

# Comparative Genomics



## *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 particular genomic location was between 3 to 50.

### Results

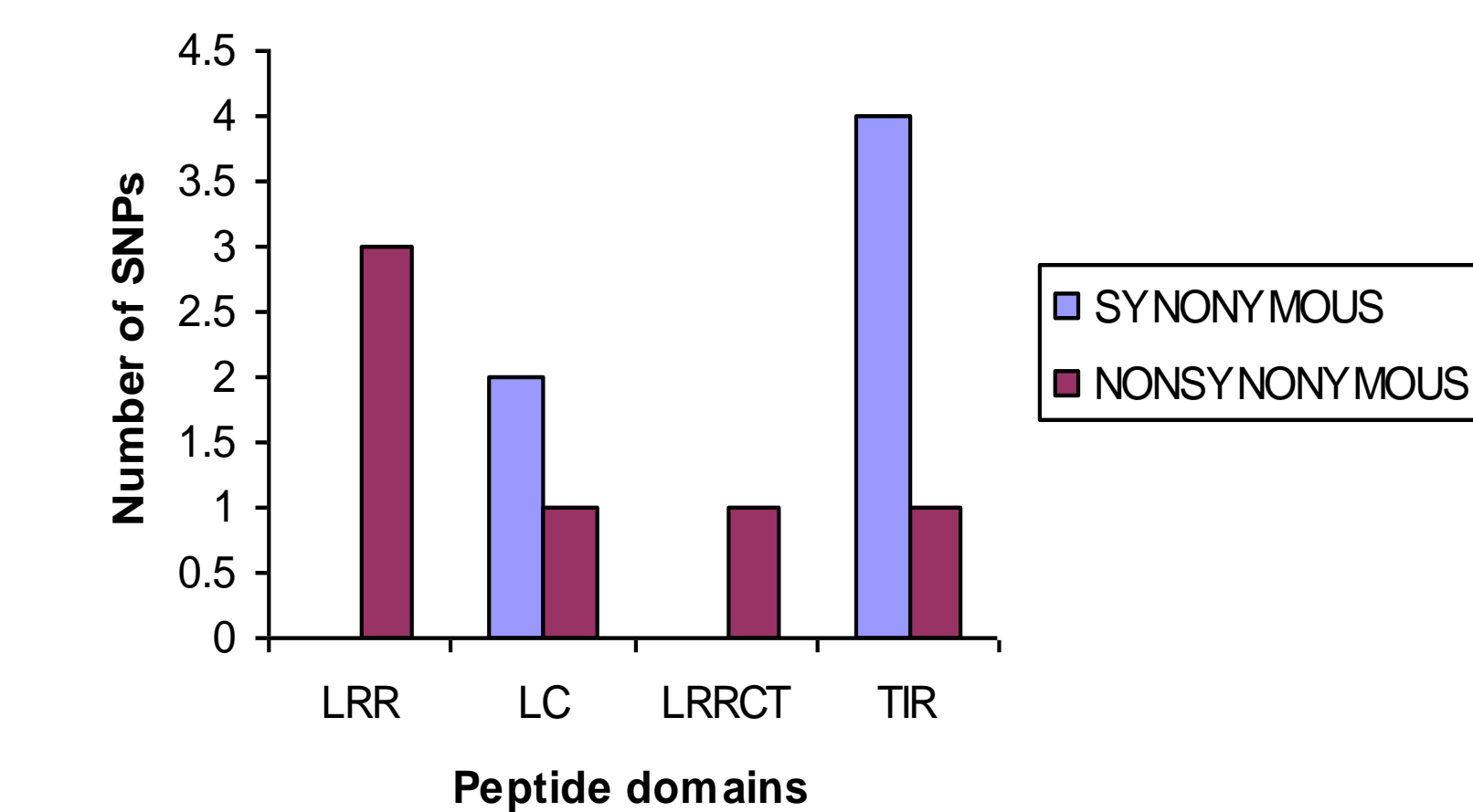


Fig 1. Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR1 across the four *Sus* species

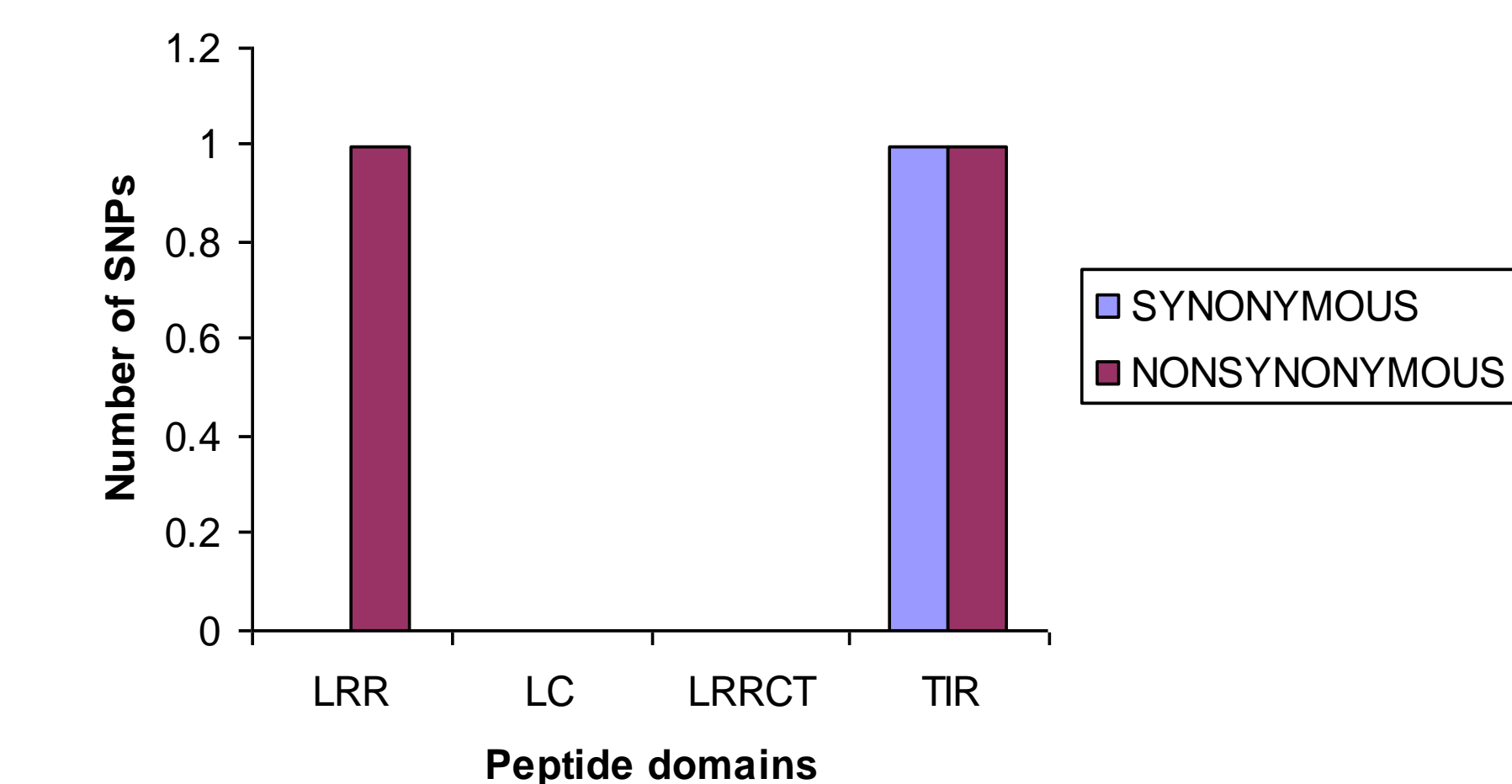


Fig 2: Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR2 across the four *Sus* species

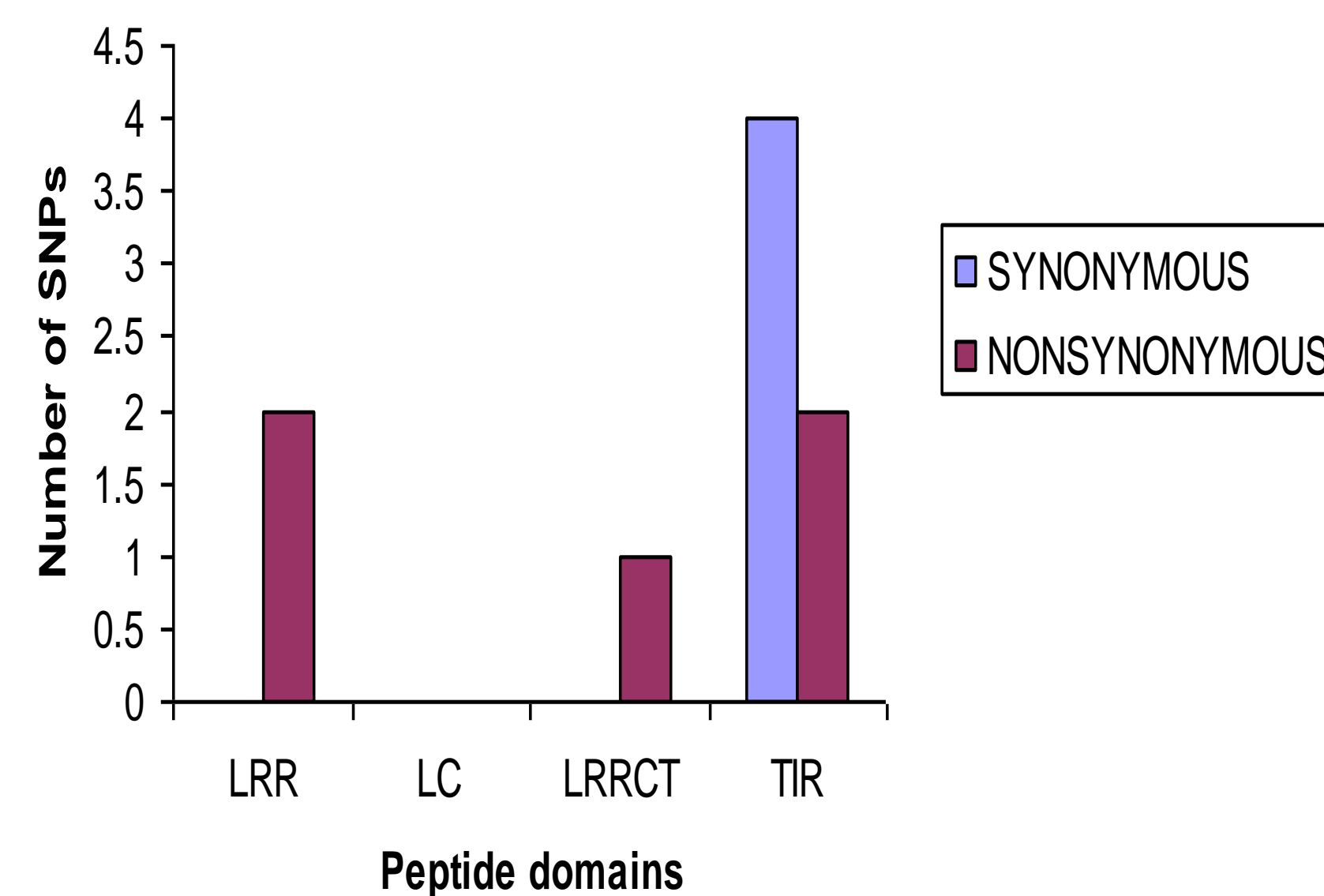


Fig.3 Number of synonymous and nonsynonymous SNPs in the peptide domains of the coding regions of TLR6 across the four *Sus* species

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

