

232. Mining post translational modifications in Arabidopsis using the ModHunter

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Project Goals: To leverage the array of proteomics data in the reference plant Arabidopsis to identify likely regions within proteins that contain post-translational modifications.

The past decade has seen the development of a plethora of online proteomics resources in Arabidopsis reflecting multiple large-scale studies. These resources exist independently and lack a level of integration. The Multinational Arabidopsis Steering Committee, Proteomics (MASCP) has addressed this issue through the development of a proteomics aggregation portal, MASCP Gator (<http://gator.masc-proteomics.org/>). The portal provides a summary of proteomics and protein information aggregated directly from ten online resources. The development of this portal has enabled us to develop a bioinformatics technique to identify likely regions of post-translational modifications in proteins of Arabidopsis. The ability to locate and identify post translational modifications experimentally by mass spectrometry is extremely challenging and there is a requirement for complementary techniques. Virtually all large-scale proteomics analyses in Arabidopsis have identified proteins with unmodified peptides. Collectively, these data reveal modified regions of a protein as unmatched areas within a protein model. Using a recent large-scale *N*-linked glycosylation survey as a test set, we could demonstrate that unmatched regions represent modification hotspots in proteins. These sites can be further targeted for investigation and characterization. We have now developed a method to locate putative regions with modifications by exploiting mass spectral data in the public domain and are attempting to develop this into a functional portal for the assessment modifications in proteomic datasets (<http://modhunter.masc-proteomics.org/>).

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