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Cannabis sativa: not just Devil’s weed

When hearing about *Cannabis sativa*, we undeniably think about marijuana and its addiction. However, *C. sativa* grown for industrial use has a Δ^9-tetrahydrocannabinol (THC, a psychoactive component) content <0.3% and has instead a high number of cellulosic fibres much valued by the textile and biocomposite sectors. Grown already in ancient China to make ropes and clothes, the cultivation of textile hemp was progressively abandoned during history because of the advent of synthetic fibres and as a consequence of the ban put on marijuana growth. We are now witnessing a « renaissance » of the agricultural interest in hemp cultivation, especially in Europe, which coincides with the need to push towards a bio-based economy. Textile hemp grows fast – much faster than woody species – it requires less water than other fibre crops (like cotton), it is naturally resistant to pests and its well developed root system helps against soil erosion.

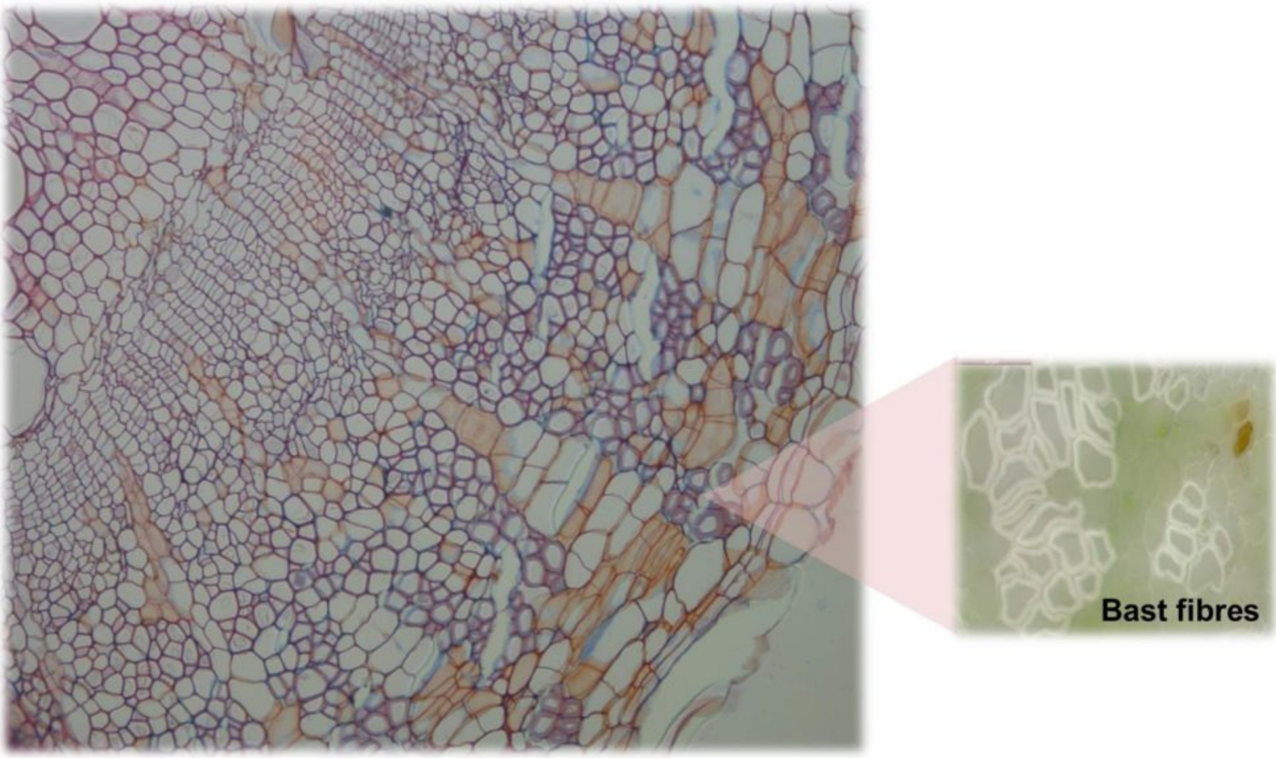

Fig. 1. Transversal cross-section of the hemp stem showing the presence of bast fibre bundles towards the stem cortex. A magnification of bast fibre bundles shows their typical « doughnut »-like appearance, due to the thick cellulosic G-layer.

What makes hemp so precious is, however, the high content of strong, long cellulosic fibres which surround a central woody core. These fibres – known as bast fibres – mechanically support the phloem (the conductive tissue transporting photosynthates) and show excellent mechanical properties which make them attractive substitutes of glass fibres for composite reinforcement. Bast fibres reach their considerable length (in some cases up to 100 mm) via a mechanism known as « intrusive » or « invasive » growth: their pointy ends diffusively extend by disrupting the middle lamellas (i.e. the pectin-rich layer glueing plant cells together) of the neighboring cells.

Elongation of bast fibres takes place in a specific region of the hemp stem and, more specifically, above the so-called « snap point », described in flax by the group of Prof. Gorshkova at the Kazan Science Centre. This region, determined empirically by tilting the stem, marks a shift in the stem mechanical properties coinciding with the transition from cell elongation to thickening. Bast fibres indeed initially elongate rapidly and then they stop, to start thickening their cell walls and mature the typical crystalline gelatinous (i.e. cellulosic) layer (G-layer) conferring the sought-after tensile properties. The presence of such a region allows high-throughput studies along the hemp stem aimed at understanding the transcriptomic signature of young elongating stem internodes and older ones.

In our recent study, carried out in the context of a project financed by the national research fund of Luxembourg (FNR), we sampled the hemp bast fibres from internodes located at different stem heights (Guerriero et al., 2017). More specifically, we analyzed fibres at the top (rapidly elongating region), middle (containing the snap point) and bottom (fully thickened bast fibres). We demonstrate that the bulk of the events associated with cell wall biosynthesis/remodelling are present at the snap point. Transcription factors involved in elongation/cell proliferation arrest and onset of secondary cell wall formation are indeed highly expressed in this stem region, accompanied by genes encoding major glycosyltransferases responsible for cellulose and xylan biosynthesis. Fibres of young stem regions show high expression of genes involved in the biosynthesis of specific secondary metabolites, notably indole glucosinolate, which mediate the response to mechanical damage and may thus regulate intrusive growth. The transcriptome of bast fibres from older stem internodes is dominated by genes involved in phytohormone biosynthesis and homeostasis, notably abscisic acid and gibberellin. Our study identifies interesting targets for functional studies. Although hemp is difficult to transform, the biotechnological progress in the field of plant biotechnology will lead to more efficient regeneration protocols and gene editing strategies improving specific characteristics of hemp bast fibres.

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Transcriptomic profiling of hemp bast fibres at different developmental stages.
Guerriero G, Behr M, Legay S, Mangeot-Peter L, Zorzan S, Ghoniem M, Hausman JF
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