rubber precursor, or involved in rubber elongation. By generating genome-wide expression data from 11 TKS tissues, Lin *et al.* were able to identify five of these genes that are predominantly expressed in roots and latex.

Altogether, these observations identify a strong set of candidate genes that may form the basis both for further enhancement of TKS rubber production and also for establishing a viable NR alternative to the Pará tree.

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Rooting for new sources of natural rubber

Global production of natural rubber (NR) depends overwhelmingly on the Pará rubber tree (*Hevea brasiliensis*), a slow-growing tropical tree that is threatened by low genetic diversity and high susceptibility to fungal blight [1]. Alternative rubber sources have been sought for more than a century, but very few species have been found that produce rubber of comparable quality [2]. One of the brightest candidates, first noticed by breeders in Soviet-era Russia, is *Taraxacum kok-saghyz* (commonly called TKS). This close relative of the common weedy dandelion has a number of attractive features. As a native of central Asia, TKS can be cultivated as a hardy, annual field crop in temperate climates. Its natural latex, produced at highest levels in the roots, yields a high-molecular-weight NR that is chemically similar to the rubber tree and far superior to synthetic rubber. And, as an added bonus, TKS produces inulin, a dietary fiber and low-glycemic-index sweetener that can be fermented for industrial bioethanol production. What TKS has lacked—until now—is an assembled reference genome that could be used for genome-enabled crop improvement and elucidation of the pathways for rubber and inulin biosynthesis. In their paper published in this issue, Jiayang Li, Hong Yu and colleagues [3] have taken a major step in rectifying that problem.

Taking advantage of the long reads provided through PacBio sequencing technology, together with the high coverage of Illumina short-read and mate-pair sequences, Lin *et al.* [3] generated a draft TKS genome assembly with an estimated size of 1.29 Gb. This draft assembly is roughly comparable in size to the ∼1.18 Gb genome inferred through flow cytometry. To bolster their gene annotations, the authors complement their genomic sequence data with RNA-seq data from multiple tissues. This approach yields important insights towards the characterization of the gene families and pathways involved in rubber and inulin biosynthesis. Identification of candidate genes and pathways is also facilitated by comparisons to non-rubber-producing members of the sunflower family, in particular the globe artichoke. Among the genes potentially implicated in rubber biosynthesis, members of the cytosolic mevalonate pathway may prove especially important. Specific gene families of particular interest for rubber elongation and stabilization include members of the CPT/CPTL gene family (encoding *cis*-prenyltransferases and rubber transferase activators) and the REF/SRPP family (encoding rubber elongation factors and small rubber particle proteins). Several candidate genes are also identified for inulin synthesis, including two promising candidates that show differentially high expression in the root.

Detailed characterization of the TKS genome still has many steps ahead, and the path will be complicated by the highly heterozygous genome of this self-incompatible species as well as the extensive proliferation of repetitive elements, which the authors estimate to make up over two-thirds of their genome assembly. But the work undertaken by Lin *et al.* [3] is a critical move in the right direction, and the genomic resources yielded by their efforts will undoubtedly serve as an important foundation for future advances in TKS research and breeding.

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