

Untapping barley's grain yield potential by mitigating floral degeneration

Gatersleben, 08.06.2023 Leaf and floral tissue degeneration are common features in plants. In cereal crops such as barley, pre-anthesis tip degeneration (PTD) starts with growth arrest of the inflorescence meristem dome. To elucidate the molecular underpinnings of inflorescence PTD, an international research team led by IPK Leibniz-Institute combined different approaches to show that barley inflorescence PTD is accompanied by sugar depletion, amino acid degradation, and abscisic acid responses. Furthermore, the research team identified *GRASSY TILLERS1 (HvGT1)* as an important modulator of inflorescence PTD. The results have been published in "Plant Cell".

Barley possesses an indeterminate 'spike'-type inflorescence that forms basic floral structures, called spikelets, in a distichous pattern along its central axis (termed rachis). Each rachis node in the barley spike produces three (one central and two lateral) spikelets.

At the end of spikelet primordia initiation along the rachis marks the stage of maximum yield potential. Subsequently, the inflorescence meristem dome starts to collapse, followed by gradual basipetal degeneration of spikelet primordia and spikelets until a specific position along the spike is reached. "We show that up to 50% of the initiated floral primordia are aborted before anthesis, representing an untapped yield potential", says Prof. Dr. Thorsten Schnurbusch, head of IPK's research group "Plant Architecture". "Understanding the molecular underpinnings of spike PTD may thus help improve grain yield in cereals."

Due to its quantitative nature and environmental sensitivity, inflorescence PTD constitutes a complex mechanism affecting final grain number. This mechanism appears to be predictable and heritable, consistent with a developmental programme. Photosynthesis, immature spike greening, and energy metabolism appear to be significant contributors to proper spikelet growth and differentiation and were restricted to basal and central spike parts. The researchers discovered, however, that the degenerating apical spike region undergoes sugar and amino acid depletion along with enhanced abscisic acid biosynthesis and signaling.

"Moreover, we functionally validated one of the apically expressed transcription factor genes, barley *GRASSY TILLERS1 (HvGT1)* an ortholog of maize *GT1*, as a growth repressor of apical spikelet development", emphasises Nandhakumar Shanmugaraj, first author of the study. Site-directed *Hvgt1* mutants in barley delayed the onset of spike PTD and produced more differentiated apical organs, resulting in significantly more fertile spikelets/florets and increased final spikelet number. "This is the first report on the

Press Release

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molecular underpinnings of barley inflorescence PTD; however, here we not only provide a molecular framework for barley but also for related cereals of the *Triticeae* tribe (e.g., wheat, rye)."

"We believe that the molecular elucidation of PTD in barley will also stimulate future research directions on the evolution of related genes on growth suppression in other plants beyond crop species", says Prof. Dr. Thorsten Schnurbusch. As barley is amongst the most important cereal crops in the world, better exploiting its spike yield potential can thus contribute to world food security and thereby directly help fight against hunger threats imposed by climate change, and natural or war disasters.

Original publication:

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A research team from the IPK Leibniz Institute has investigated the molecular underpinning of spike formation in barley. The aim is to better develop the yield potential of the cereal plant. Photo: IPK Leibniz Institute/ T. Schnurbusch