



Category: Plant Genomics

Towards enhancement of yield by molecular stacking of yield contributing genes in rice (*Oryza sativa* L.)

B.R. Yamini¹, M.M. Bharghavi¹, G.R. Eswar², K. Gopalakrishna², B.N. Jeevula², B.N. Swarajyalakshmi², E.N. Suresh², K.R. Hariprasad² and Lakshminarayana R. Vemireddy^{2*}

¹S.V. Agricultural College, Acharya NG Ranga Agricultural University (ANGRAU), Tirupati, INDIA

²Institute of Frontier Technology, Regional Agricultural Research Station (RARS), ANGRAU Tirupati, INDIA

*Corresponding author: drvlnreddy@gmail.com

Abstract

Rice (*Oryza sativa* L.) is a staple food for over half of the global population. Rice yield is mainly determined by three complex traits i.e., number of panicles per plant, number of grains per panicle and grain weight which are governed by many genes with minute effect called quantitative trait loci (QTL). As of now, more than 30 QTLs governing yield and its component traits have been cloned and molecularly characterized. Stacking of harmonious QTLs/genes into a single elite variety proved to show higher yields. To this end, in the present study, two strategies have been contemplated to raise the yield ceiling in rice. In the first strategy, the validated known yield genes would be pyramided into a single elite variety by marker-assisted backcross breeding. For this, the validation of majority of the yield gene-specific markers from known high yielding varieties has been completed. In all, 17 markers showed polymorphism with the recurrent parent MTU1010. Using these polymorphic markers as foreground markers, the BC₁F₁ plants obtained from MTU1010/MTU3626 (Donor for *DEP1*, *GW5* and *GW8*) and MTU1010/Swarna (Donor for *GS5* and *qSS7*) were confirmed for the presence of the yield genes. Later, the confirmed BC₁F₁ plants will be intercrossed to pyramid the yield genes. In the second strategy, the candidate genes for the yield component traits would be mapped and then pyramided into a single elite variety. To this end, the rice varieties MTU3626 and NLR33892 have been chosen as donors for grain weight and grain number, respectively and BPT5204, a fine grain variety has been chosen as recurrent variety. The F₂ populations of the crosses BPT5204/ MTU3626 and BPT5204/NLR33892 are being grown in the field. The DNA from 20 plants with extreme phenotype for the targeted traits would be bulk sequenced along with the parents for rapid detection of QTLs using QTL-seq method. Later, the major QTLs would be introgressed into BPT5204 and evaluated for its yield enhancement.

References

- [1] Bai, X., Wu, B. and Xing, Y. (2012) Yield-related QTLs and Their Applications in Rice Genetic Improvement. *J Integr Plant Biol* 54: 300–311. <https://doi.org/10.1111/j.1744-7909.2012.01117.x>
- [2] Takagi, H., Abe, A., Yoshida, K., Kosugi, S., Natsume, S., Mitsuoka, C., Uemura, A., Utsushi, H., Tamiru, M., Takuno, S., Innan, H., Cano, L.M., Kamoun, S. and Terauchi, R. (2013) QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations. *Plant J* 74: 174-183. <https://doi.org/10.1111/tpj.12105>

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