

Peer Review

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

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## Review report on Genetic Basis of Immunity in Indian Cattle as Revealed by Comparative Analysis of Bos Genome

### I. Abstract:

- **Strengths:** The abstract concisely summarizes the study's aim, methods, and key findings. It highlights the unique resilience of *Bos indicus* cattle and the novel comparative genomic approach.
- **Weaknesses:** The abstract could be improved by explicitly stating the significance of the findings. What are the practical implications for disease resistance in cattle breeding? Quantifying the impact of the identified genomic variations on specific traits would strengthen the abstract.

### II. Introduction:

- **Strengths:** The introduction effectively sets the stage by describing the economic importance of *Bos indicus* cattle, their resilience, and the existing research gaps. The rationale for comparing *Bos indicus* and *Bos taurus* genomes is clearly explained.
- **Weaknesses:** The introduction could benefit from a more focused and streamlined narrative. Some sentences feel somewhat descriptive rather than analytical. Consider tightening the writing by removing redundant phrases and emphasizing the key arguments that lead to the study's specific aims. The paragraph on innate immunity could be more concise.

### III. Materials and Methods:

- **Strengths:** The methods section provides a good overview of the bioinformatics tools used (SyMAP, GSAalign, SyRI). The workflow diagram is a helpful visual aid.

- **Weaknesses:** This section needs significant improvement. It lacks crucial details. For example:
  - **Data Sources:** More detail is needed on the specific versions and assemblies of the genomes used. Accession numbers are helpful but not sufficient.
  - **Parameter Selection:** The rationale for choosing specific parameters in SyMAP, GSAalign, and SyRI should be explicitly stated and justified. (e.g., Why 60% sequence similarity as a cutoff?)
  - **QTL Analysis:** More detail is needed on the QTL database used, the specific QTLs considered, and the method used to link QTLs to genes.
  - **Validation:** The validation process needs a more rigorous explanation. How were the results from the three tools compared? What criteria determined consensus?
  - **Statistical Analysis:** Were any statistical tests used to assess the significance of the identified variations? This is critical and missing. The methods for this are needed.

#### IV. Results:

- **Strengths:** The results are presented in a relatively clear and organized manner. Tables and figures appear to summarize the data effectively.
- **Weaknesses:** The results section needs more interpretive analysis. The sheer volume of numbers and genomic locations can be overwhelming. Focus more on trends and significant findings, rather than just presenting the raw data. Discuss the biological significance of the observed genomic variations. For instance, what are the functional implications of the specific gene variations identified? Do they result in altered protein structure or expression levels? Consider using fewer tables and figures; perhaps combine some of the data.

#### V. Discussion:

- **Strengths:** The discussion attempts to interpret the results in the context of the existing literature. There's a good attempt to connect the findings to the biological functions of the identified genes and their role in immunity. The points on chromosome X and QTL mapping are well-discussed.
- **Weaknesses:** The discussion needs to be more critical and nuanced. Some statements feel speculative and need to be better supported with evidence. The connection between genomic variations and specific phenotypic traits should be further explored and strengthened with statistical data. There is room for integrating information regarding the known immune pathways and regulatory networks impacted by the affected genes. The conclusion about the implications of the findings for cattle breeding should be more direct and strongly supported by the data.

## VI. Conclusion:

- **Strengths:** The conclusion summarizes the main findings concisely.
- **Weaknesses:** The conclusion should be strengthened by explicitly stating the implications of the study for cattle breeding and disease management. Highlight the study's limitations as well.

## Overall Assessment (Tentative):

This paper requires major revisions before it can be considered for publication. The major weakness is the lack of detail and rigor in the Materials and Methods section and the insufficient interpretive analysis in the Results and Discussion sections. The statistical analyses are completely missing. Addressing these issues would require extensive rewriting and potentially additional analyses.

## Recommendations for the Authors:

1. **Expand the Materials and Methods:** Provide detailed information on the data sources, parameter choices, validation strategy, and statistical analysis.
2. **Revise the Results:** Focus on the most significant and biologically relevant findings. Provide a more in-depth interpretation of the genomic variations and their implications.
3. **Strengthen the Discussion:** Provide more critical analysis, strengthen the connection between genomic variations and phenotypic traits, and clearly state the study's limitations.
4. **Improve the figures and tables:** Make them clearer and more concise; use fewer figures and tables if necessary.
5. **Add more statistical analyses:** Include appropriate statistical tests to assess the significance of the identified variations.

## Declarations

**Potential competing interests:** No potential competing interests to declare.