



# Cloning and characterization of a novel fructan 6-exohydrolase strongly inhibited by sucrose in *Lolium perenne*

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Auteur	Lothier, Jérémy [1], Van Laere, André [2], Prud'homme, Marie-Pascale [3], Van den Ende, Wim [4], Morvan-Bertrand, Annette [5]
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Résumé en anglais	Main conclusion The first 6-fructan exohydrolase (6-FEH) cDNA from <i>Lolium perenne</i> was cloned and characterized. Following defoliation, <i>Lp6</i> -FEHa transcript level unexpectedly decreased together with an increase in total FEH activity. <i>Lolium perenne</i> is a major forage grass species that accumulates fructans, mainly composed of $\beta(2,6)$ -linked fructose units. Fructans are mobilized through strongly increased activities of fructan exohydrolases (FEHs), sustaining regrowth following defoliation. To understand the complex regulation of fructan breakdown in defoliated grassland species, the objective was to clone and characterize new FEH genes in <i>L. perenne</i> . To find FEH genes related to refoliation, a defoliated tiller base cDNA library was screened. Characterization of the recombinant protein was performed in <i>Pichia pastoris</i> . In this report, the cloning and enzymatic characterization of the first 6-FEH from <i>L. perenne</i> is described. Following defoliation, during fructan breakdown, <i>Lp6</i> -FEHa transcript level unexpectedly decreased in elongating leaf bases (ELB) and in mature leaf sheaths (tiller base) in parallel to increased total FEH activities. In comparison, transcript levels of genes coding for fructosyltransferases (FTs) involved in fructan biosynthesis also decreased after defoliation but much faster than FEH transcript levels. Since <i>Lp6</i> -FEHa was strongly inhibited by sucrose, mechanisms modulating FEH activities are discussed. It is proposed that differences in the regulation of FEH activity among forage grasses influence their tolerance to defoliation.

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## Liens

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