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A DELETION IN THE *ent-KAURENOIC ACID OXIDASE1* (*HaKAO1*) GENE AFFECT THE *dwarf2* (*dw2*) MUTANT OF SUNFLOWER

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Dwarf mutants in plants are crucial to elucidate regulatory mechanisms for plant growth and development. This character is also favored in breeding [Hedden, (2003) Trends Genet. 19: 5-9]. Identification of the genes responsible for these traits shown that they control gibberellins (GAs) metabolism and/or perception. A dwarf mutant, *dwarf2* (*dw2*) of sunflower (*Helianthus annuus*), showed an extreme reduced size of stem, leaves, petioles and flower organs and a retarded flower development. Pollen and ovules were produced but most disk flower failed to open. The *dw2* phenotype was mainly because of reduced cell size. The mutant responded to the application of bioactive GAs. In *dw2* seedlings, the levels of *ent*-7α-hydroxykaurenoic acid, GA_{19}, GA_{20} and GA_1 were severely decreased relative to those in its wild type (WT). *ent*-Kaurenoic acid was actively converted to *ent*-7α-hydroxykaurenoic acid in WT plants but quite poorly in *dw2* plants. All together these data suggested that the *dw2* mutation severely reduced the flux through the biosynthetic pathway leading to active GAs by hampering the conversion of *ent*-kaurenoic acid to GA_{12}. Two *ent*-kaurenoic acid oxidase (*KAO*) genes were identified. *HaKAO1* was expressed everywhere in sunflower organs, while *HaKAO2* was mainly expressed in roots. The *HaKAO1* of *dw2* displayed an ample deletion (403 nucleotides) encompassing partial sequences of the last intron, the entire last exon and a partial sequence of 3'-UTR. Consequently, the AG required for the positioning of splicing was lost from the last intron. This mutation leads to aberrant processing of the resultant pre-RNA. [Fambrini et al., (2011) Plant Mol. Biol. 75:431-450]. In *dw2* calli, *Agrobacterium*-mediated transfer of WT *HaKAO1* cDNA restored the WT endogenous levels of GAs. In segregating BC_1 progenies, the deletion co-segregated with the dwarf phenotype. The deletion was generated near to a breakpoint of a more complex chromosome rearrangement.