contrast, B cell deficient mice were unable to control bacteremia. Collectively, our results indicate that a GC-independent but T cell-dependent germline IgM being the major effective antibody specificity. Our results further highlight the importance IgM and potentially anti-CPS antibodies in clearing *S. suis* infections and provide insight for future development of *S. suis* vaccines.

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099 - *Streptococcus suis* surface-antigen recognition by antibodies and bacterial elimination is influenced by capsular polysaccharide structure

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Streptococcus suis is an encapsulated bacterium that can cause severe invasive diseases in pigs. The bacterial capsular polysaccharide (CPS) is a critical virulence factor that provides resistance against host phagocytic cells. The antigenicity of the CPS defines 29 distinct serotypes of *S. suis*, with some serotypes being more commonly associated with clinical disease than others. For instance, the serotype 2 is the most prevalent worldwide. Our hypothesis was that the structure of the CPS influences survival in the host and resistance against antibodies targeting subcapsular antigens (such as proteins) at the bacterial surface. Therefore, serotype-switched mutants of *S. suis* serotype 2 were employed to compare the role played by the CPS structures of serotypes 2, 3, 4, 7, 8, 9 and 14, since the only difference between these strains is the CPS expressed. Primary and secondary infections in a mouse model showed that strains expressing the CPS of the serotypes 3 and 4 were the most susceptible to host defences during a primary infection. During the secondary infection, strains expressing the CPS of serotypes 3, 4 and 14 were the most eliminated. Furthermore, CPS structure was found to influence antigen recognition by antibodies. The CPS of serotypes 3, 4 and 14 allowed more IgG binding to subcapsular antigens (such as proteins) than the CPS of serotypes 2, 7, 8 and 9. This feature consequently affected antibody capacity to induce opsono killing of *S. suis*. Results suggest that the different CPS structures of *S. suis* provide varying levels of protection by influencing antigen availability and elimination by the host immune system. This finding is of importance for vaccine development and highlights the need to closely monitor cross-protection when designing *S. suis* vaccines since the CPS structure might eventually affect the efficacy of vaccines targeting subcapsular antigens at the bacterial surface.

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Theme 7. Immunology of parasite diseases

028 - Ovine resistance against *Haemonchus contortus*: Does a breed or a β-globin subtype feature?

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Background: Hair sheep breeds, as Santa Inês, are well-known for improved natural resistance and/or resilience against gastrointestinal infections, especially by Haemonchus contortus, compared to wool breeds, such as Dorper and Texel. Several studies have also pointed out to significant association of resistance against hemonchosis and β-globin polymorphisms.

Objectives: Compare phenotypic, Th2 profile and inflammatory responses during infection with H. contortus in different sheep breeds (Santa Inês-SI, Texel-TX and White Dorper-DO) harboring different β-globin haplotypes (AA, AB, BB).

Methods: Four male lambs of each group (SI-AA, SI-AB, SI-BB, TX-BB and DO-BB) were dewormed and, after 14 days, received 4000 L3 H. contortus (D0). Animals were weekly evaluated for packed cell volume (PCV), fecal egg counts (FEC) and blood gene expression until D28.

Results: For DO and TX, there were no AA animals in the flock, while rare AB were found, therefore they were not included in this study. Comparing BB haplotype lambs, all three sheep breeds presented similar PCV. However, SI-AA lambs presented significantly higher PCV compared to DO-BB and TX-BB from D7 to D21, and to SI-BB on D21. Despite no significant differences, higher FEC levels were observed for DO and lower levels for SI-AA. Differential Th2 profiles were observed among groups, higher IL4/IL13 levels were detected in SI animals (especially SI-AA), while IL5 was most prominent in TX and secondly in DO. Inflammatory response was IL1B polarized in SI, but TNFA in TX. Significant higher levels of MS4A2 (high affinity IgE receptor gene) were observed in SI breed.

Conclusion: Based on similar PCV values among SI-BB, DO and TX groups, but superior PCV for SI-AA animals, we hypothesized that resistance against hemonchosis may be more associated to the β-globin subtype than to the breed feature. Differential Th2 and inflammatory responses were also distinct among these groups.

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191 - Evaluation of global immune responses in goats infected with *Haemonchus contortus* using RNA sequencing

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Haemonchus contortus is an extremely pathogenic resident gastrointestinal nematode in tropical and subtropical regions worldwide, causing significant production and economic losses in small ruminants. During infection, this nematode feed by sucking blood from the abomasum mucosa. Over the years, anthelmintic drugs have been used to manage this nematode; however, drug resistance is becoming a problem. There is only one registered vaccine (Wirevax®) in South Africa, and it is approved for use in sheep. Therefore, there is an urgent need to develop alternative vaccines for goats as well. *H. contortus* infection is usually associated with the Th2 immune responses. However, the detailed host immune mechanisms and pathways involved in protection against *H. contortus* infections are not well-understood. This study aims to evaluate the immune response mechanisms and pathways involved during *H. contortus* infection in goats using RNA sequencing (RNA-seq). To achieve this, goats will be orally infected twice with *H. contortus* L3 larvae in five-week intervals. The innate and adaptive immune responses following primary and secondary infection will be evaluated in peripheral blood mononuclear cells (PBMC) separated using magnetic-activated cell sorting (MACS). Immune transcriptome analysis will be done in individual cell populations using RNA-seq. This will provide insights into the immune mechanisms and pathways involved in goat immune responses to *H. contortus.* Understanding the immune response mechanisms and pathways involved will lay a foundation for developing alternative vaccines against *H. contortus.*

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