



VARIANT DISCOVERY IN GENES IDENTIFIED AS DIFFERENTIALLY EXPRESSED GENES BETWEEN THE ABOMASAL LYMPH NODE TRANSCRIPTOME OF RESISTANT AND SUSCEPTIBLE ADULT SHEEP TO *Teladorsagia circumcincta* INFECTION

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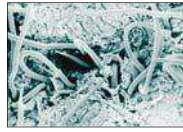


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Churra sheep

Introduction



Teladorsagia circumcincta (Robin et al. 2007)

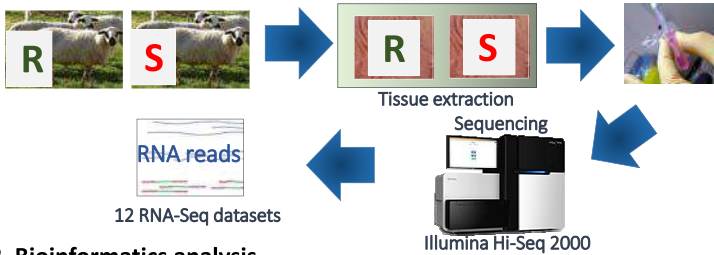
- Gastrointestinal nematode (GIN) infections are one of the major health issues facing grazing sheep populations. The resistance/susceptibility trait appears to be a highly complex trait.
- Several QTL mapping studies have tried to identify genomic regions and mutations^{1,2} but the detection of causal mutations for this trait is still a challenge for the research community.
- The RNA-Seq technology provides the opportunity to perform gene quantification, differential gene expression and detection of variants with high-throughput transcriptome data from a specific tissue.
- In a previous study, we identified a list of 106 differential expression genes (DEGs) based on RNA-Seq dataset obtained from the abomasal lymph nodes of 12 adult sheep³.

Objective: In the present study, we have performed a variant calling analysis on the same RNA-Seq dataset with a focus on the list of the reported 106 DEGs. We present a list of functionally relevant variants that could underlie the genetic control of resistance/susceptibility to *T. circumcincta* in adult sheep.

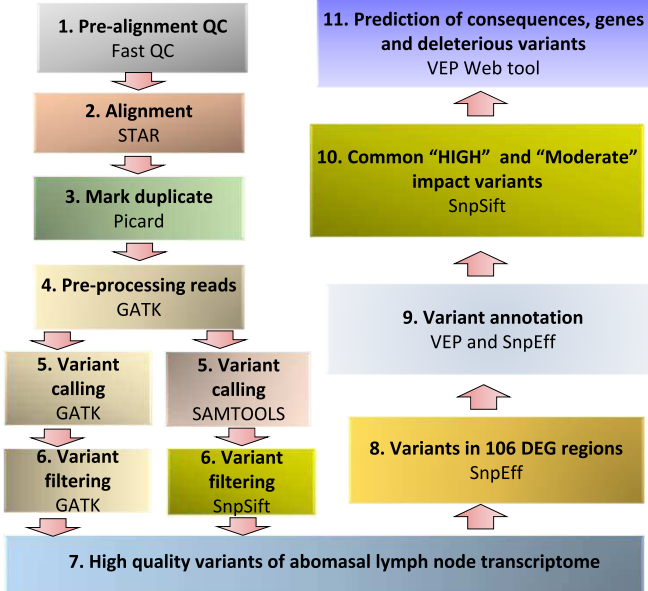
Materials and methods

1. Experimental infection, RNA extraction and RNA-Seq

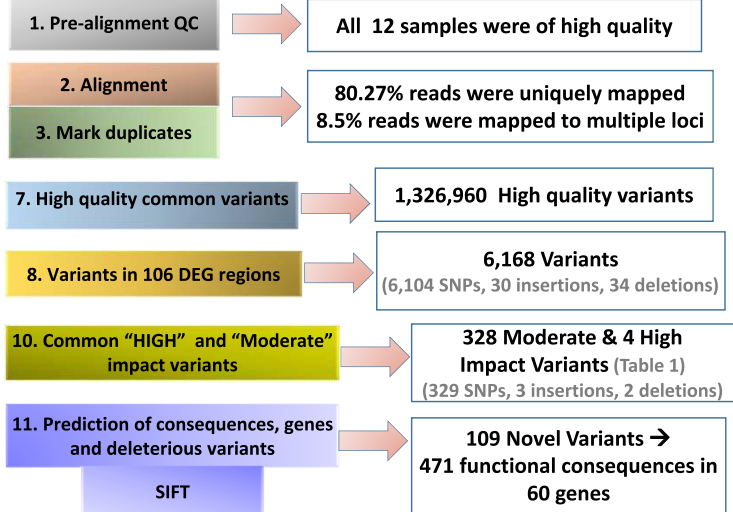
- 12 adult Churra ewes previously classified as 6 resistant (R) and 6 susceptible (S) to *T. circumcincta* were subjected to an experimental infection (EI). After seven days after, animals were humanitarian sacrificed.
- RNA samples were extracted from abomasal lymph node tissue, sequenced through an Illumina RNA-Seq protocol.



2. Bioinformatics analysis



Results and Discussion



- We found 50 deleterious missense consequences, 25 of them located in 15 genes with known symbol ID.
- Some of these genes harboring missense were related to the immune response according the literature review.

Immune response

BPIFB1⁴, KRT20⁵, SLC38A2⁶, FNDC1⁷.

Cell proliferation in response to skin injury

MMP28⁸

Table 1: "High" Impact variants identified by both VEP and SnpEff.

S. No	Gene	Location	Consequence
1	LGALS4	OAR14:47718975-47718975	splice acceptor variant
2	SLC38A2	OAR3:139947003-139947003	stop lost
3	ASIC3	OAR4:113023157-113023157	stop gained and splice acceptor variant
4	SULF1	OAR9:46254552-46254553	frameshift variant

Conclusion

- This study has identified genetic variants in genes previously identified as differentially expressed in relation to GIN resistance/susceptibility in adult sheep.
- The variants predicted to have a potential functional impact should be assessed through future studies as potential relevant variation underlying the genetic architecture of sheep GIN resistance in adult sheep.

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Acknowledgements

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