival of these defense cells and its absence can reduce the proportion and number of mature B cells in the body, influencing the adaptive immune response (Cohen et al., 2012, Cohen and Shachar, 2013).

B cells act in the humoral immune system and when activated can store memory of the first infection and thus make the adaptive immune response more optimized in cases of relapse (Mesquita Júnior et al., 2010).

IGF1 : In humans, the IGF1 gene modulates IgE production in B cells (Kim, et al., 2003, van Bilsen et al., 2008).

CRACR2A : is a modulator of calcium-release-activated calcium (CRAC) channels acting on T cells (Srikanth et al., 2010, Wilson et al., 2014, Woo et al., 2018) and it is suspected that this protein may play an active role in the activation of other cells of innate and adaptive immunity (Wu et al., 2021).

LAX1 : The LAX1 gene also has relevance in encoding membrane-associated adaptor proteins of B and T lymphocytes (Hoang et al., 2019).

**Take-away**

Here we present Evidence that Angus females present resistance to Anaplasma marginale and the genes cited could be associated with the trait.

If there is any question, please check out my contact info in the QRcode on the poster.

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