

Structural proteomics applied to plant membrane protein complexes

Original

Structural proteomics applied to plant membrane protein complexes / Albanese, P., Tamara, S., Scheltema, R.A., Pagliano, C.. - In: TRENDS IN PLANT SCIENCE. - ISSN 1360-1385. - ELETTRONICO. - 25:9(2020), pp. 945-946. [10.1016/j.tplants.2020.04.002]

Availability:

This version is available at: 11583/2842960 since: 2020-08-25T13:23:33Z

Publisher:

Elsevier Ltd

Published

DOI:10.1016/j.tplants.2020.04.002

Terms of use:

This article is made available under terms and conditions as specified in the corresponding bibliographic description in the repository

Publisher copyright

Elsevier postprint/Author's Accepted Manuscript

© 2020. This manuscript version is made available under the CC-BY-NC-ND 4.0 license
<http://creativecommons.org/licenses/by-nc-nd/4.0/>. The final authenticated version is available online at:
<http://dx.doi.org/10.1016/j.tplants.2020.04.002>

(Article begins on next page)

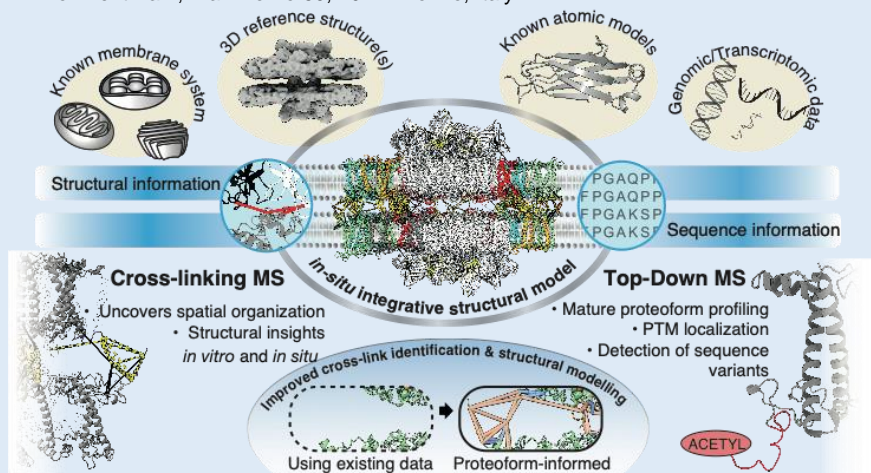
Structural proteomics applied to plant membrane protein complexes

Pascal Albanese^{1,2,*}, Sem Tamara^{1,2}, Richard A. Scheltema^{1,2}, Cristina Pagliano^{3,*}

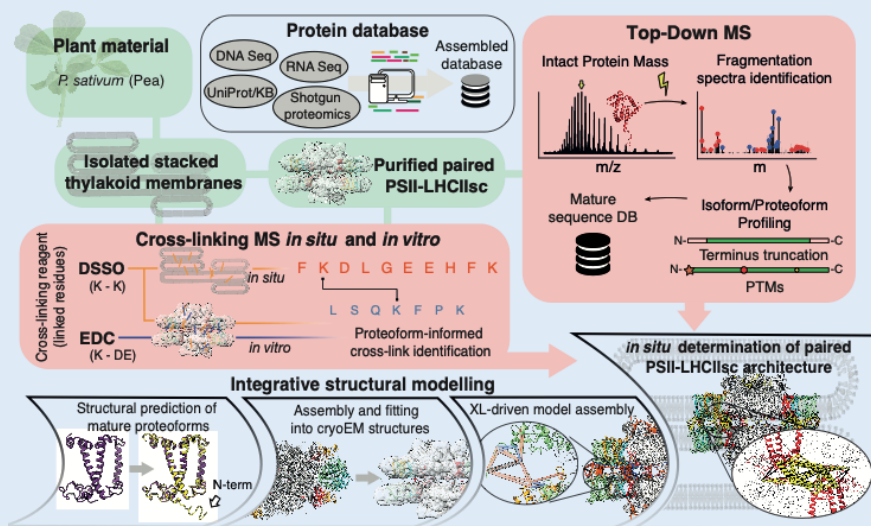
¹Biomolecular Mass Spectrometry and Proteomics, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, University of Utrecht, Padualaan 8, 3584 CH, Utrecht, The Netherlands

²Netherlands Proteomics Centre, Padualaan 8, 3584 CH, Utrecht, The Netherlands

³Applied Science and Technology Department–BioSolar Lab, Politecnico di Torino, Environment Park, Via Livorno 60, 10144 Torino, Italy



Membrane protein complexes are fundamental in many biological processes. Nevertheless, their structural details are difficult to resolve, especially in their cellular milieu. The combination of top-down (TD) mass spectrometry (MS), profiling post translational modifications (PTMs) and sequence variants, and cross-linking (XL) MS, for uncovering the spatial organization and interactors of protein complexes, provides a novel approach to study the structural behavior of protein complexes in their close-to-native environment.



In plants, grana-stack formation is still debated. By using TD-MS and XL-MS, *in vitro* on purified paired PSII-LHCII supercomplexes (PSII-LHCIIsc) and *in situ* on their sourcing isolated stacked thylakoid membranes, we uncovered the spatial organization of paired PSII-LHCIIsc, revealing their role in grana stacking. Samples were isolated from pea, a plant for which transcriptomic data and a cryo-electron microscopy (cryo-EM) 3D structure of paired PSII-LHCIIsc are available.

Advantages:

Analysis suitable for large membrane protein complexes, either detergent-solubilized (*in vitro*) or embedded in the native membrane (*in situ*), provided the availability of genetic and 3D structural information.

3D structures of large membrane protein complexes at intermediate resolution, achievable by cryo-EM, are sufficient to reveal the overall organization.

TD-MS uncovers mature proteoforms, namely different forms of a protein arising from a given gene with a variety of sequence variants and PTMs. As such, it complements the public sequence databases by providing an exhaustive list of mature proteoforms.

XL-MS, informed by the TD-MS results, uncovers protein interactions and complements cryo-EM results providing protein localization within the 3D structure.

Integration of multiple tiers of structural information completes the picture of the overall membrane protein complex organization.

Challenges:

Initial availability of plant genetic information, at genomic or transcriptomic level, is required.

Protocols for sample isolation in close-to-native state need to be optimized for membrane protein complexes and native sourcing membranes.

It is difficult to confidently identify high-molecular weight (≥ 100 kDa) proteoforms by TD-MS.

Efficient cross-linking reagents for *in situ* XL-MS specifically target lysine amino acid residues, which have to be abundant and accessible in the target protein complex.

*Correspondence: p.albanese@uu.nl (Pascal Albanese) cristina.pagliano@polito.it (Cristina Pagliano)

Acknowledgments

CP would like to thank John F. Allen (University College London, UK) for stimulating discussions about the plant *grana* stacking “enigma”.

Literature

1. Albanese, P. et al. (2020) How paired PSII–LHCII supercomplexes mediate the stacking of plant thylakoid membranes unveiled by structural mass-spectrometry. *Nat. Commun.* 11, 1361
2. Albanese, P. et al. (2017) Pea PSII–LHCII supercomplexes form pairs by making connections across the stromal gap. *Sci. Rep.* 7, 10067
3. Allen, J.P. (2019) Recent innovations in membrane-protein structural biology. *F1000Research* 8, 211
3. Daum, B. et al. (2010) Arrangement of Photosystem II and ATP Synthase in Chloroplast Membranes of Spinach and Pea. *Plant Cell* 22, 1299–1312
4. Su, X. et al. (2017) Structure and assembly mechanism of plant C2S2M2-type PSII–LHCII supercomplex. *Science* 357, 815–820
5. Albanese, P. et al. (2018) Thylakoid proteome modulation in pea plants grown at different irradiances: quantitative proteomic profiling in a non-model organism aided by transcriptomic data integration. *Plant J.* 96, 786–800
6. Klykov, O. et al. (2018) Efficient and robust proteome-wide approaches for cross-linking mass spectrometry. *Nat. Protoc.* 13, 2964–2990
7. Steigenberger, B.A. et al. (2019) (2019) PhoX: an IMAC-enrichable Crosslinking Reagent. *ACS Cent. Sci.* 5, 1514–1522
8. van de Waterbeemd, M. et al. (2018) Dissecting ribosomal particles throughout the kingdoms of life using advanced hybrid mass spectrometry methods. *Nat. Commun.* 9, 2493
9. Steigenberger, B. et al. (2020) To Cleave or Not To Cleave in XL-MS? *J. Am. Soc. Mass Spectrom.* 31, 196–206