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Abstract

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THE NEED FOR NUTRIENT EFFICIENT RICE VARIETIES: STATUS AND PROSPECTS

Vinod, K K.¹, M. Nagarajan¹, S. Gopalakrishnan², Prolay K Bhowmick², and Ashok K Singh²

¹Indian Agricultural Research Institute, RBGRC, Aduthurai

²Indian Agricultural Research Institute, New Delhi

Email:kkvinod@iari.res.in

Best agro-management in rice always required large quantum of agronomic inputs such as fertilizers. Modern rice varieties need high positive nutrient balance in the soil to throw their best yields. Nitrogen and phosphatic fertilizers are required by rice crop plants in large quantities. Overdependence of mineral fertilizers for agricultural production envisions problems such as, (a) soil nutrient deficiency, (b) non-recyclable nutrient loss, (c) loss of nutrients by soil processes, (d) nutrient pollution, (e) atmospheric pollution, (f) depletion of natural resources, (g) geographic resource confinement, (h) booming fertilizer costs, (i) constrained fertilizer affordability to farmers (j) no alternate fertilizer resources. To curb ill-effects of indiscriminate fertilization and sustain rice production reduction in soil nutrient input needed. Ability of plants to withstand nutrient starvation is leveraged by a variety of mechanisms such as root system architecture, root exudations and root microfloral symbiosis, besides uptake and transport. Crop tolerance to nutrient deficiency is called as low nutrient tolerance or nutrient starvation tolerance. Considerable genetic variations are reported for nutrient efficiency (NtE) in rice. Experience shows that the key to this genetic variation does not lie with the genes directly responsible for nutrient uptake, transport and assimilation but on the genes that regulate the processes. Nutrient starvation tolerance genes may be better sourced from older germplasm. Molecular isolation of large effect QTLs for phosphorus starvation tolerance and low nitrogen response have also been mapped in rice. Improved rice varieties with better NtE developed using modern molecular breeding technology would lead the agriculture in future.

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NEXT GENERATION SEQUENCING- A REVOLUTION IN GENOMIC SCIENCE

Poornima Jency J

Tamil Nadu Agricultural University

E-mail:poomimajames@gmail.com

Next Generation Sequencing (or massively parallel sequencing) refers to a group of new DNA sequencing technologies that can rapidly sequence DNA on the gigabase scale. This method is now replacing Sanger sequencing, which was the dominant sequencing technology from the late 1970 to the late 2000 and was used for all of the initial genome sequencing projects (*H. influenzae*, *Drosophila*, *Arabidopsis*, human). Using next-generation sequencing technologies it is possible to resequence