



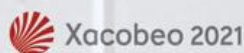
Dr. Beatriz Orosa

Lecture Title: *Deciphering ubiquitin and SUMO signalling to enhance plant performance in a changing environment*

School of Biological Sciences – The University of Edinburgh

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Abstract

Plants are sessile organisms, unable to modify their surroundings; therefore, they must constantly and rapidly adjust to environmental changes. To cope with the large variety of biotic and abiotic stresses, plants employ a dynamic proteome, where post-translational modifications as ubiquitin and ubiquitin-like or SUMO are key. The Arabidopsis genome project identified more than a thousand genes encoding components of ubiquitin-like pathways, which represent about 10% of the entire plant proteome. I will use two case studies where plants use posttranslational modifications to cope with biotic and abiotic stresses to highlight their crucial role in plant-environment interactions. For instance, SUMO plays a major role in the regulation of root branching, a process of vital agronomic importance since it determines the efficiency of water uptake and nutrient acquisition in crops. Basically, plants develop lateral roots on the side of the main root in contact with water, but rarely on the dry side. This process is highly dependent of the transcription factor ARF7, and its transcriptional activity is regulated by the posttranslational modification SUMOylation.

In response to drought, SUMO negatively regulates ARF7 DNA binding activity, rapidly blocking gene expression associated with lateral root initiation. Similarly, posttranslational modifications are key in plant immunity. Ubiquitination is highly versatile, as it enables the addition of eight different ubiquitin chain linkages to substrates, thereby regulating their stability or cell signalling properties. Ubiquitin signalling is an indispensable component of the plant immune system and plays key roles in modulating the stability of immune receptors and transcriptional regulators.

Nonetheless, how different ubiquitin topologies contribute to the establishment of immunity remains completely unknown. By developing a new linkage-specific ubiquitin proteomics workflow, I demonstrated for the first time that all eight ubiquitin topologies exist in plants and that chain branching is pervasive. Moreover, diverse ubiquitin topologies accumulated upon activation of plant immunity regulate key cellular processes that contribute to immune development, including transcription reprogramming, epigenetic regulation of chromatin and DNA damage repair.

In summary, posttranslational modifications enable a swift and reversible response to environmental stressors; synthetic exploitation of these modifications and their underlying regulatory mechanisms represents an untapped resource to enhance the performance of plants of agricultural interest.

Researcher profile:

My scientific career started with a PhD with Dr Blanca SanSegundo at the University of Barcelona (Spain), where I studied the defence of Arabidopsis plants to fungal pathogens and acquired invaluable knowledge on plant pathogen interactions.

During a sabbatical period from my PhD I had the opportunity to work on human autoimmunity at the Institute of Health Research (Santiago de Compostela, Spain), focusing on deciphering the molecular signals that induce autoimmunity. My results provided a promising new target for therapeutic treatments that led to a patent and four peer-reviewed manuscripts as first author. Although my experience in the biomedical field was very rewarding, I have always been fascinated by the ability of plants to perceive, anticipate, and swiftly respond to environmental changes and pathogens. Therefore, I moved to Prof Ari Sadanandom group (Durham University) to study how plants employ protein posttranslational modifications for fast and accurate regulation of stress responses. My four years in Durham led to a series of exciting discoveries, which resulted in nine peer-reviewed manuscripts, including three as first author in high impact journals (SCIENCE, NATURE COMMUNICATIONS and PLoS GENETICS). I revealed how posttranslational modifications play a key role in perceiving and responding to environmental stress, which has direct relevance to agritech approaches to boost the ability of crops to cope with a changing environment.

My increasing interest in posttranslational modifications led me to the University of Edinburgh where I independently developed new proteomic tools to investigate for the first time how linkage-specific ubiquitin signalling orchestrates plant immunity. While ubiquitin chain diversity is intensively studied in mammalian immunity and pharmacology, by contrast little is known about its role in establishing plant immunity.

This has left a wide-open research niche and great potential for biotechnological innovation of novel agritech approaches to food security. My future goal is to establish myself in this open research niche and to translate my frontier research on ubiquitin signalling into directly applicable methodologies for crop protection.