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Phosphoproteomic approaches to understanding ABA signaling networks in plants

Monday 1 July 2013 3.00 – 4pm

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Slatyer seminar room R.N. Robertson Building (Bldg. 46), Linnaeus Way, ANU



Abscissic acid (ABA) is a phytohormone that regulates diverse plant processes, including seed germination and the response to dehydration. In the major ABA signaling pathway, three members of SNF1-related protein kinase 2 (SnRK2) family transmit ABA-induced signals through phosphorylation of downstream substrates. To identify such substrates, we screened thousands of phosphoproteins in Arabidopsis by mass spectrometry-based phosphoproteomics. We identified proteins that were phosphorylated in Arabidopsis wild-type plants, but not in mutants lacking SnRK2s (srk2dei), treated with ABA or subjected to dehydration stress. Comparative analysis revealed that 35 peptides were differentially phosphorylated in wild-type but not in srk2dei plants. Biochemical and genetic studies of candidate SnRK2-regulated phosphoproteins showed that SnRK2 promoted the ABA-induced activation of MAPK(s), AtMPK1/2; that SnRK2 mediated phosphorylation of Ser45 in a bZIP transcription factor, AREB1, and stimulated ABA-responsive gene expression;

and that a previously unknown protein, SnRK2-substrate 1 (SNS1), was phosphorylated in vivo by ABA-activated SnRK2s. Reverse genetic analysis revealed that SNS1 acts as a negative regulator of ABA responses. Thus, by integrating genetics with phosphoproteomics, we identified multiple components of the ABA-responsive protein phosphorylation network.

Presented by
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**Medicine, Biology
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