

Peer Review

Review of: "Genetic Basis of Immunity in Indian Cattle as Revealed by Comparative Analysis of Bos Genome"

Md Azizul Haque¹

1. Department of Biotechnology, Yeungnam University, Korea, Republic of

The manuscript presents an in-depth comparative analysis of the genetic basis of immunity in Indian cattle breeds, particularly focusing on *Bos indicus* (Nelore and Gir) and *Bos taurus* (Hereford). While the study presents valuable information, several important revisions are needed to improve the manuscript's impact and contribution to the field.

Major Comments

Abstract

1. The abstract needs a sharper conclusion to highlight the practical applications of the findings. For example, explain how the identified immunity genes could support breeding programs or disease management strategies.

Introduction

1. Provide a clearer explanation of how this study addresses gaps in genomic knowledge between *Bos indicus* and *Bos taurus*.

2. The mention of Vechur cattle is interesting but feels somewhat disconnected from the study's main focus. If the goal is to highlight disease resistance, briefly connect this example to the genomic variations under investigation.

Materials and Methods

1. The data filtering criteria, particularly the 60 percent sequence similarity cutoff for low similarity genes, should be better justified. Explain how this threshold was chosen and what biological significance it holds.

Results

1. The observation of Chromosome X losing 50 Mbps is noteworthy. Provide more context on how this loss might influence immunity or phenotypic traits, especially since no genes were lost.
2. The manuscript identifies numerous SNPs, insertions, and deletions. Grouping these variations into functional categories such as immune pathways or cell signaling genes would make the results more biologically meaningful and easier to interpret.
3. Several genes are labeled as immunity genes. Clarify whether this classification is based on keyword matching alone or supported by functional validation such as databases or previous studies.

Discussion

1. The discussion would benefit from stronger connections between findings and practical outcomes. For example, explain how the observed genetic differences contribute to disease resilience.
2. The segment on Chromosome X raises interesting points. Expand on why this chromosome might show such variability between breeds.
3. The mention of QTLs linked to milk and health traits is valuable. To enhance practical relevance, explain how this information could guide breeding strategies such as marker-assisted selection.

Conclusion

1. The conclusion lacks a strong future direction statement. Consider addressing how these findings might influence upcoming genomic studies or inform cattle breeding programs in other tropical regions.

Minor Comments

1. The term chromosome by chromosome appears inconsistently alongside chromosome-by-chromosome. Choose one and maintain consistency throughout the manuscript.
2. The phrase Bos indicus (Nelore breed) repeats frequently. Consider varying the expression.

3. Gene names such as *VSTM1L*, *Galectin-9*, *HDAC5*, and *POLH* should follow standard genetic formatting guidelines, with gene symbols italicized.
4. Figure references such as Fig. 2 should follow a consistent format. Choose between Fig. or Figure and apply it uniformly.
5. Figures 3, 5, 6, 9, and 11 need improved resolution. The text within these figures is difficult to read.

Declarations

Potential competing interests: No potential competing interests to declare.