The root-derived bps signal induces ABA-dependent and ABA-independent changes in gene expression.

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The Arabidopsis *bypass1* (*bps1*) mutant shows a severe seedling growth arrest phenotype. This growth arrest is a response to a novel mobile metabolite that is over-produced in its roots, and that is also sufficient to arrest growth of a wild-type plant. Our goal is to determine whether the *bps* signal is a plant hormone that has not been previously described. One of our approaches is to characterize responses of wild-type tissues to the *bps* signal using transient micrografts. We place a wild- type scion and *bps1* or wild-type (control) rootstock in a grafting collar, separated by an agarose block. Wild-type scions show robust responses to the *bps* signal within 24h. Evidence for the *bps* signal controlling gene expression came from using scions carrying GUS markers (*CYCB1:1::GUS* and the stem-cell marker *pWUS::GUS*). To characterize the genome---wide responses to the *bps* signal, we carried out RNAseq on wild-type scions grafted to *bps1* or wild-type roots. This analysis identified 353 up-regulated and 81 down-regulated genes. GO analysis showed over-representation of water deprivation, salt stress, and ABA response genes. Although *bps1* double mutants that abrogate ABA synthesis are phenotypically identical to *bps1*, we considered that ABA might be mediating a *bps* signal---initiated physiological response. To test this, we carried out RNAseq on scions from transient micrografts that coupled *aba3* mutant scions with either *aba3* or *bps1 aba3* roots. This analysis revealed a core set of genes that respond to the *bps* signal independently of ABA, a second set of genes regulated through *bps* signal-ABA cross talk, and a third large set of ABA-specific genes. These findings are consistent with the *bps* signal being a novel plant hormone that functions upstream of ABA production, and that also controls development through ABA-independent regulation of gene expression.