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An *in-silico* analysis of the genetic diversity of *ABRE-BP* among Sri Lankan rice varieties: could a polymorphism in *ABRE-BP* be diagnostic of salinity tolerance?

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The *ABRE-BP* (*Abscisic Acid Responsive Element binding protein*) is a key gene in the abscisic acid (ABA)-dependent plant salinity stress-responsive regulon. The gene transcribes for a transcriptional factor and binds with the ABRE*cis*-acting element in salinity stress responsive genes, regulating its expression. A greater diversity in salinity tolerance has been reported in Sri Lankan rice germplasm while *Pokkali*c has been consistently identified as a tolerant variety. In the current *in-silico* study, we assessed the nucleotide diversity of the *ABRE-BP* genic region of 47Sri Lankan rice varieties to identify putative diagnostic sites associated with salinity responses. The *ABRE-BP* sequences were retrieved from the Rice SNP-Seek data base and the exon/intron regions and protein domains were annotated. DNA polymorphisms leading to non-synonymous mutations were identified compared to *Pokkali*. A cluster analysis was carried out considering the non-synonymous mutations and the nucleotide diversity index (Pi) were calculated. The entire *ABRE-BP*genic region consists, 208 single nucleotide polymorphisms (SNPs) including 13 singletons and 195 parsimony variables. The *ABRE-BP* coding sequence (CDS; Pi:0.00617) was generally conserved comparing to the genic region (Pi:0.00817). The intron region of *ABRE* consisted of 179 SNPs. In the CDS, the exon one has the highest polymorphism with 23SNPs followed by exon five (3), exon two (2), and exon three (1). The exon four was conserved across all varieties. The *ABRE-BP* polypeptide chain consisted of 12 non-synonymous mutations where, 11 in exon one and one in exon three, that clustered the selected varieties in to four groups. The exon three contains the bZIP domain which produces the ABRE transcription factor. The bZIP domain was annotated to be longer in six varieties compared to the rest, enclosing the non-synonymous mutation at exon 3 (lysine to asparagine). The cluster of 26 varieties contained, tolerant varieties *Pokkali, Kuruluthudu* and *Kotteyaran* with known intolerant varieties *Pachchaperumal* and *Hondarawalu*. The *ABRE-BP* sequence of *Pokkali* differed from the rest, by a single non-synonymous mutation (Tyrosin to Aspartate) on exon 1, however, could not be associated with salinity tolerance. Thus, the tolerance of *Pokkali* and other tolerant varieties could not be diagnostically associated to the polymorphisms detected in the *ABRE-BP* genic region.