

Modifications in Modulating Plant Development

Phillip Andrew*

Huxley Faculty Fellow, Department of Ecology and Evolutionary Biology, Rice University, USA

Editorial

Plant Development during a Nut Shell

Plant development is an overarching term for a plethora of processes, including embryonal development, seed maturation and germination, and growth of the vegetative plant with specialized roots, shoots, leaves and flowers. It's been shown that sugars, glycoproteins and glycolipids play an important role in various pathways like hormone signaling, cellular trafficking, development and growth.

Seed development is universal and includes embryogenesis, maturation and germination. Embryogenesis follows after flower pollination and ovule fertilization by pollen grains, and is taken into account because the beginning of each plant's life cycle. The method starts with sequential coordinated cell divisions of the zygote, resulting in a globular embryo, a cluster of undifferentiated cells. During embryogenesis, the evolving embryo receives endless flow of nutrients from the parental plant. Later on, the first meristems develop. Cell divisions within the protoderm and within the embryo cause the event of the longer term epidermis on the one hand and therefore the ground meristem and procambium on the opposite hand, which successively will develop to ground tissue and plant tissue, respectively.

Developmental Consequences of Glycosylation: From Flowers to Germinating Seeds

The importance of glycosylation for flowers, fertilization, seeds, developing embryos, germinating seeds and developing roots and leaves is illustrated by the multitude of research articles addressing this subject. Most of those reports make use of mutant plants, mostly in *Arabidopsis thaliana* L., during which one or multiple proteins involved within the glycosylation pathway are knocked out, knocked down or over-expressed, allowing to look at which modifications play an important role within the glycosylation pipelines.

Functionality of Protein Glycosylation

DELLA proteins cause growth repression through transcriptional reprogramming of various genes involved in cellular division, expansion and differentiation. The change in transcription levels for these genes is modulated through protein-protein interactions between DELLA proteins and a number of other transcription factors. REPRESSOR OF GA1-3 (RGA), a DELLA protein, is SPY-dependent O-fucosylated. It had been reported that RGA extracted from the spy mutant displayed reduced binding activity compared to the DELLA protein obtained from wild type plants. Additionally, it had been shown that O-GlcNAcylation by SEC inhibited the interaction of RGA with four of its interactors, suggesting opposite roles for O-GlcNAcylation and O-fucosylation in RGA. These results provided evidence that O-fucosylation and O-GlcNAcylation influence specific functions of RGA.

Another example showcasing the importance of glycosylation for a specific

**Address for Correspondence:* Phillip Andrew, Huxley Faculty Fellow, Department of Ecology and Evolutionary Biology, Rice University, USA, E-mail: phillipandrew814@gmail.com

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protein, is that the endo- β 1, 4-glucanase glycoprotein KORRIGAN1 (KOR1), necessary for cellulose biosynthesis. Recombinant KOR1 with mutated N-glycosylation sites yielded proteins with reduced glucanase activity. Additionally, aberrant N-glycosylation of KOR1 also changed its localization within the different subcellular compartments.

Despite the considerable number of studies that specialize in elucidating the biological role of glycosylation enzymes, their characteristics and respective phenotypes, less attention is paid in performing analyses for specific glycoproteins. Only a couple of examples exist where glycosylation functionality is approached at the extent of one glycoprotein. Two striking examples include the MTR1 glycoprotein and therefore the SCR/SRK glycoprotein, which are important for flower development and reproduction. Site-directed mutagenesis of the N-glycosylation sequon in MTR1 revealed that this modification is crucial for normal anther development and pollen fertility. Its role was confirmed with subsequent analysis of the glycosylation profile through PNGaseF treatment. Similarly, the extent of glycosylation of the SCR/SRK tandem determined the pollen haplotype, allowing the stigma to discriminate between self and non-self and henceforth evoking self-incompatibility. Similarly, glycosylation of pattern recognition receptors is required to mediate plant immune signaling.

Sugar Signaling because the Puppet Master of Plant Development

Plants as autotrophic organisms produce sugars in mature photosynthetic leaves (source organs) which are subsequently wont to support the storage and growth in sink tissues like the roots, young leaves and fruits. Aside from driving growth as metabolic substrates, sugars also function signaling entities, interacting with environmental stimuli and metabolic signals to manage cell growth through the remobilization of nutrients and storage compounds. Free soluble sugars like Glc and Fru are thus directly associated with the cellular energy status of the cell. As such, sugars are linked to the regulation of growth and stress responses, but also as important cues during developmental decisions like germination, vegetative phase change, flowering and senescence. However, the interplay between soluble sugars and glycol conjugates in plants remains largely underexplored.

Perspectives

Glycosylation of proteins and lipids represents a crucial and sophisticated post-translational modification governing a broad sort of developmental processes, regulation of biotic and abiotic stress responses, also as signaling pathways. Over the last decades, particular attention was paid to all or any aspects of N-glycosylation. However, recent findings associated with O-glycosylation means that there are still missing links that prevent a profound understanding. Whereas the N-glycosylation pathway also because the nature and significance of N-glycoproteins are well-studied, more detailed studies are needed to succeed in an equivalent level of comprehension for the O-glycosylation process and O-glycoproteins, but also to know the interplay between both N- and O-glycosylation and therefore the link with sugar and hormone signaling. There's more to research concerning the structure, distribution and evolutionary aspects of glycoproteins and glycolipids across plants, and interactomics at the extent of specific pathways and processes during particular developmental stages.

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