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Data Article

Quantitative proteome changes in *Arabidopsis thaliana* suspension-cultured cells in response to plant natriuretic peptides

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ABSTRACT

Proteome changes in the *Arabidopsis thaliana* suspension cells in response to the *A. thaliana* plant natriuretic peptide (PNP), AtPNP-A (At2g18660) were assessed using quantitative proteomics employing tandem mass tag (TMT) labeling and tandem mass spectrometry (LC–MS/MS). In this study, we characterized temporal responses of suspension-cultured cells to 1 nM and 10 pM AtPNP-A at 0, 10 and 30 min post-treatment. Both concentrations we found to yield a distinct differential proteome signature. The data shown in this article are associated with the article “Plant natriuretic peptides induce a specific set of proteins diagnostic for an adaptive response to abiotic stress” by Turek et al. (Front. Plant Sci. 5 (2014) 661) and have been deposited to the ProteomeXchange with identifier PXD001386.

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Specifications table

Subject area	Biology
More specific subject area	Plant science, Arabidopsis cell suspension proteome
Type of data	MS data and annotations
How data was acquired	TMT labeled peptides were analyzed using LTQ Orbitrap Velos mass spectrometer (Thermo Fisher Scientific, Germany)
Data format	Analyzed output data
Experimental factors	*A. thaliana* suspension-cultured cells were treated with AtPNP-A or water (mock treatment) and total protein was extracted, digested with trypsin and the peptides were labeled with TMT
Experimental features	The peptides resulting from in-solution tryptic digestion of total proteins from treated cells were labeled with TMT, OFFGEL-fractionated and analyzed using LC–MS/MS
Data source location	Thuwal, Saudi Arabia
Data accessibility	The data available in this article is related to [1] and deposited to the ProteomeXchange with identifier PXD001386 (http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD001386)

Value of the data

- A total of 4641 proteins were identified in response to 1 nM AtPNP-A and 3447 proteins in response to 10 pM AtPNP-A at a false discovery rate (FDR) of 0.7% for protein and 1.6% for peptide.
- 11 proteins are differentially expressed in response to 1 nM AtPNP-A and 15 proteins in response to 10 pM AtPNP-A. These differentially expressed proteins are mainly enriched for functional categories of translation and response to salt, heat and oxidative stress.
- Cellular responses to PNPs are highly concentration-dependent.
- We propose that AtPNP-A, possibly signaling through cGMP, has a key role in oxidation-reduction processes as well as response to salt stress.
- The data are valuable for understanding the molecular mechanism of AtPNP-A action and are key for further exploration of the PNP signaling.

1. Experimental design

Quantitative proteomic changes in response to *Arabidopsis thaliana* PNP (AtPNP-A; At2g18660) was performed as outlined in Fig. 1. Total soluble proteins were extracted from 10 to 30 min Arabidopsis cell suspension culture samples either treated with water or with different concentrations (1 nM and 10 pM) of AtPNP-A. A total of three biological replicates of the mock-treated and three biological replicates of cells treated with each concentration of AtPNP-A were used per each time-point considered in this study. We performed a proteomic analysis using LTQ Orbitrap Velos after OFFGEL fractionation of the TMT-labeled tryptic peptides. The acquired mass data identification was performed using MASCOT and SEQUEST search engines and the interpretation was done using Scaffold Q+ software. The proteomics data presented here include the protein and spectrum identification results, gene ontology (GO) functional category and transcriptional profiling results. Here, 4641 proteins were identified in response to 1 nM AtPNP-A and 3447 proteins in response to 10 pM AtPNP-A, at FDR of 0.7% for protein and 1.6% for peptide. 11 unique proteins were differentially expressed in response to 1 nM AtPNP-A while expression of 15 proteins was significantly regulated upon treatment with 10 pM AtPNP-A. The functional categories of the proteins with significantly altered expression in response to AtPNP-A were annotated using TAIR GO search (http://www.arabidopsis.org/tools/bulk/go/index.jsp). The transcriptional profile of these proteins was also analyzed using Genevestigator (https://www.genevestigator.com/gv/plant.jsp) [2].