Title
The role of sugar supply and signalling in the regulation of maize leaf growth

Description
Light drives the generation of sugars by photosynthesis and sugars act as signalling molecules that regulate developmental processes including cell division and expansion. Studies on growth regulation by sugars have been done largely in *Arabidopsis*, but we use the maize leaf due it its larger size that allows to perform analyses of the sugar metabolism, particularly in proliferating and expanding cells that drive growth. Using this system, we studied the effect of light treatments and mutants affected in the sugar metabolism, that so far have not been studied in the context of organ growth regulation

We identified different mutations of sugar metabolism and transport genes (e.g., ramosa3 (*ra3*, encoding T6P phosphatase (TPP): increased leaf length), miniature1 (*mn1*, encoding cell wall invertase gene, short and narrow leaves), *ae* (coding amylase extender gene) and *sut1-m4* (encoding sucrose transporter 1 gene, short leaves). Our spatitemporal analyses of carbon metabolism and growth of thee sugar related mutants indicated that plants coordinate growth with carbon availability. However, we currently do not know how the diurnal dynamics of sugar depletion and growth rate are related. Therefore, we developed a leaf length tracker to measure leaf elongation of maize leaf at a time scale of minutes to perform a high-resolution phenotyping of the leaf growth. This will enable us to pinpoint at which time during the day/night cycle the mutations have the smallest and strongest effect on the growth rate, providing a basis for more detailed cellular (cell division and expansion), metabolic (different sugars and hormones), biochemical (enzyme activities) and transcriptional (mRNA) analyses.

Techniques
The selected mutants will also be subjected to extended detailed kinematic analysis to quantify rates of cell division and expansion along the growth zone, allowing to determine the contribution of these processes in the overall phenotype.

We also use a leaf length tracker, as a novel, and cheap approach to measure leaf elongation of cereals at a time scale of minutes to provide enough statistical power to differentiate between LER curves under controlled growth conditions.

Also, a range of protocols is available in our laboratory and operational for the measurement of different sugar metabolite levels (e.g., Glc, Fru, Suc, T6P, starch, etc.) and enzyme activities (e.g., amylase, invertases, sucrose synthase, starch synthase, etc.) in the 10 segments collected along the leaf blade.

Based on RNAseq results, The expression profile of few genes of interest will be confirmed and refined using up to 10 segments along the growth zone by QPCR

Supervisor
Dr. Hamada AbdElgawad
Prof. Dr. Gerrit Beemster

- There is a PowerPoint presentation for this topic