Transposon-mediated gene tagging and editing in oat

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Among various functional genomic tools to characterize genes in plants, transposon-based insertional mutagenesis approach offers great potential, especially in plant species, which possess large genomes and genetic transformation is not a routine. Oat (*Avena sativa*) is a globally-important cereal crop species with documented benefits to human health. However, oat has lagged behind other cereals with respect to genomic resources, due in part to the complexity of its hexaploid genome. Our aim in the current project is to introduce the *Ac/Ds* transposable elements in oat species for the development of a gene tagging resource with its potential for gene editing. Highly regenerative calli derived from mature oat seeds of oat cultivar 'Park', were successfully transformed with several *Ac/Ds* constructs, using a biolistic delivery system. Twenty-two independent transgenic events were obtained using two different antibiotic selection schemes. Our data indicate that co-transformation of *Ac* and *Ds* constructs led to 5% of primary *Ds* transpositions at T_o stage. Generation advance of T_1 plants containing both *Ac* and *Ds* elements from four different events established the transposition frequency between 11 to 30%. Movement of *Ds* element was confirmed by histochemical and molecular assays. Homozygous oat lines containing individual *Ac* and *Ds* elements are being hybridized for further remobilization of *Ds* transposons in the oat genome. Reactivation of *Ds* elements from its original position has a great potential for gene editing of the insertion sites. Prospects of transposon- based gene editing will be discussed.