

P119

Phenotypic and genotypic screening of rice accessions for salt tolerance

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Abstract

Rice (*Oryza sativa* L.) is one of the major crops that is seriously impacted by global soil salinization. Rice is among those crops where most of the high-yielding cultivars are highly sensitive to salinity. The key to a plant survival under NaCl salt stress is by maintaining a high K^+/Na^+ ratio in its cells. Selection for salinity tolerance genotypes of rice based on phenotypic performance alone is less reliable and will delay in progress in breeding. Recent advent of molecular markers, microsatellites or simple sequence repeats (SSRs) were used to find out salt tolerant rice genotypes. In the current experiment phenotyping and genotyping studies were correlated to differentiate different rice accessions for salinity tolerance. Eight rice accessions along with check plant Dongjin were screened by physiological studies using Yoshida solution with 50mM NaCl stress condition. The physiology studies identified four tolerant and four susceptible accessions based on their potassium concentration, sodium concentration, K^+/Na^+ ratio and biomass. 17 SSR markers were used to evaluate these rice accessions for salt tolerance out of which five molecular markers were able to discriminate tolerant accessions from the susceptible accessions. Banding pattern of the accessions was scored comparing to the banding pattern of Dongjin. The study identifies accessions based on their association of K^+/Na^+ ratio with molecular markers which is very reliable. These markers identified can play a significant role in screening large set of rice accessions for salt tolerance; these markers can be utilized to improve salt tolerance of commercial rice varieties with marker-assisted selection (MAS) approach.

Key words: Rice, Salinity, K^+/Na^+ ratio, Molecular markers.

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