



Participants

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The specimens were cultivated at Mauguio in collaboration with the DIAPHEN platform.

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Histological quantification of maize stem sections from FASGA-stained images

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Quantifying the histological profile of maize ear internodes to unravel plant response to hydric stress

Carefully controlled crop irrigation is crucial for sustainable agriculture. In this respect, the development of drought-adapted plant varieties is desirable, but only possible if knowledge is available regarding differential responses of plants exposed to water deficits of variable duration and intensity. Moreover, plant degradability and plant agronomic properties (such as drought-resistance) are both crucial factors that depend on plant-growth development and variations in plant cell-wall composition. Therefore, it is the diversity of these responses that can serve to identify genotypes combining stable agronomic performances with good degradability under varying environmental conditions.

► RESULTS

We custom-developed an automated image processing and analysis procedure for quantifying the histological tissue-type pattern of maize stem sections using high-res colour-stained input images digitalized with whole-slide scanners. The method involves segmenting different tissue regions based on variations in the colour and morphology of the plant structures, which gives an anatomical ID of the section that can then be run through an automated analysis to quantify the colour and morphology of the tissue regions. The information output can be cross-correlated against information from other analytical methods (typically biochemistry and/or spectroscopy) to assess the relationships between the composition, histology and degradability of crop plants under contrasting water supply regimes. Plant response to water deficit can then be characterized and integrated at each of these levels.

► FUTURE OUTLOOK

Our custom-developed methodology has already served to study several maize genotypes that experienced variable cell-wall degradability and that were cropped under different irrigation regimes. The high throughput processability achieved makes it possible to characterize several hundred samples per week, which raises prospects for studying the basic genetics involved in biochemically and histologically variable phenotypes and their responses to hydric stress. The approaches developed here are transposable to other crop grasses, including major biomass-feedstocks plants like *Miscanthus*.

Illustrative example of sample-image acquisition of FASGA-stained sections from the same genotype cultivated under two different irrigation scenarios (with irrigation, at left, and without irrigation, at right), and output results of the image segmentation workflow on these same images segmented into distinct tissue-class regions.

