Analysis of Endogenous Sirevirus in Germinating Barley (Hordeum vulgare L.)

Authors : Nermin Gozukirmizi, Buket Cakmak, Sevgi Marakli

Abstract : Sireviruses are genera of copia LTR retrotransposons with a unique genome structure among retrotransposons. Barley (Hordeum vulgare L.) is an economically important plant and has been studied as a model plant regarding its short annual life cycle and seven chromosome pairs. In this study, we used mature barley embryos, 10-day-old roots and 10-day-old leaves derived from the same barley plant to investigate SIRE1 retrotransposon movements by Inter-Retrotransposon Amplified Polymorphism (IRAP) technique. We found polymorphism rates between 0-64% among embryos, roots and leaves. Polymorphism rates were detected to be 0-27% among embryos, 8-60% among roots, and 11-50% among leaves. Polymorphisms were observed not only among the parts of different individuals, but also on the parts of the same plant (23-64%). The internal domains of SIRE1 (gag, env and rt) were also analyzed in the embryos, roots and leaves. Analysis of band profiles showed no polymorphism for gag, however, different band patterns were observed among samples for rt and env. The sequencing of SIRE1 gag, env and rt domains revealed 79% similarity for gag, 95% for env and 84% for rt to Ty1-copia retrotransposons. SIRE1 retrotransposon was identified in the soybean genome and has been studied on other plants (maize, rice, tomatoe etc.). This study is the first detailed investigation of SIRE1 in barley genome. The obtained findings are expected to contribute to the comprehension of SIRE1 retrotransposon and its role in barley genome.