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Seed shattering in weedy rice is not similarly regulated as in cultivated rice

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ABSTRACT

Although seed shattering is one of the main causes of weedy rice persistence it still is poorly understood. The aim of this study was to identify the main genes related with the occurrence of seed shattering in weedy rice. Gene expression and DNA sequencing of the coding and promoter region and a whole genome sequencing were performed in weedy and cultivated rice with contrasting seed shattering. The main genes associated with the seed shattering in cultivated rice *Sh4*, *qSH1* and *SHAT1* were not important in weedy rice. The expression of the gene *OsCPL1* was positively associated with high seed shattering in weedy rice, which is the opposite than in cultivated rice. This result is related to the absence of four SNPs and an indel in the *OsCPL1* gene in weedy rice. The analysis of the expression of six genes related to cell wall synthesis/degradation pioneering revealed the importance of the genes *OsXTH8* and *OsCel9D* to seed shattering in weedy rice. The nucleotide variability of eight genes identified on a genome-wide re-sequencing study in cultivated rice indicated that only the genes *Os01g0849100* and *Os08g0512400* were associated with seed shattering in weedy rice. The whole genome sequencing of genotypes with high seed shattering indicates a variation on the promoter region of the gene *OsXTH8*. An insertion of G or C on this region next to the gibberellin motif was identified in all weedy rice genotypes with high seed shattering. This study evaluated jointly a series of genes involved in rice seed shattering and indicated that genes *qSH1*, *Sh4* and *SHAT1* are not important in weedy rice, and that the genes *OsCPL1*, *OsCel9D*, *OsXTH8*, *Os08g0512400* and *Os01g0849100* should be considered in studies of weedy rice evolution and in the development of mitigation approaches gene flow between cultivated and weedy rice.

Key words: Abscission layer, *Oryza sativa*, *qSH1*, red rice, seed dispersal, *Sh4*.