

Stories from One Thousand and Two *Secale* Samples: Insights into the evolutionary history of domesticated rye and its wild relatives

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As a minor crop with only local importance our understanding of the evolutionary history of domesticated rye and the relationship to its wild relatives are still limited. In contrast to wheat and barley, rye is not considered as a founder crop of Neolithic agriculture, even if the wild progenitors of all three cereal crops share the same area of distribution in Southwest Asia. Instead, rye is assumed to be a secondary domesticate that became widely used in Central and Eastern Europe only after its introduction as a weed in the course of the expansion of domesticated wheat and barley. The ability to thrive on poor soils and the high frost tolerance has enabled rye to become a suitable crop under harsh conditions as found in the northern areas of Europe.

Here, we use the combination of genotyping-by-sequencing and whole genome

resequencing data on 1002 *Secale* samples mapped to the recently assembled high quality reference genome to study the population history of the small genus *Secale*. Overall, the weak genetic differentiation between wild and domesticated rye points to ongoing gene flow and a fairly recent speciation leading to incomplete lineage sorting and low fertility barriers.

The analysis of the population genomic history of domesticated rye within the complex population structure of the different wild *Secale* species points to the idiosyncratic characteristics of the domestication process of rye. Combining these newly available genomic resources with archaeological and linguistic evidence enables us to explore the differences in use and perception of rye in different geographic areas as a result of the underlying past processes.