

A novel gene controlling tiller development in barley

Tillering or branching is an important agronomic trait closely related to crop yield. It is well documented that the yield of cereal crops, including wheat, rice and barley can be improved by manipulating tillering. The “Green Revolution,” characterized by the development of semi-dwarf rice and wheat cultivars, dramatically increased yield potentials mainly due to enhancement tillering and spike-forming ability. Moreover, tillering is also important for cereal crops to fight against weeds. Tillers in grass plants are initiated and developed from the axillary meristem (AM) of basal nodes with little-elongated internodes. Each tiller has the potential to grow independently into the primary stem, by virtue of its adventitious roots, to generate its own spike. Barley (*Hordeum vulgare* L.) is the fourth largest cereal crop in terms of planting area in the world. It has been used as a model plant of Triticeae because of its diploid nature and wide genetic diversity. Compared with other species of Triticeae, such as wheat and rye, barley is weaker in tillering capacity and fewer in spikes per plant.

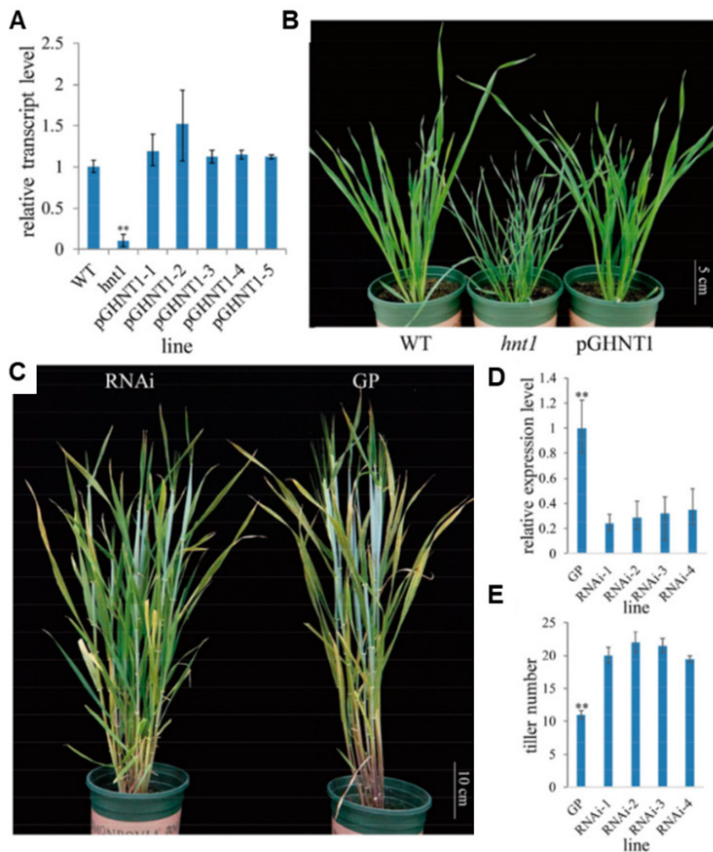


Fig. 1. Transgenic analysis of the *hnt1* mutant. A–B were genetically complementary transformation experiments. (A) Relative gene expression levels in leaves of WT, *hnt1* mutant and the positive T1 lines (pGHNT1-5) by quantitative real-time PCR analysis. (B) Phenotype of WT, *hnt1* mutant and positive T1 lines (pGHNT1) at tillering. C–E provide information on the *Hvhnt1*-RNAi lines and wild-type (cv. Golden Promise, GP). (C) Phenotypes of RNAi lines and GP at heading stage; (D) Relative gene expression levels in the leaves of GP and the positive RNAi lines by quantitative real-time PCR analysis; and (E) Tiller number of GP and positive RNAi lines.

In this study, we identified a *high number of tillering* (*hnt1*) mutant from a segregating population of a γ -ray treated barley cultivar Vlamingh, showing more tillers per plant, narrower leaves and shorter plants relative to the wild parent. Histological anatomy experiment showed that the more tiller number per plant in the *hnt1* mutant resulted from the accelerated outgrowth of tiller buds, and the narrower leaves were attributed to a reduction in vascular tissue and cell number. Genetic analysis revealed that more tillers per plant and narrower leaves in the *hnt1* mutant are controlled by a novel gene, encoding a trypsin family protein with 648 amino acids. A 2-bp deletion in the gene was responsible for the *hnt1* mutant phenotype. Gene function was further confirmed by transgenic complementary and RNAi experiments. *Hvhnt1* was expressed in vascular tissue, leaf axils and adventitious root primordia, and negatively regulated tiller development. The *Hvhnt1* mutation resulted in the accumulation of a putative cyclophilin-type peptidyl-prolyl cis/trans isomerase (PPIase), which physically interacts with the HvHNT1 protein in the nucleus of plant cells. Hence, it may be assumed that HvHNT1 controls barley tiller development and leaf width through PPIase.

The identification of novel genes is important for genetic studies and crop breeding. In this case, the *Hvhnt1* gene could be useful in barley breeding as it controls tiller development, plant height and leaf size. In addition, we found the involvement of trypsin in controlling tiller development, plant height and leaf size in barley or even other cereal crops.

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Publication

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