

IPK scientists discover gene that ensures slim inflorescence shape of barley

Gatersleben, 12.10.2020 The inflorescences of grasses often have very different shapes. An international research team led by IPK has now succeeded in identifying a gene that plays a decisive role in ensuring that barley develops its characteristic slender inflorescences, called spikes. Compared to other grasses, the COMPOSITUM1 (COM1) gene has acquired a new function during grass evolution. The results have today been published in *Nature Communications* magazine.

The "spikelet meristem" (SM) plays a central role during the development of the grass inflorescence. Meristems are plant cells or tissues that have the capacity to produce new organs - in this case spikelets. To do this, however, cells destined to become SM must first attain the SM identity. This is achieved, among other things, by gene regulation. As a result, cells develop normally from meristem to organ. The process thus runs from the undifferentiated plant cell to the differentiated organ.

To better understand grass inflorescence architecture, mutants can be very revealing to geneticists. The COM1 barley mutant e.g. is compromised in a way that the corresponding cells cannot perceive or convert the SM identity signal. "Ultimately, the signal transmission does not function properly, so that the cells cannot attain their correct cell identity," explains Dr. Naser Poursarebani, first-author of the study and discoverer of the COM1 gene. To put it simple, the cell does not know what to do in this situation. "Thus, spikelet formation along the main axis of the barley spike, the rachis, cannot proceed normally."

Ultimately, instead of producing a spikelet, a kind of "branch" occurs that looks like a small secondary spike. "Such 'branching', however, is very untypical for all spike-forming grasses belonging to the tribe Triticeae", Prof. Dr. Thorsten Schnurbusch, head of the independent research group Plant Architecture, HEISENBERG Professor of the IPK and the Martin Luther University Halle-Wittenberg and initiator of the study confirms.

In barley, COM1 normally ensures that meristem cells develop into spikelets by influencing the properties of their cell walls and thus ultimately controlling cell growth. COM1's contribution to this identity signal is also its newly discovered function, which is not found in other grasses such as rice, maize, sorghum or twigs (*Brachypodium distachyon* L.). Barley COM1 function is thus fundamentally different from those above-mentioned grass species, in which the gene rather promotes the formation of inflorescence branches. "From a botanical point of view, COM1 is therefore in any case an important genetic factor for spike formation and shape, about which little has been known until now", explains Prof. Dr. Schnurbusch.

Barley belongs to the grass family (Poaceae) and was domesticated from the wild barley (*Hordeum spontaneum*) ancestor in the area of the Fertile Crescent about 10,000 years ago. Scientists suspect that the simplified, less complex spike architecture of Triticeae species is related to the spread of those species into zones with a more temperate climate



Scientific Contact

Prof. Dr. Thorsten Schnurbusch
Tel.: +49 39482 5341
schnurbusch@ipk-gatersben.de

Media Contact

Christian Schafmeister
Tel. +49 39482 5461
schafmeister@ipk-gatersleben.de

and adaptation to cooler conditions. The newly gained insights into spike development can aid to better understand grass inflorescence evolution but possibly may also help to increase barley's yield potential.

Original publication: Poursarebani *et al.* (2020), COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals.

Nature Communications.

DOI: 10.1038/s41467-020-18890-y

Photo (for free use):

<https://ipk-cloud.ipk-gatersleben.de/s/LDrZKMfskDsmrBw>



Barley develops the characteristic slender spikes. Photo: IPK



A field of barley near Halle.
Photo: Nadja Sonntag

