

FUNCTIONAL CHARACTERIZATION OF MUTATIONS IN A BARLEY STRIGOLACTONE BIOSYNTHESIS GENE

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Hordeum vulgare, *Strigolactones*, *mutants*

Strigolactones (SL) are a diverse class of plant hormones that were shown to affect a wide range of traits including shoot branching and root architecture, responses to drought and other abiotic stresses, as well as interactions with arbuscular mycorrhizal fungi and germination of parasitic plant seeds. Research in model species revealed the main upstream steps of the SL biosynthesis pathway, but the existence of different so-called canonical and noncanonical SLs prompted investigations into the biological roles of these different molecules and the processing steps involved in producing such structural diversity. Moreover, genetic tools allowing the selective biosynthesis of specific SLs may be useful for tailoring crop plants with improved features without undesired pleiotropic effects. One such locus, *LATERAL BRANCHING OXIDOREDUCTASE* (*LBO*), encoding a 2-oxoglutarate and Fe (II)-dependent dioxygenase, has been identified as a gene acting specifically in noncanonical SL biosynthesis in *Arabidopsis*.

To better understand SL diversity and the underlying biosynthesis pathways in major crops of the Triticeae tribe, we targeted the barley (*Hordeum vulgare*) *LBO* ortholog (*HvLBO*) for functional analysis by gene-editing, TILLING and heterologous complementation tests in *Arabidopsis*. A range of phenotypic analyses under controlled conditions supported a conserved role of the gene in repression of shoot branching, as previously shown in *Arabidopsis*. As *lbo* mutants are predicted to be defective only in non-canonical SLs, the study of *lbo* mutants may be useful for revealing any noncanonical SLs specific effects, which we will discuss.

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