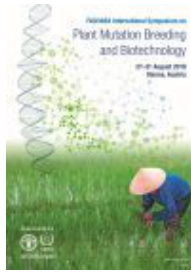


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DEVELOPMENT OF A NEW RICE MUTATION BREEDING METHOD FOR THE SELECTION OF HIGHER YIELD PHYSIOLOGICAL MUTANTS

The selection of higher yield physiological mutants had not yet been achieved in the 90 years history of crop mutation breeding. This is because physiological traits which cause higher yields than existing high yield varieties were unknown and we did not have any practical methods for selecting unknown physiological traits. We developed a new mutation breeding method of rice in which plant selection by all panicle weight per plant in M2 and M3 generations were conducted followed by usual yield trial of rice breeding sectors in M4 and 10 times replicated yield trials in M5. By using this method, we could select three higher yield rice mutants. FukuhibikiH6, YamadawaraH3 and MochidawaraH1 showed significantly higher yields compared with their original varieties. Their original varieties, Fukuhibiki, Yamadawara and Mochidawara are the highest yield varieties in some areas or for a specific usage in Japan. The yield advantages of these three mutants were 3 to 5%. In the selection of M2 and M3 generations, their yield advantages over surrounding plants were 10 to 40 % which were much higher than in M5 generation. In the M2 and M3 fields, they were surrounded by ordinary plants and they must have had advantages against the surrounding ordinary plants which suffered a disadvantage from them and became smaller. However, yield traits differences between them and their original varieties were very small and inconsistent. Higher yield is likely to be caused by physiological traits rather than phenotypical agronomic traits such as panicle and grain size. By gamma ray mutation induction, it is relatively easy to isolate the relevant genes because the number of mutated genes is limited, usually around ten in the whole rice genome. The isolated genes can then be used in genome editing for enhancing gene functions and for breaking the present yield barriers.

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