Internal Report

Deliverable D3.2A:

Identification of all public knowledge resources related to plant immune signaling

National Institute of Biology Version 1 FINAL

Abstract: To improve further downstream analyses, we have identified the main important public knowledge sources related to immune signaling. Three important layers of biological regulation were chosen, namely protein-protein interactions, transcription factor regulation and regulation via small RNA molecules. For each separate source, we covered highly reliable, often manually curated corrections, enhancing them with data from high-throughput experimental datasets and also computational predictions, when deemed necessary.

Document administrative information	
Project acronym:	HinLife
Project number:	J7-7303
Deliverable number:	D3.2
Deliverable full title:	Identification of all public knowledge resources related to plant immune signaling
Document identifier:	HinLife D3.2 v1.FINAL
Lead partner short name:	NIB
Report version:	Version 1, FINAL
Report preparation date:	09/02/2017
Lead author:	Kristina Gruden
Co-authors:	Živa Ramšak
Status:	Final

Introduction

Identification of important public knowledge sources enveloped main publically available data sources, particularly for Arabidopsis thaliana (as the main model plant organism). Highly reliable protein-protein interactions included the manually curated subset of the AtPIN database (Brandao et al., 2009) and STRING-v10 connections with a score larger than 0.9 (Szklarczyk et al., 2015), transcription factor regulation dataset was extracted from the atRegNet and ATRM databases (Jin et al., 2015; Palaniswamy et al., 2006) and micro RNA dataset from miRTarBase (Chou et al., 2015). Datasets resulting from high-throughput experiments or computational predictions of protein-protein interactions (Arabidopsis Interactome Mapping Consortium, 2011; Jones et al., 2014), transcription factor regulation (Chang et al., 2013; Liu et al., 2015) and miRNA regulation (Zhang et al., 2010; Yi et al., 2014) were also included. As highly reliable protein-protein interactions were more abundant, only predictions of transcription factor regulation (Srivastava et al., 2010) and miRNA regulation (Yi et al., 2014) were included. To enhance the knowledge on plant-virus interactions, datasets on host component interaction with virus components (Elena et al., 2011) or bacterial effector proteins were added (Mukhtar et al., 2011). Each connection was ranked based on its reliability in the following hierarchical order: (1) most reliable curated knowledge from literature, (2) connections resulting from high-throughput experiments and (3) in silico computationally predicted connections. For the connections that were present in different data sources the highest reliability level available was assigned. Selected datasets with their corresponding literature references are listed in Table 1, with an indication of data type and data reliability level.

Results

Table 1: In the connections table, the first two columns describe the data type and it's quality level (manually curated sources > high-throughput studies > in silico predictions). PPI – protein-protein interactions; TR – transcriptional regulation; miRNA – miRNA regulation.

Data Type	Quality Level	Source	Connections #
PPI	manually curated	AtPIN (Brandao et al., 2009) STRING-v10 (Szklarczyk et al., 2015) PPI individual	6637 9140 31
PPI	HT studies	Arabidopsis interactome (Arabidopsis Interactome Mapping Consortium, 2011) membrane interactome (Jones et al., 2014) viral component interactions (Elena et al., 2011) immune component interactions (Mukhtar et al., 2011)	11351 12102 175 2795
TF	manually curated	atRegNet (Palaniswamy et al., 2006) ATRM (Jin et al., 2015) TF individual	4540 1440 34
TF	HT studies	atRegNet (Palaniswamy et al., 2006) ChIP-seq (EIN3) (Chang et al., 2013) ChIP-seq (WRKY33) (Liu et al., 2015)	12334 1314 214
TF	in silico predictions	Arabidopsis transcription factor targets (Srivastava et al., 2010)	12333
miRNA	manually curated	miRTarBase (Chou et al., 2015) miRNA individual	68 36
miRNA	HT studies	PMRD (Zhang et al., 2010)	1999
miRNA	in silico predictions	PNRD (Yi et al., 2014)	1617

References

Arabidopsis Interactome Mapping Consortium (2011). Evidence for Network Evolution in an Arabidopsis Interactome Map. Science (80-.). **333**: 601–607.

Brandao, M.M., Dantas, L.L., and Silva-Filho, M.C. (2009). AtPIN: Arabidopsis thaliana protein interaction network. BMC Bioinformatics **10**: 454.

Chang, K.N. et al. (2013). Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. Elife **2013**: 1–20.

Chou, C.-H. et al. (2015). miRTarBase 2016: updates to the experimentally validated miRNA-target interactions database. Nucleic Acids Res. **44**: gkv1258-.

Elena, S.F., Carrera, J., and Rodrigo, G. (2011). A systems biology approach to the evolution of plant-virus interactions. Curr. Opin. Plant Biol. **14**: 372–377.

Jin, J., He, K., Tang, X., Li, Z., Lv, L., Zhao, Y., Luo, J., and Gao, G. (2015). An arabidopsis transcriptional regulatory map reveals distinct functional and evolutionary features of novel transcription factors. Mol. Biol. Evol. **32**: 1767–1773.

Jones, A.M. et al. (2014). Border control--a membrane-linked interactome of Arabidopsis. Science (80-.). **344**: 711–716.

Liu, S., Kracher, B., Ziegler, J., Birkenbihl, R.P., and Somssich, I.E. (2015). Negative regulation of ABA Signaling By WRKY33 is critical for Arabidopsis immunity towards Botrytis cinerea 2100. Elife **4**: 1–27.

Mukhtar, M.S. et al. (2011). Independently evolved virulence effectors converge onto hubs in a plant immune system network. Science (80-.). **333**: 596–601.

Palaniswamy, S.K., James, S., Sun, H., Lamb, R.S., Davuluri, R. V., and Grotewold, E. (2006). AGRIS and AtRegNet. A Platform to Link cis-Regulatory Elements and Transcription Factors into Regulatory Networks. Plant Physiol. **140**: 818–829.

Srivastava, G.P., Li, P., Liu, J., and Xu, D. (2010). Identification of transcription factor's targets using tissue-specific transcriptomic data in Arabidopsis thaliana. BMC Syst. Biol. **4 Suppl 2**: S2.

Szklarczyk, D. et al. (2015). STRING v10: Protein-protein interaction networks, integrated over the tree of life. Nucleic Acids Res. **43**: D447–D452.

Yi, X., Zhang, Z., Ling, Y., Xu, W., and Su, Z. (2014). PNRD: a plant non-coding RNA database. Nucleic Acids Res.: 1–8.

Zhang, Z., Yu, J., Li, D., Zhang, Z., Liu, F., Zhou, X., Wang, T., Ling, Y., and Su, Z. (2010). PMRD: plant microRNA database. Nucleic Acids Res. **38**: 806–813.