Principal component analysis in RIL population derived from the cross of Improved Samba Mahsuri and Phougak in rice (*Oryza sativa* L.)

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ABSTRACT

Rice is one of the principal cereal food crops which fulfills carbohydrate needs and nutritional requirement of half of the world's population. Despite its agricultural significance, rice production faces severe threats from many diseases, notably sheath blight (ShB), caused by *Rhizoctonia solani*. ShB leads to substantial yield losses, ranging from 4-50% based on environmental conditions and disease severity. The present study aimed to evaluate recombinant inbred line (RIL) population, derived from a cross between susceptible elite cultivar ('Improved Samba Mahsuri') and a ShB-tolerant landrace ('Phougak'), for traits associated with ShB tolerance and yield. Using principal component analysis (PCA), nine ShB and yield-related traits were evaluated in two environments, yielding nine and eleven principal components (PCs) for the dry season and wet season respectively. In both environments, the first three PCs explained 50% of observed phenotypic variance, with traits relative lesion height (RLH) and standard evaluation scores (SES) as primary contributors. PCA results revealed that yield contributing traits-tiller number, panicle number, and panicle length are positively correlated with grain yield, emphasizing their breeding relevance. Biplot analysis indicated critical trait interactions for RLH and SES and their strong influence on trait divergence. This research helps rice breeding efforts targeting ShB resistance with improved yield, by identifying promising genotypes for sustainable rice production.

Key words: *Eigen value, Principal components, Sheath blight, Variability.*