

Summary:

- The *Jekyll* gene, first described in 2006, plays an important role in the sexual reproduction of barley (*Hordeum vulgare*).
- Researchers from the IPK in Gatersleben have discovered that *Jekyll* exists in two strongly diverged allelic variants in barley. Further they found that *Jekyll* is a lineage specific gene, which likely functioned as a driver for the separation of the Bromeae and Triticeae lineages within the Poaceae.
- The paper made the cover of The Plant Journal.

The two faces of the *Jekyll* Gene – Dual allelic state of *Jekyll* discovered

Gatersleben, 20.06.2019. **Genes which are specific to a species or group of species can reflect important genetic changes within lineages. Often, such lineage-specific genes are found to play a role within sexual reproduction, thus promoting reproductive isolation and, consequently, speciation. Whilst investigating the *Jekyll* gene which is essential for the procreation of barley, researchers from the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK in Gatersleben) have discovered that *Jekyll* occurs in form of two highly divergent allelic variants. The corresponding genes are lineage-specific for the grass tribes Triticeae and Bromeae and functioned as drivers for the speciation process within the Poaceae.**

The *Jekyll* gene was first described in 2006 by researchers from the IPK in Gatersleben. They found that while it was crucial for sexual reproduction and fertility in barley (*Hordeum vulgare*), it was also partially similar to the Cn4 toxin produced by scorpions and played a role in cell autolysis. Inspired by this seemingly two-faced nature of the gene, the researchers had named it after Dr. Jekyll, the main character with the split personalities Dr. Jekyll and Mr. Hyde and from the eponymous gothic novella. A follow-up study by the same group of IPK researchers, led by Dr. Ljudmilla Borisjuk, has now shown how stunningly apt their choice of name was.

Whilst working on *Jekyll*, Dr. V. Radchuk discovered that the gene exists as two different and much diverged allelic variants, *Jek1* and *Jek3*. The *Jek1/Jek3* sequences are located at the same chromosomal locus and are inherited in a monogenic Mendelian fashion, whilst *Jek1* and *Jek3* share identical signal peptides, conserved cysteine positions and direct repeats. Although the encoded protein sequences might just have over 50% similarity, the researchers found that *Jek3*

actually complements the function of *Jek1* in *Jek1*-deficient plants. Further investigations showed that *Jekyll* likely emerged in the common ancestor of the tribes of the Triticeae, such as barley, and Bromeae, therefore functioning as a lineage specific gene and probable driver for the separation of the lineages within the Poaceae.

The dual allelic nature of *Jekyll* made the cover of The Plant Journal and was featured in the belonging Research Highlight. In the meanwhile, the authors have started looking into the newly arisen questions of the cause and benefits of this allelic diversity in barley.

Characters: 2.532 (inkl. Leerzeichen)

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<https://doi.org/10.1111/tpj.14363>

Figure:

<https://ipk-cloud.ipk-gatersleben.de/s/NSLzWWP6JpqfzFe>

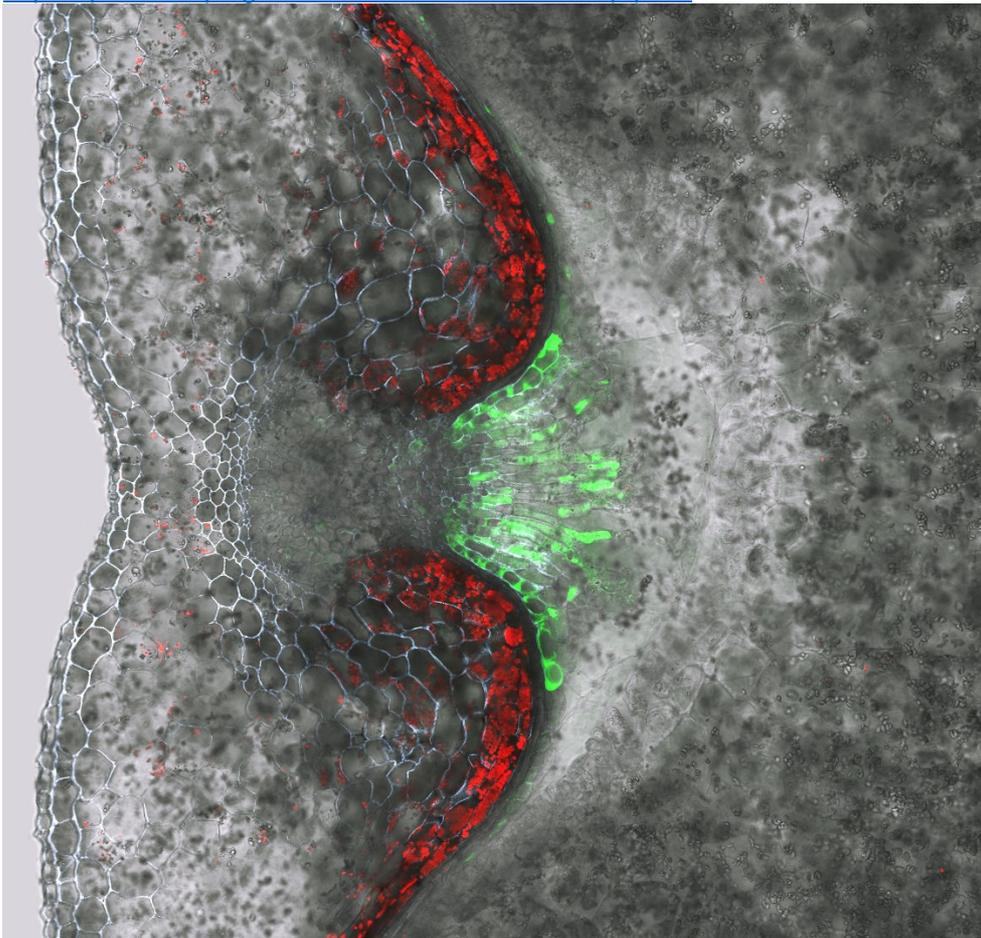


Figure: Activity of *Jekyll* promoter as visualised by expression of Jekprom: GFP (green signal). Stefan Ortleb & Twan Rutten

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