

# Cell Wall Polysaccharide Synthases are Located in Detergent-Resistant Membrane Microdomains in Oomycetes

by

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**Running title: Lipid rafts and glycan synthases in *Saprolegnia***

**Table S1.** Identification of some of the major proteins present in the DRM fraction from *S. monoica* by mass spectrometry and peptide fingerprint after trypsin digestion.

Spot number <sup>a</sup>	Accession number <sup>b</sup>	Protein identity <sup>c</sup>	Theoretical MW/pI	Sequence coverage <sup>d</sup> (%)
1	Pr 72463	Hsp70	71900/5.15	<b>24</b>
	Ps 108711		71386/5.27	<b>24</b>
2	Pr 49002	V-type ATPase, subunit A	62174/5.59	<b>28</b>
	Ps 108996		68454/5.49	<b>27</b>
3	Pr 49002	V-type ATPase, subunit A	62174/5.59	<b>27</b>
	Ps 108996		68454/5.49	<b>28</b>
4	Pr 49002	V-type ATPase, subunit A	62174/5.59	<b>31</b>
	Ps 108996		68454/5.49	<b>33</b>
5	Pr 41867	V-type ATPase, subunit B	54006/5.47	<b>34</b>
	Ps 108790		55270/5.35	<b>36</b>
6	Pr 41867	V-type ATPase, subunit B	54006/5.47	<b>26</b>
	Ps 108790		55270/5.35	<b>26</b>
7	Pr 41867	V-type ATPase, subunit B	54006/5.47	<b>28</b>
	Ps 108790		55270/5.35	<b>28</b>
8	Pr 41867	V-type ATPase, subunit B	54006/5.47	<b>32</b>
	Ps 108790		55270/5.35	<b>33</b>
9	CAA42559	Actin ( <i>Achlya bisexualis</i> )	41851/5.30	<b>38</b>
10	DQ323662	Annexin ( <i>S. monoica</i> )	36055/5.41	<b>39</b>
11	DQ323662	Annexin ( <i>S. monoica</i> )	36055/5.41	<b>42</b>
12	DQ323662	Annexin ( <i>S. monoica</i> )	36055/5.41	<b>38</b>

<sup>a</sup>The spot numbers given in this column correspond to those in Fig. S1.

<sup>b</sup>Pr and Ps, accession numbers in the genome databases of *Phytophthora ramorum* and *Phytophthora sojae* (<http://genome.jgi-psf.org/>); other accession numbers are from the EMBL database and the corresponding detailed information can be retrieved from <http://www.expasy.org>.

<sup>c</sup>Proteins exhibiting significantly high scores using the Mascot algorithm (55; <http://www.matrixscience.com/>).

<sup>d</sup>Fraction of the protein sequence covered by the identified peptides.

FIG. S1. 2D-PAGE analysis of the proteins present in the purified DRMs.

A. Protein profile obtained after silver staining of a 2D gel in which 100  $\mu\text{g}$  protein was loaded (theoretical amount). In this typical example, the isoelectric focusing was performed using a non-linear pH gradient in the range 3-10. The numbers indicate the spots that could be identified by mass spectrometry as detailed in Table S1.

B. As in A, but in the case of a gel containing 250  $\mu\text{g}$  protein.

