Comparative analysis of intron regions in grass genomes

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Members of the Family Poaceae show extensive sequence conservation in their genomes. In orthologous genes, exon sequences are found to be more conserved among species due to functional conservations, than intron sequences. Thus, comparative analyses of intron regions in grasses provide a useful means of detecting genetic variation between closely related taxa.

In this study a comparative analysis was carried out, of ten introns, each from a randomly selected gene, in eight different grass species that included *Oryza sativa* subsp *indica*, 4 wild rice species (i.e *O.rufipogan*, *O.rhizomatis*, *Hygroryza aristata*, *Leersia hexandra*), *Saccharum officinarum*, *Zea mays* and *Eleusine coracana*. Ten pairs of intron-flanking polymerase chain reaction (PCR) primer pairs complementary to conserved exonic regions of *O. sativa* subsp *japonica* were employed to amplify these particular introns in all grasses studied. The PCR products were analyzed following agarose gel electrophoresis for the presence or absence of a particular intron region in the above taxa, and for any possible variation that might be revealed by the size of the PCR product, such as large insertions or deletions within the introns.

The results indicated that the two introns amplified by the primer pairs PRSC1_004 and PRSC1_022 were conserved throughout the grass species, the respective primers amplifying a single band of equal size in all the species examined. The intron region amplified by the primer pair SRSC4_011 was also highly conserved and was absent only in *Zea mays*. All other introns were found only in *O. sativa* and its wild relatives except for the region amplified by SRSC4_016. This region was absent in *O.sativa*, but was observed in some wild relatives and in *S. officinarum*. In *O. sativa*, 9 of the 10 primer pairs used, amplified their respective introns. This underlines the sequence similarity shared between *O.sativa* subsp *indica* genome and *O.sativa* subsp *japonica*. Amplification products of primer pair SRSC4_003 in *O.sativa*, *O. rhizomatis* and *L. hexandra* always produced two bands of nearly equal size on the gel, indicating the presence of a duplication of this region in these genomes. However, no PCR products were observed for this region in other species, indicating the absence of this region from their genomes. Similarly the region amplified by the primer pair SRSC4_062 also appeared to be duplicated in *O. sativa* and *O. rufipogan* but only one band was observed in *H. aristata* and *L. hexandra*, and was absent from the other species. A size-variation in PCR products was only observed in the intron region amplified by primer pair SRSC4_062, in which the region amplified in *H. aristata* markedly differed in size with a smaller fragment compared to other species.