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Seed priming with selenium improves growth, yield and anti-oxidative machinery in salt-stressed mungbean (*Vigna radiata* L. Wilczek) plants

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Salt stress is one of the vital reasons that adversely affect the productivity of crops; hence suitable strategies are required to mitigate its adverse effects on plants. Exogenous selenium (Se) has been reported to mitigate the salinity effects under lab conditions, but its effects in soil-grown salt-stressed mungbean plants with seed-priming technique have not been reported yet. In a preliminary experiment, the comparative response of mungbean plants to different salt stress levels (applied with NaCl) revealed nearly 70% reduction in pod number and seed yield per plant at 100 mM concentration. Subsequent studies showed that 100 mM NaCl caused substantial damage to membranes, chlorophyll, photosynthetic ability, stomatal conductance and leaf water status. Se seed priming at 1 and 2.5 ppm to salt-stressed plants revealed significant alleviation of stress damage. With 1 ppm Se concentration, resulting in enhanced plant biomass (12%) and seed yield/plant (22%) as compared to salt-treated plants. These plants accumulated significantly less Na⁺ (42%) in their leaves but Cl⁻ accumulation was not affected. The oxidative damage, measured as lipid peroxidation and hydrogen peroxide, was considerably lower in Se-primed salt-stressed plants. The activity of antioxidants such as catalase, ascorbate peroxidase, glutathione reductase and glutathione peroxidase was significantly improved with 1 ppm Se application to salt-stressed plants. These findings indicated that Se seed-soaking at low concentration increased Se uptake but reduced the Na⁺ uptake and, consequently improved the plant function in mungbean plants growing under salt stress.

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Identification and characterization of a gene controlling tiller trait of wheat

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Tiller number is one of the important agronomic traits in cereals such as rice, wheat and barley that directly correlates with yield, but is highly regulated by environmental and endogenous factors. Tillers in wheat are considered to be the axillary branches arising from the crown giving plant shoot architecture. Various genes are known to suppress lateral branching including lateral suppressor (LS) of tomato, *MOC1* of rice, and *LAS* of *Arabidopsis*. Mutants in these orthologous genes showed suppression of lateral branches. Furthermore, these mutations turned out to be in the conserved GRAS domain. However, the molecular mechanism regulating tillering in wheat has been poorly understood. The main objective of this study is to identify and characterize a gene responsible for number of tillers in wheat. So far, rice *MOC1* is the only cloned and characterized gene among cereals controlling tillering. Thus, we selected rice gene as the query sequence to identify its ortholog in wheat. Detailed bioinformatic and sequence analyses identified a gene in wheat showing high sequence similarity with *MOC1*. All three homoeologous copies of the candidate gene have been cloned and mapped. The gene showed similar expression pattern as that of *MOC1* in different developmental tissues. Transient as well as stable silencing of the *TaMOC1* resulted in reduced tiller number in wheat suggesting its role in tillering. Microscopic analysis of the silenced plants showed the absence of bud formation in the axil of leaf, directly implicating the role of the gene in tiller bud initiation. The research will focus towards the sustainable agriculture in this era of diminishing available resources.

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