ABSTRACT

"LEAF growth: from images to molecular networks"

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Growth of plants and plant organs is orchestrated by complex molecular networks that integrates both intrinsic development signals encoded by the genome as well as a wide variety of environmental cues such as light, availability of water and minerals, temperature, e.a. Understanding the molecular composition and topology of these networks ultimately will accelerate advanced breeding and gene engineering for higher yielding crops. We have chosen leaves as a model organ to understand growth and size control mechanisms. As leaf growth is a quantitative trait, several (semi-) automated growth analysis platforms were developed to analyze leaf growth over time. Detailed cellular and molecular analysis of numerous Arabidopsis mutants revealed the existence of at least five mechanisms that contribute to final leaf size: i) the initial size of the leaf primordium; ii) cell cycle duration; iii) the developmental timing of the transition from cell division to cell expansion; iv) the timing of meristemoid division; and v) cell expansion. For each mechanism, multiple genes have been identified that when overexpressed or mutated enhance leaf organ size. For example, cell cycle duration appears to be controlled by the ANAPHASE PROMOTING COMPLEX, a multi-protein E3 ligase that is involved in mitosis. On the other hand the transition from cell division to cell expansion during leaf development is mediated by the gibberellic acid (GA) dependent activity of a chromatin remodeling complex. GA levels in the growth zones are regulated by the activity of two stress responsive transcription factors ERF5 and ERF6 and our experimental data show that these transcription factor have a pivotal role in regulation growth in response to the environment. Furthermore, GA also was shown to have an important function in mediating leaf growth in maize and by engineering GA metabolism maize leaves that have a 40% increase in length were obtained. We will discussed our current understanding of growth regulatory networks and how we can use this information to improve crop yield.