

Breeding research on Russian Dandelion (*Taraxacum koksaghyz*) as a rubber producing crop

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Russian Dandelion (*Taraxacum koksaghyz*, TKS) has the ability to produce and store high quality rubber in its roots. With the lack of alternative sources for natural rubber next to the Para rubber tree (*Hevea brasiliensis*), whose cultivation is problematic due to economical and ecological reasons, TKS has turned out as the most promising new resource crop for natural rubber demanding industries.

Since TKS shows high diversity and relatively weak growth, it is still considered a wild type. This work aims to gain insights into the genetic background of this plant and provide important information for breeding programs, in order to develop a new rubber producing crop.

As part of a network of different research institutions and private companies, the JKI Institute for Breeding Research is part of a value chain from breeding up to the finished product made of dandelion rubber. In close cooperation with a breeding partner, the comprehensive genetic variability of TKS shall be used for the development of new varieties with high level and quality of rubber.

On that account, different agronomic traits, such as the formation of a large,

clear tap-root with high contents in rubber, early and uniform flowering time, improved tillering in the first year of cultivation, as well as different disease resistances have been defined as breeding objectives.

In order to support these objectives, the genetic diversity of available germplasm of TKS was analyzed and first genetic maps were constructed based on a mapping population segregating for rubber content. By the application of a Genotyping-by-Sequencing (GBS) approach and combination with other molecular marker sources, a relatively high-density genetic map of TKS could be drafted.

This genetic map represents the basis for mapping QTLs regarding rubber content and other traits. Consequently, field trials with the cloned mapping population have been initiated over three years at three different locations for the exact quantification of rubber contents. Furthermore, transcriptomic sequence data (RNAseq, MACE) will be used for annotation of rubber related genes and inclusion in the genetic map. Combined, this information shall be used for the development of selection markers in marker assisted breeding approaches.