



Identification of functional INDELs responsible for splice site effect in acute stress response grazing sheep exposed to gastrointestinal nematode infection

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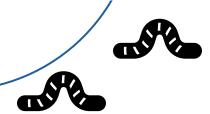
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Gastrointestinal nematode (GIN)





 GIN can also bring massive economic losses due to production losses and treatments.

McLeod, 1995; Saddiqi et al. 2012; Galyon et al. 2020.

Overreliance on anthelmintics





 Increased concerns over the residue of drugs in the food and environment.

Khusro et al. 2004; Saddiqi et al. 2012; Falzon et al. 2013 Sallé et al. 2021



Immune response





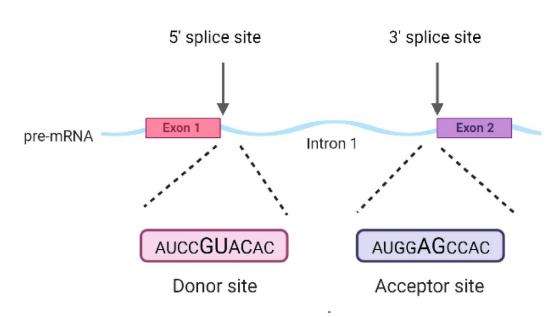
 Identify variants responsible for functional consequences in sheep with different responses to acute inflammatory stress.

You et al. 2008; Benavides et al. 2016; Lam et al. 2020





Splice Site



Adapted from Zabardast et al. 2023

- Regions responsible for signaling specific places for cleavage of introns, located at the boundary of exons and introns.
- Creation or deactivation of splice sites.
- Exclusion of exon and inclusion of introns.
- Change the expression ratio between mRNAs isoforms.

De Conti et al. 2013





Objective



Identification of short insertion and deletions (INDELs) responsible for possible splice site effect in Rideau x Dorset crossbred sheep with different immune profiles under natural exposure to gastrointestinal nematodes using RNA-Sequencing.







Material and Methods





Tissue sampling

Variant Identification

Functional Annotation





Sheep with different immune profiles

Grazed GINcontaminated pasture



High acute phase immune responders n = 15

Medium acute phase immune responders n = 15

*H: one animal removed

Unexposed animals n = 4

Grazed GIN-free pasture



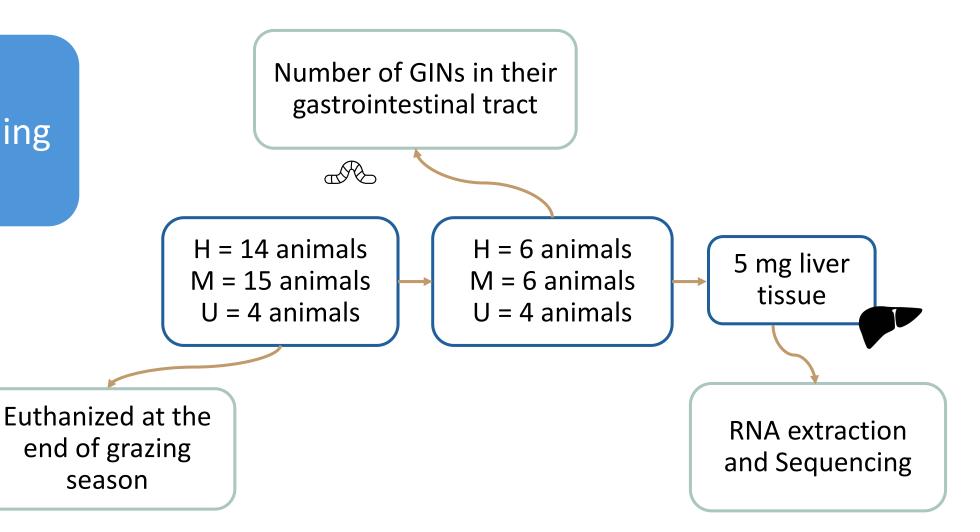
Rideau x Dorset population (n=180)

Challenged with lipopolysaccharide

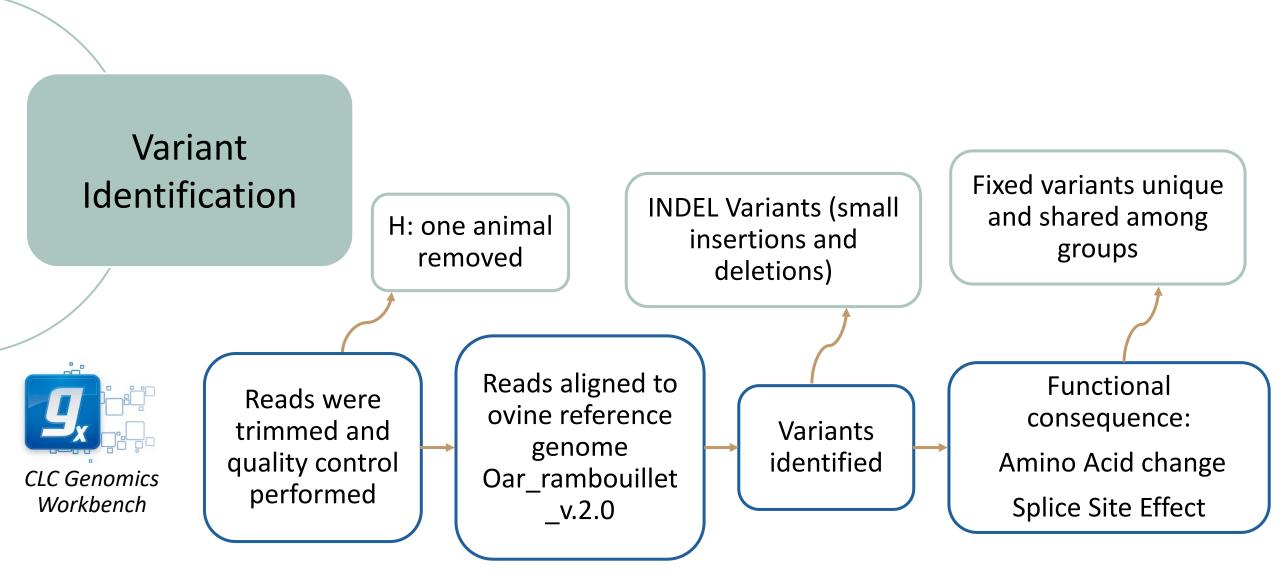
You et al. 2008



Animal Sampling







Functional Annotation

Annotation of genes associated with each INDEL



INDEL Variants

Functional analysis: Enriched metabolic pathways

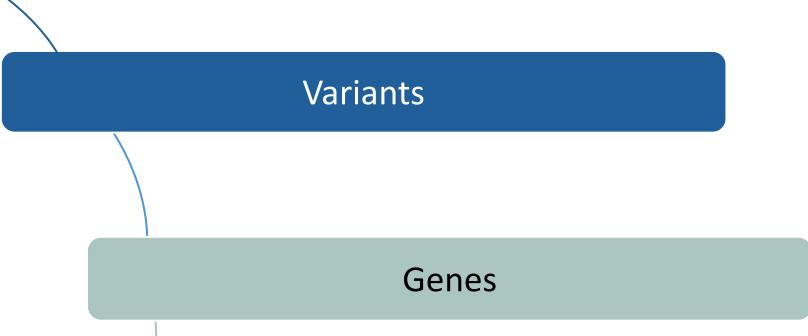






Results and Discussion





Metabolic Pathways





Variants

Table 1. Number total of INDEL variants, INDELs that led to amino acid change (AAC) and to splice site effect (SSE) unique and shared among groups

Group	Variants	AAC	SSE
H	34,168	1,938	1,614
M	39,380	2,026	2,980
U	19,610	1,414	1,396
H/M/U	27,032	1,587	1,777
H/M	12,531	571	719
H/U	5,381	307	376
M/U	8,301	405	558
Total	146,403	8,248	9,420

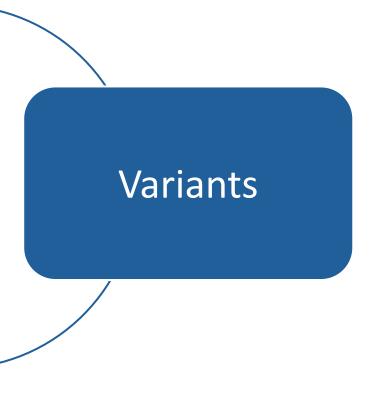
H: High-stress responders; M: Medium-stress responders; U: control group not exposed to gastrointestinal nematodes.

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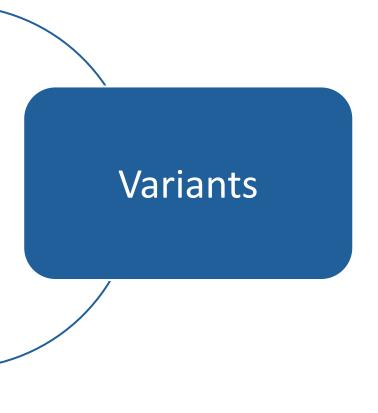
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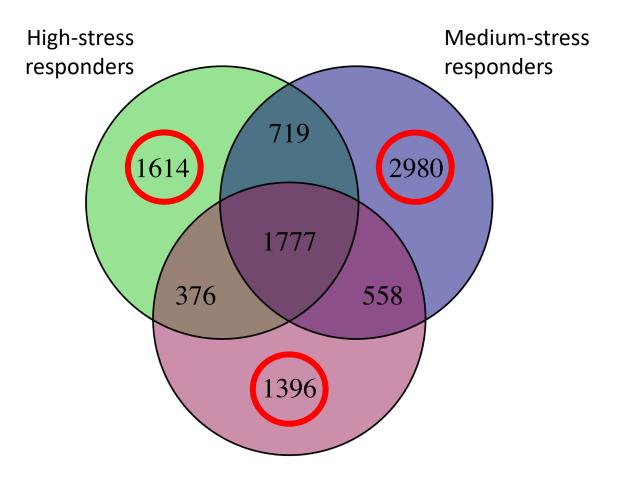




Unexposed animals

Figure 1. Number of INDELs identified

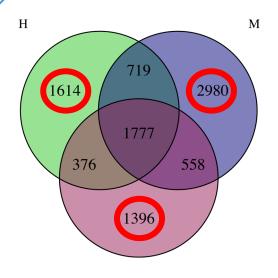




Unexposed animals

Figure 1. Number of INDELs identified

Genes



U



Genes M 719 2980 1614 1777 376 558 U

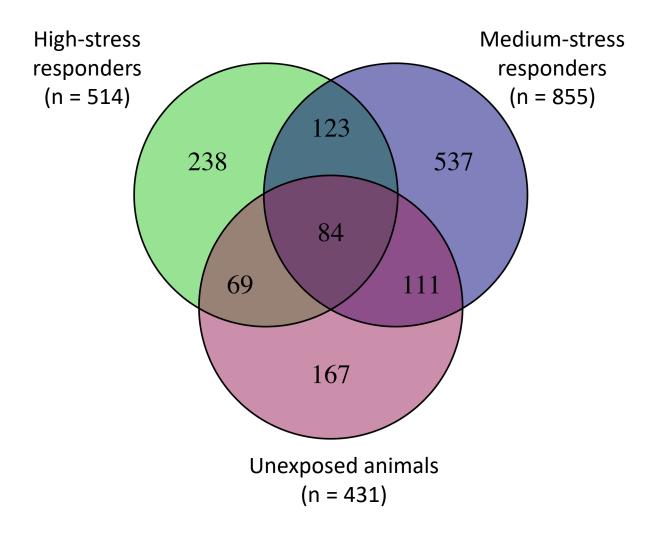


Figure 2. Number of genes identified

Genes M 719 2980 1614 1777 376 558 U

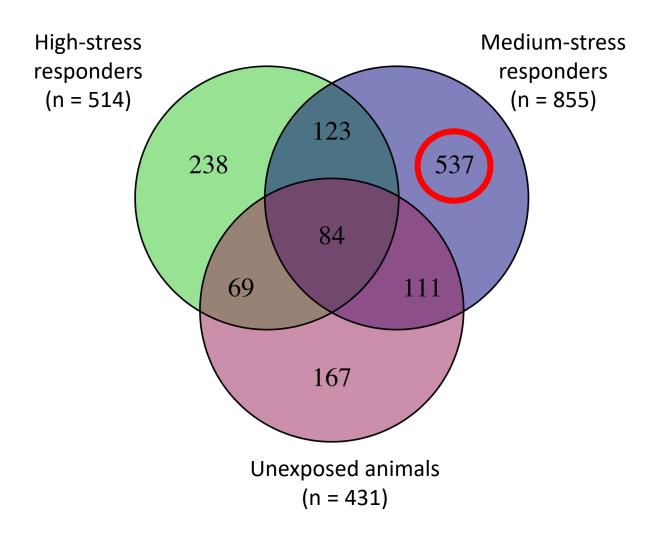


Figure 2. Number of genes identified





CFI

Genes

- The **complement system** is one of the **first responses** to be activated in a **nematode infection**.
- **Up-regulated in resistant lambs** in different studies when compared to susceptible and control groups.
- Identified in genome-wide association studies associated with traits measuring resistance to nematode.

Alba-Hurtado and Muñoz-Guzmán 2013; Guo et al. 2016; Toscano et al. 2019; Zhang et al. 2019; Estrada-Reyes et al. 2019; Niciura et al. 2022



LBP

Genes

- Encodes the Lipopolysaccharide Binding Protein that plays an important role in the acute-phase immune response to gramnegative bacteria.
- LBP blood concentration was significantly different between uninfected and infected animals.
- LBP can be used as a biomarker in H. contortus infection.

Bernheiden et al. 2001 and Zhong et al. 2014

STAT6

Genes

- STAT6 gene is responsible for several **T-cell responses**, the **development of Th2 response**, and the **release of Interleukin-4 (IL-4)**.
- IL-4 is a major cytokine for the activation and expansion of the Th2 response.
- Th2 response is the **primary adaptative immune response in helminth infection in sheep.**

Goenka & Kaplan, 2011; McRae et al. 2015; Stear et al. 2023

Functional analyses

	Group	Pathway name	TGV	TGP	FDR (p<0.05)
	М	Cross-presentation of soluble exogenous			
		antigens (endosomes)	14	53	0.001
	М	Downstream signalling events of B Cell			
	1*1	Receptor (BCR)	18	91	0.002
	М	NIK>noncanonical NF-kB signalling	14	61	0.003
	М	Activation of NF-kappaB in B cells	15	72	0.003
	М	Dectin-1 mediated noncanonical NF-kB			
	1*1	signaling	14	66	0.004
	М	ER-Phagosome pathway	18	106	0.007
	M	Antigen processing-Cross presentation	20	128	0.008
	M	TNFR2 non-canonical NF-kB pathway	16	104	0.028
	M	Interleukin-1 signaling	18	125	0.029
	M	Terminal pathway of complement	4	8	0.037
	M	CLEC7A (Dectin-1) signaling	17	120	0.042



Functional analyses

Nuclear Factor Kappa B (NF-κB) related process

- NF-kB is a family of transcription factors that regulate different processes in the innate and adaptive immune systems.
- Effective participation of NF-κB in mice's inflammatory response to nematode infection.
- Playing roles in the regulation of macrophage-killing capabilities.

Artis et al. 2002; Bąska & Norbury, 2022



Functional analyses

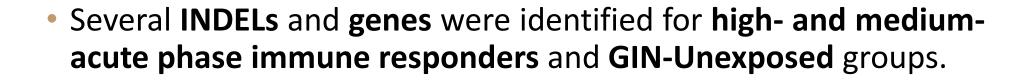
Cross-presentation of antigen

- It is an immunological process not well characterized.
- Cross-presentation is a mechanism used by antigenpresenting cells (APCs) when they encounter extracellular antigens.
- Nematode antigens are presented by APCs to naïve T cells, leading to their differentiation.

Amigorena and Savina, 2010; Joffre et al. 2012; Karrow et al. 2014; McRae et al. 2015



Take Home Messages



• The *CFI*, *LBP*, and *STAT6* genes seems to play important roles in the inflammatory response to GIN infection.

 Enriched metabolic pathways associated with NF-κB, crosspresentation of antigen, and the complement system were identified.

 This study brought additional information to understand the complex immune response to GIN in sheep.



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Cánovas Lab [UofG] and Delma Kennedy [OMAFRA] at the Breezy Ridge Farm, April 2022.







FOOD FROM THOUGHT



Ministry of Agriculture, Food and Rural Affairs





Thank you!

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