

differences between studies are likely to reflect inconsistencies in statistical definitions rather than true biological variation. This issue is particularly pronounced in multi-population or cross-environment comparisons, and thus harmonizing analytical frameworks is essential to avoid misleading interpretations.

Based on these considerations, a more integrative conceptual framework can be proposed: SNP heritability is not an intrinsic biological constant of a trait, but rather a statistical function dependent on specific models, data structures, and LD patterns. This perspective is especially important for reinterpreting the “missing heritability” problem. Traditional explanations often attribute low SNP heritability to unobserved genetic variation, whereas in reality, model assumptions and LD mismatches can also lead to systematic underestimation (Yang et al., 2015).

Overall, this study not only reveals structural differences among estimation methods but also highlights a fundamental issue: the numerical value of heritability has no independent meaning outside its statistical definition. Only when its estimation context and model conditions are clearly specified can the results be scientifically interpretable. This perspective provides a more robust analytical framework for future genetic studies and contributes to improving the comparability and methodological consistency of research findings.

Author Contributions

Xuanjun Fang conducted this study, including literature review, data analysis, and the drafting and revision of the manuscript. The author has read and approved the final version of the manuscript.

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