

Rice second florigen is crucial for expansion of its' cultivation areas: A Bioinformatics.

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Abstract

Flowering state is an important agronomic trait in determining the plant cropping season and best ecological examples between plant and its existing ecosystem. Rice is a model plant for molecular studies and pertinent for flowering development analysis. Rice Flowering Locus T1 (RFT1) is the second rice florigen which promotes flowering under long-day (LD) condition. This study investigates the correlation between RFT1 gene established accessions towards an expansion of rice cultivation areas in Asia using bioinformatics tools. Fourteen (14) different RFT1 accessions were collected including 9 indica and 5 japonica, and analyzed for molecular evolution. Also, the protein 3-dimensional (3D) structure were predicted and validated. The genes appeared to be highly conserved and functional across the diverse accessions. Cultivars from the two sub-species form a separate sub-group except for Koshihikari, Akamai and Nara aswari which form a major group, while Basmati370 was in the same clade with japonica cultivars. The 3D model indicated that the protein accessions has slight differences and VERIFY 3D model refinement has the best stereochemistry score at 99.38. The study clarified on the cultivars' evolutionary relationships and suggested that diverse functional RFT1 variants is crucial for expansion of rice cultivation areas.

Keywords: Rice, RFT1 gene, Accessions, Phylogenetic tree and 3D model.

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Received: 2017/12/07

Accepted: 2018/07/10

DOI: <https://dx.doi.org/10.4314/njtr.v13i2.10>