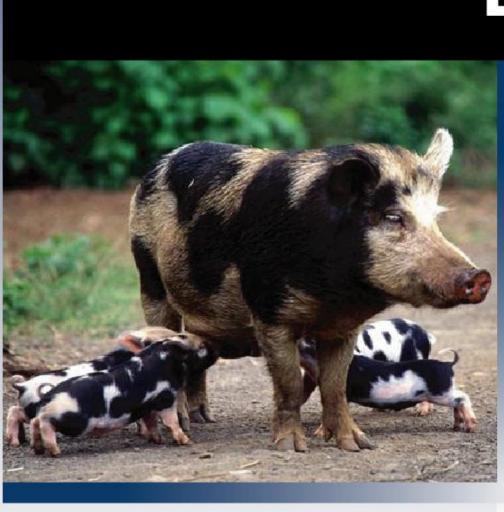


# Laboratory of



# Sus species polymorphism in coding regions of Toll-like receptor (TLR) 1, TLR2 and **TLR6 genes**

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# Introduction:

Toll-like receptors (TLRs) are pattern-recognition receptors which detect pathogens and initiate immune response (Akira and Takeda, 2004). The coding regions of TLRs encode proteins whose peptide domains consists of Leucine rich repeats which bind pathogens and Toll-interleukin 1 receptor involved in intracellular signaling. Polymorphism within these domains are associated with variations in disease resistance in Livestock. Polymorphism within positively selected sites within these domains may have functional changes that can have consequences for host-pathogen interactions (Werling et al, 2008). In pigs, the TLR2/TLR6 heterodimer is activated by Mycoplasma hyopneumoniae. TLR2 also forms heterodimer with TLR1. In this study we identified polymorphisms within the coding regions of TLR1, TLR2 and TLR6 for four Sus species.

# Materials and Methods:

•Paired-end reads from Illumina sequencing technology for Sus barbatus, Sus verrucosus, Sus celebenesis and Phacochoerus africanus were aligned to Sus scrofa TLR genes as a reference genome from Ensemble. •Mozaik Aligner software was used in aligning reads to the reference genome. •Gigabayes software was used in calling SNPs (Single Nucleotide Polymorphisms) •.Read depth to call a SNP at a paricular genomic location was between 3 to 50.

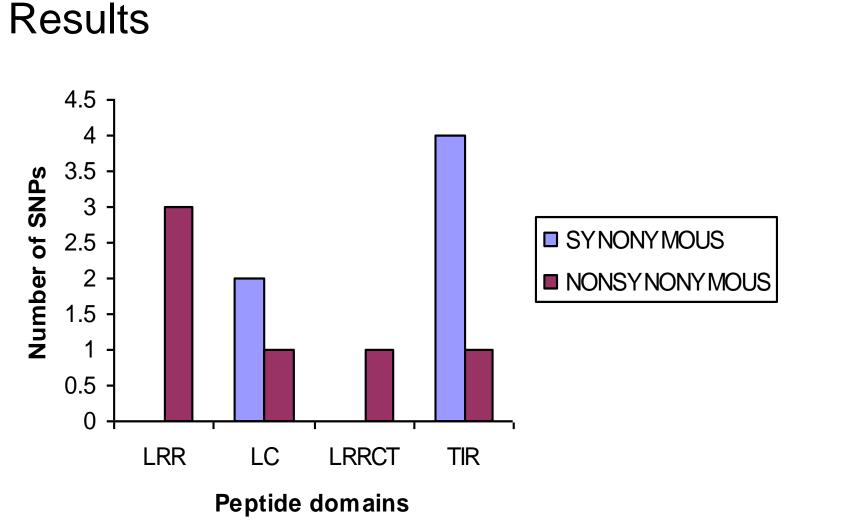


Fig 1. Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR1 across the four Sus species

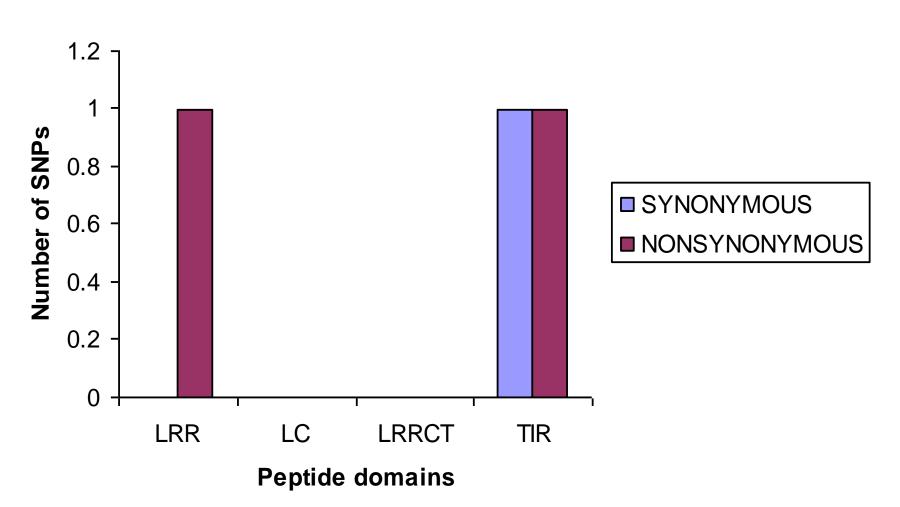


Fig 2: Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR2 across the four Sus species

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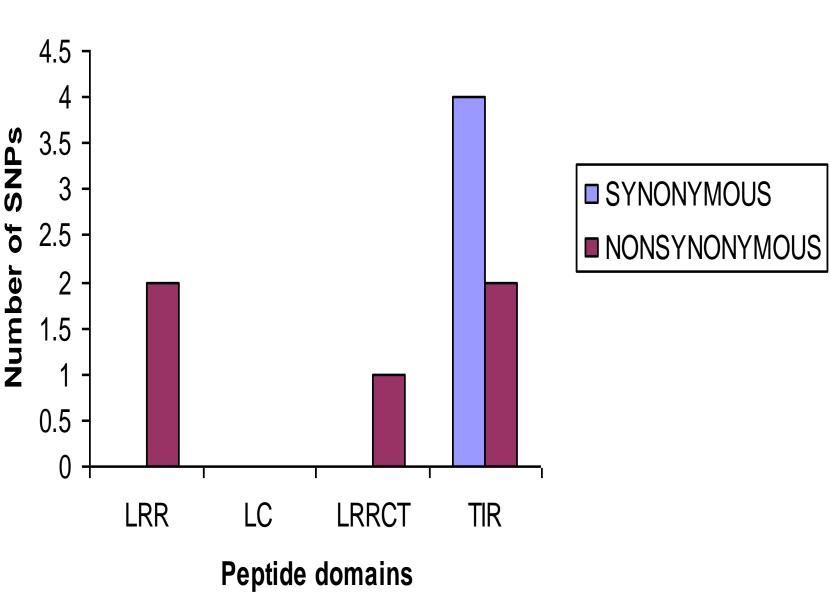


Fig.3 Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR6 across the four *Sus* species

Keys for peptide domains of protein encoded by coding regions of the TLR genes

LRR-Leucine Rich Repeat

LRRCT-Leucine Rich Repeat C terminal

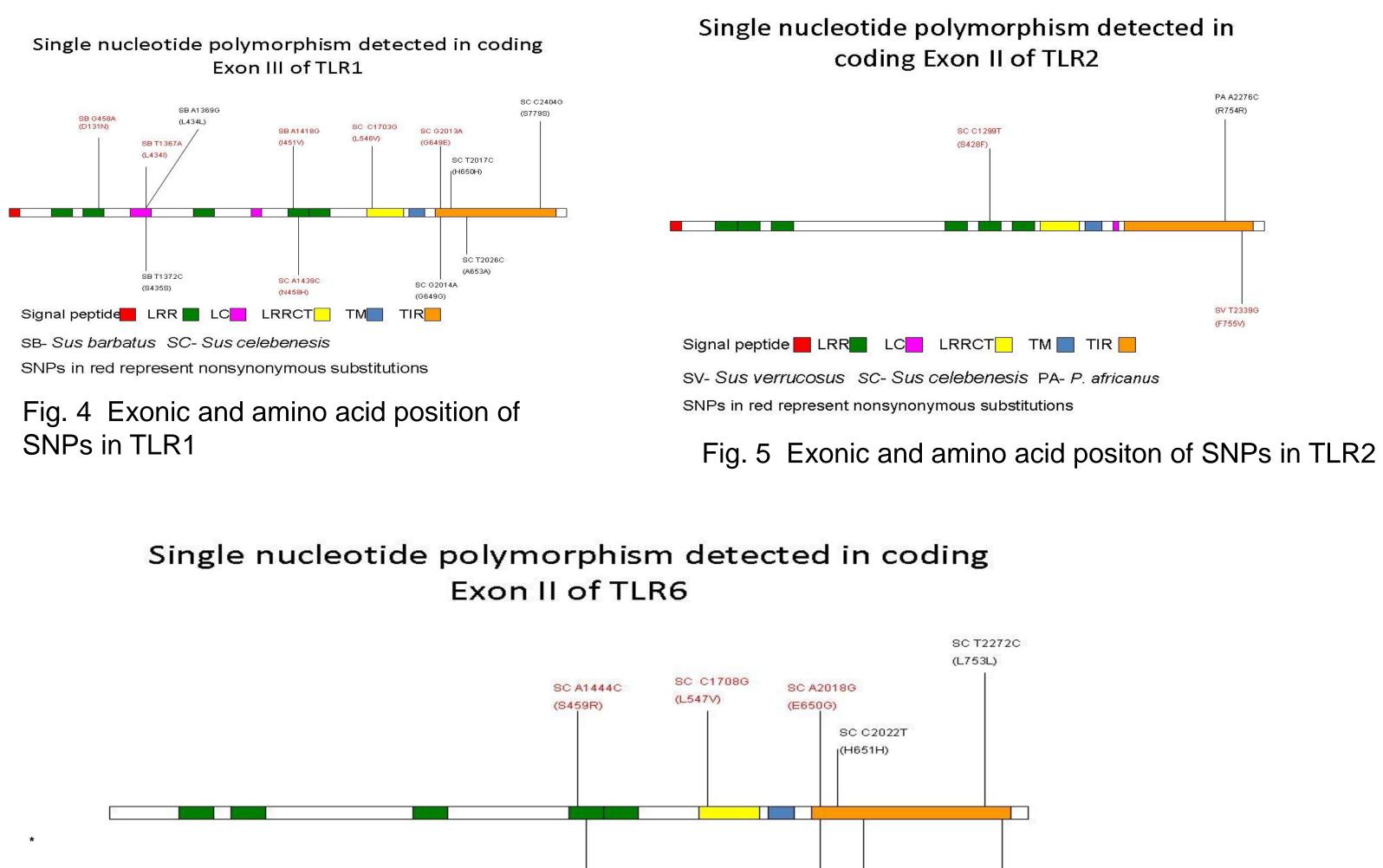
LC-Low complexity

TM-Transmembrane

TIR-Toll/interleukin 1 receptor

# **Results continued:**

•The Leucine rich repeat domains of all TLR gene coding regions had only nonsynonymous SNPs •The TIR domain had both synonymous and nonsynonymous SNPs for both for all the



SC P738S

C 2281T

SC T2043C (N658N) SC A1439C SC A2019G (N458H) (E650E) LRRCT LRR | TIR Signal peptide SC-Sus celebenesis

**Conclusions and future work:** 

The location of both synonymous and nonsynonymous SNPs within the various peptide domians of the coding regions of TLR1, TLR2 and TLR6 across the four Sus species have been determined. The Leucine rich repeat domain that binds to pathogens had only nonsynonymous SNPs at this site. This observation could have implications for host pathogen interactions. A future work will include determining positively selected sites in the coding regions and determine the nonsynonymous SNPs that fall within these sites, as well as their implications on disease susceptibility.

# **References:**

.Akira S, Takeda, K (2004) Toll-like receptor signalling. Nat Rev Immunol 4:499-511. doi:10.1038/nri1391 Werling D, Jann, OC, Offerd V, Glass, E.J, Coffey, T.J (2009). Variation matters: TLR structure and species-specific pathogen recognition. Trends Immunol.30:124-130.



SNPs in red represent Nonsynonymous substitutions

Fig. 6 Exonic and amino acid positon of SNPs in TLR3

