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## Cloning and characterization of an endosperm-specific legumin-type seed storage protein gene of common buckwheat (*Fagopyrum esculentum* Moench)

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Seed storage proteins of grain crops meet the major dietary protein requirement of over half of the world population, therefore intensive research on isolation and characterization of these proteins and their genes is an important aspect for improvement of nutritive value in human food and animal feed. These seed storage proteins during seed development are abundant during the mid-maturation period and decline towards maturation. The isolation and complete nucleotide sequencing of 1.7 kb (acc. KM488332) legumin type protein gene was determined using primer walking strategy. BLAST analysis of the sequence revealed >90% homology with legumin gene nucleotide sequences bearing accession numbers D87980, GQ358524 and AY245536. The deduced amino acid sequence from the open reading frame coded for a 64 kDa pre-protein. BLASTp analysis of the sequence revealed 98% homology with 13S globulin seed storage protein from common buckwheat (acc.no.O23878) showing a characteristic barrel domain of the 'cupin' superfamily which comprises the 11S and 7S plant seed storage proteins and germins. Analysis of the deduced amino acid sequence revealed the presence of α and β subunit linked ASN-GLU linkage. This gene was cloned into pJET1.2 blunt cloning vector (Fermentas) and further sub-cloned into pCAMBIA1304 through directional cloning strategy which would enable us to characterize its further candidature in research programmes aimed at improvement of the nutritional quality of conventional crops deficient in essential amino acids.

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## Molecular analysis of Basmati×*indica* (salt tolerant) derived segregating populations in rice (*Oryza sativa* L.)

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Rice (*Oryza sativa* L), is the most important food crop for over half of the world's population and supplies 20 percent of daily calorie intake. Salinity is one of the major abiotic stresses that adversely affect crop productivity and quality. Rice is found to be sensitive to soil salinity with salinity threshold level of 3.0 dS $m^{-1}$ and 12 percent reduction in grain yield per degree increase in electrical conductivity (EC) beyond this threshold value. The problem of soil salinity is further increasing because of the use of poor quality water for irrigation and poor drainage. The yield reduction in salt soils can be overcome by soil reclamation or by improving salt tolerance in target crops. The use of molecular markers, permit the genetic dissection of the progeny at each generation and increase the speed of the selection process. Molecular markers could be used to tag quantitative trait loci (QTLs) and to evaluate their contributions to the phenotype by selecting favorable alleles at these loci in a marker-assisted selection scheme. Of the available molecular markers, microsatellite markers (SSRs) being co-dominant, highly polymorphic and economically assayed by PCR have been preferentially used for genotyping and genetic diversity analysis in rice. Seeds harvested from Pusa1121×CSR10 $F_1$ plants are being used in the present study. The seeds are being treated initially at 25-50 mM of NaCl and plants showing resistance towards salt stress are being carried forward to next generation. The selected plants would be also tested for BAD2 locus specific for aroma as well as an array of SSR's would be used to help in the detection of QTL's related to salt tolerance.

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