



## Vesicular fractions of sunflower apoplastic fluids are associated with potential exosome marker proteins

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### ABSTRACT

**Based on the presence of phospholipids in the extracellular fluids (EFs) of sunflower seeds, we have hypothesized on the existence of vesicles in the apoplastic compartment of plants. Ultracentrifugation of sunflower EF allowed the isolation of particles of 50–200 nm with apparent membrane organization. A small GTPase Rab was putatively identified in this vesicular fraction. Since Rab proteins are involved in vesicular traffic and their presence in exosomes from animal fluids has been demonstrated, evidence presented here supports the existence of exosome-like vesicles in apoplastic fluids of sunflower. Their putative contribution to intercellular communication in plants is discussed.**  
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### 1. Introduction

Mammalian cells release membrane vesicles into the extracellular environment. Among them, the best known are exosomes, which are derived from multivesicular bodies (MVB) and can fuse the plasma membrane resulting in the secretion of their luminal vesicles of 40–100 nm [1]. Although the physiological role of exosomes in vivo is still a matter of study, it is apparent that they function in a multitude of processes, including cell–cell communication and tissue developmental processes [2–4]. Particularly, a relevant role of exosomes in intercellular communication is being recognized [5,6]. These secreted membranes have been characterized for their protein composition revealing several transmembrane or peripheral proteins with affinity for ligands on other cell membranes that may direct exosomes to their target cells [7]. In

addition, some cytoskeleton related proteins and proteins involved in membrane traffic and fusion have been found [5,8].

With the discovery of exosome-like vesicles in *Drosophila*, it has become clear that they have conserved functions in evolution [9,10]. Moreover, spherical vesicles of unknown function are also released from the outer membrane by certain bacteria [11]. On the other hand, plant exosomes have not been described yet. However, it has recently been shown that MVBs participate in a cell wall-associated defense response in barley leaves attacked by the fungus *Blumeria graminis* f. sp. *hordei* [12]. These MVBs would be able to fuse to the plasma membrane to release their internal content into the paramural space. This evidence has led to speculate on the existence of exosomes in plants [13], although no demonstration of their presence was reported.

We have recently shown the existence of phospholipids in extracellular fluids (EF) of imbibed sunflower (*Helianthus annuus*) seeds [14]. Lipid profiling using electrospray ionization tandem mass spectrometry (ESI-MS/MS) revealed a particular phospholipid composition, with phosphatidic acid and phosphatidylinositol as major components. Besides, phosphatidylinositol phosphate was also found in the extracellular milieu of tomato cell suspensions by using a labelling strategy [15]. To our knowledge, these were the first reports on the presence of phospholipids as extracellular components of plants and their origin and significance in an aqueous medium constitutes a relevant issue for plant sciences. The

**Abbreviations:** EF, extracellular fluid; ESI-MS/MS, electrospray ionization tandem mass spectrometry; FSGTP1, small GTPase from *Fagus sylvatica*; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; MALDI-TOF, matrix-assisted laser desorption/ionization – time of flight; MVB, multivesicular bodies; MW, molecular weight; SE, seed extract; TEM, transmission electron microscopy

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occurrence of several phospholipid types in the EF of sunflower seeds may be indicative of the existence of bilayers or micelles, that in an aqueous compartment such as the apoplast, could be organized in vesicular structures, as it is the case in animal fluids. However, to our knowledge this possibility has not been explored in plants. The purpose of this work was to analyze the existence of exosome-like vesicles in sunflower fluids. To that aim, we have applied a biochemical approach already established for exosomes of animal origin, which allowed the isolation of vesicles in EFs of seeds.

## 2. Materials and methods

### 2.1. Plant material and collection of extracellular fluid

Intact sunflower seeds (*H. annuus* L., line 10347 Advanta Semillas) were subjected to imbibition during 2 h in water and then carefully peeled to remove the pericarp previous to the extraction of the EF. The EF was collected by a standard technique based in a vacuum infiltration-centrifugation procedure. Briefly, seeds were immersed in 50 mM Tris-HCl pH 7.5, 0.6% NaCl, 0.1% 2-mercaptoethanol (infiltration buffer) and subjected to three vacuum pulses of 10 s, separated by 30 s intervals. The infiltrated seeds were recovered, dried on filter paper, placed in fritted glass filters and centrifuged for 20 min at 400×g at 4 °C. The EF was recovered in the filtrate and evaluated for the absence of intracellular contamination as previously described [14].

A seed extract (SE) was obtained by pulverization of decoated seeds previously imbibed in water for 2 h. The resultant powder was immersed in 5 vol. of infiltration buffer and clarified by centrifugation at 10 000×g for 15 min.

### 2.2. Preparation of vesicles

The EF from 20 g of seeds was filtrated through a 0.5 µm membrane and subjected to fractionation by successive centrifugation steps at 10 000×g for 30 min, 40 000×g for 60 min and 100 000×g for 60 min according to a procedure described previously for animal exosomes [16]. The first pellet was discarded while the 40 000×g and 100 000×g pellet fractions were suspended in 30 µl of 20 mM Tris-HCl pH 7.5, being the fractions potentially enriched in vesicular material. As a control, the SE obtained from 1 g of seeds was also filtrated and subjected to fractionation by successive centrifugation as described for EF.

### 2.3. Transmission electron microscopy (TEM)

The pellets obtained by successive centrifugation steps (40 000×g and 100 000×g) were subjected to phosphotungstic acid negative staining on Formvar carbon-coated electron microscopy grids [17]. Twenty microliters of each sample were applied to the

grid and after 5 min excess solution was wicked off the grid with filter paper. An equal part of 2% phosphotungstic acid was added to the grid and after 2 min the grids were placed in a Petri dish containing filter paper for 15 min. The preparations obtained were examined at 90 kV with a JOEL 1200 EXII electron microscope (INTA Castelar, Argentina).

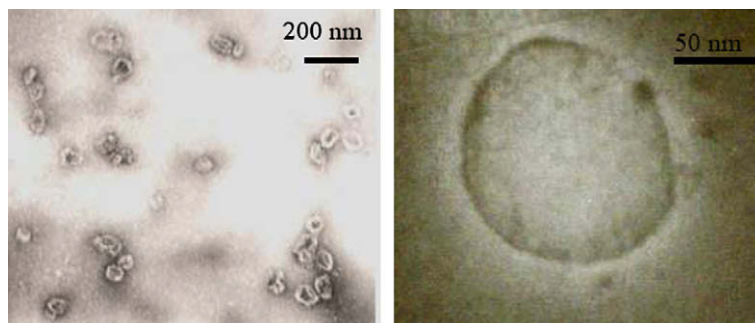
### 2.4. Protein and lipid analysis

The 40 000×g and 100 000×g pellet fractions of EF obtained from 20 g of seeds or SE obtained from 20 mg of seeds were suspended in 20 microliters of standard sample buffer [18]. Electrophoretic separation was performed in 12% SDS-PAGE gels [18]. Gels were then stained with Sypro reagent and bands were automatically excised from the gel (Investigator ProPic robotic workstation, Genomic Solutions). The gel pieces were digested with trypsin and MS analyses of peptides were performed in a 4700 Proteomics Station (Applied Biosystems, USA) as previously described [19]. Protein identification was assigned by comparing the obtained peptide mass fingerprinting with the non-redundant plant database, using Mascot 1.9 search engine (Matrixscience, UK). Immunodetection of GAPDH was assayed by Western blot according to standard procedures [14].

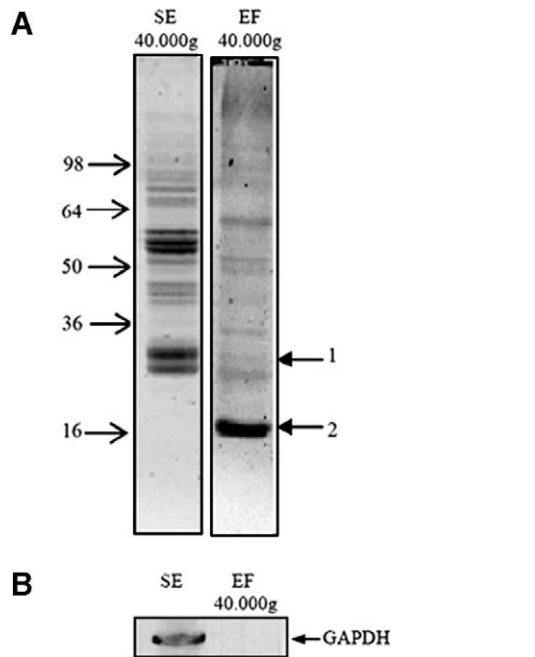
Lipid extraction and phospholipid measurement were performed as previously described [14]. Briefly, the vesicular fraction was subjected to lipid extraction with 4.5 vol. of chloroform:methanol:HCl (200:100:1, v/v/v) and 1 vol. of 0.9% (w/v) NaCl. The organic phase was obtained by centrifugation, washed with 4.5 vol. of chloroform:methanol:1 M HCl, 3:45:47, v/v/v and finally evaporated under nitrogen stream. The lipid pellets obtained were analyzed by ESI-MS/MS at the Facility of the Kansas Lipidomics Research Center (Kansas State University, USA).

## 3. Results

Taking into account our previous results demonstrating the existence of phospholipids in the apoplast of *H. annuus* seeds, we decided to explore whether vesicular structures were present in EFs. To that aim, seeds were imbibed for 2 h and the EF, containing the apoplastic fraction of the seeds, was isolated by infiltration-centrifugation. This fraction was tested for the absence of significant intracellular components as previously described [14] and showed the absence of detectable levels of actin, oleosin and Glu-6-P dehydrogenase. The EF was then fractionated by sequential centrifugation at 10 000×g, 40 000×g and 100 000×g. The first pellet was discarded and the 40 000×g and 100 000×g pellets, expected to be enriched in exosome-like vesicles [16], were further analyzed. Electron transmission microscopy (TEM) showed the presence of vesicular bodies of 50–200 nm in diameter in both fractions, although a higher density of vesicles was apparent in



**Fig. 1.** Presence of vesicles in the extracellular fluids (EFs) of sunflower seeds. TEM images obtained by negative staining with phosphotungstic acid of the EF 40 000×g vesicle fraction. Left panel: whole mount. Right panel: detailed visualization of a vesicle. Bars indicate the scale in nm.



**Fig. 2.** SDS-PAGE analysis of EF vesicles. (A) Protein profile of SE 40 000×g and EF 40 000×g fractions. Twenty-five micrograms of protein was subjected to SDS-PAGE and Sypro stained. The arrows on the right panel indicate the EF 40 000×g protein bands identified by MALDI-TOF peptide mass fingerprinting. The migration of molecular weight markers is indicated on the left. (B) SE proteins obtained of 4 mg of seeds (positive control) or EF 40 000×g proteins obtained from 400 mg of seeds were immunodetected with 1:25 000 anti-GAPDH antiserum.

the 40 000×g pellet (Fig. 1). TEM images also revealed the presence of a phospholipid layer, visualized by negative staining with phosphotungstic acid [17] (Fig. 1, right panel). In addition, the content of phospholipids in the vesicular fraction was assessed by ESI-MS/MS analysis and resulted in 3.2 pmol/g seed. These vesicles do not stem from cell damage and membrane release, since the protein profile observed in the 40 000×g pellet isolated from the EF is completely different from that obtained in the microsomal pellet resulting from centrifuging total SEs (Fig. 2A). Moreover, the cytosolic marker glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is not detected in the vesicular fraction (Fig. 2B).

SDS-PAGE revealed similar protein patterns in the 40 000×g and 100 000×g pellet obtained from the EF. Hence, further studies were only performed on the 40 000×g pellet fraction (Fig. 2A). In an effort to identify proteins present in this fraction, bands were submitted to trypsin digestion followed by matrix-assisted laser desorption/ionization – time of flight (MALDI-TOF) and identity assignment by peptide mass fingerprinting. These analyses provided limited information as most bands gave low scores on database searching, thus avoiding their putative identification. It must be taken into account the scarce number of sequences from *Helianthus* and other Compositae available in databases. However, two bands showed a good agreement between the expected and observed molecular weight (MW) and resulted above the cut off Mascot score of 63. Table 1 summarizes the data obtained. Band 2 (Fig. 2) matched agglutinin I, a lectin from *Helianthus tuberosus*

**Table 1**  
Proteins identified in the 40 000×g vesicle fraction by peptide mass fingerprinting.

Band No.	Matched protein	Origin	UniProt accession	Experimental MW (theoretical) in kDa	Matching peptides	Sequence coverage (%)	Mascot score
1	FSGTP1	<i>Fagus sylvatica</i>	Q39755_FAGSY	22.4 (24.1)	8	44	63
2	Agglutinin I	<i>Helianthus tuberosus</i>	Q9FS32_HELTU	17.9 (15.5)	3	35	189

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MARRADEEYDYLFKVVLIGDSGVGKSNLLSRFTRNEFCLESKSTIGVEFA
TRLQVEGRIVKAQIWDTAGQERYRAITSAYYRGAVGAALLVYDVTKPTTF
EQVWLKELRDHADSNIIVIMLIGNKTDLKHSAVRTEDAQQGFMLRKKALSF
IETSALKATNVEKAFQTILCLRFTGIISKKSLSSDEPAPSVIKEAVKHIV
VGGSEANTKKPCCSN
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**Fig. 3.** A putative sunflower Rab11A protein in the EF vesicular fraction. Amino acid sequence of FSGTP1, a Rab11A GTPase from *F. sylvatica*, and matching peptides from sunflower band 1. Peptides detected upon MALDI-TOF/MS analysis from sunflower EF vesicles are presented in gray boxes.

belonging to the jacalin-related protein family [20]. In addition, a 24 kDa protein (band 1 in Fig. 2) was putatively identified as similar to FSGTP1, a small GTPase from *Fagus sylvatica* whose gene product accumulates in dormant seeds [21]. In fact, FSGTP1 displays 68% identity with human Rab11A and is 81% identical to *Arabidopsis thaliana* Rab GTPase 11C. As shown in Fig. 3, a high sequence coverage was observed between FSGTP1 and the sunflower protein detected in the vesicular fraction of EFs, including the N-terminal residues perfectly conserved in the Rab family.

#### 4. Discussion

Exosomes are routinely isolated from mammalian fluids by ultracentrifugation. Hence, we have applied this technique in order to verify if similar structures could be present in sunflower apoplastic fluids. TEM has shown the presence of 50–200 nm vesicle-like particles with apparent phospholipid membrane in the EFs. Several controls allowed to discard that these vesicles could result from contamination with cellular debris. A striking observation is the presence of a protein similar to Rab11 GTPases in the vesicular extracellular fraction. Rab-related proteins have been implicated in regulating the formation of vesicles at the donor membrane, the movement, tethering and docking of vesicles, as well as their fusion with the acceptor membrane, not only in animal systems but also in plants [22–24]. Rab11 GTPases are key regulators of vesicular trafficking events in the eukaryotic cell and play a central role in exosomes [25]. In fact, Rab proteins have already been detected in exosomes derived from several cell types [8,5]. Concerning Rab11 GTPases in plants, several lines of evidence indicate that they are involved in secretion and recycling of cell wall components [23]. In tomato, for instance, the inhibition of Rab11 results in complex developmental abnormalities and delayed ripening, attributed to impaired cell wall deposition [26]. On the other hand, the role of Rab11 GTPases during germination has not been studied yet.

A lectin was also found in the vesicular fraction of sunflower apoplast. It is intriguing that lectins such as galectin-3 have already been described in exosomes from animal origin [8]. Galectins are glycan-binding proteins that appear to be a novel class of adhesion-modulating proteins, clearly involved in cancer, inflammation, and autoimmunity [27,28]. It is tempting to speculate that lectins can help driving exosomes to their targets.

Among its multiple functions, the apoplast of plants (including cell walls, intercellular spaces and conducting cells of the xylem) is a dynamic compartment involved in plant signalling and communication. We have already reported that seeds treated with the

plant hormones abscisic acid and jasmonic acid modulate the levels of apoplastic phospholipids [14]. In fact, phospholipids involved in signalling events such as phosphatidic acid and phosphatidylinositol phosphate are accumulated in the EF upon hormonal treatments. This observation has prompted us to suggest that these phospholipids may be contributing to the intercellular communication [14]. We now present evidence that at least part of the phospholipids present in sunflower fluids are organized in vesicular structures. Taking into account that animal exosomes are considered “bioactive vesicles” that function to promote intercellular communication [1] and act as signalling device [29], the occurrence of similar structures in the plant apoplast point out for a new concept related to intercellular signalling. In this sense, the presence of a cell wall in plant cells may be considered an impediment for the production and perception of vesicles. However, since vesicular transport across cell wall has already been demonstrated in fungi [30], an analog mechanism could be operating in plants. Alternatively, vesicles could reside near to the plasma membrane without moving through the cell wall. In conclusion, our description of exosome-like vesicles in sunflower fluids highlights a still unexplored aspect of intercellular communication: the vesicle-based information transfer in plants.

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### References

- [1] Schorey, J.S. and Bhatnagar, S. (2008) Exosome function: from tumor immunology to pathogen biology. *Traffic* 9, 871–881.
- [2] Denzer, K., Kleijmeer, M.J., Heijnen, H.F., Stoorvogel, W. and Geuze, H.J. (2000) Exosome: from internal vesicle of the multivesicular body to intercellular signaling device. *J. Cell Sci.* 113, 3365–3374.
- [3] Stoorvogel, W., Kleijmeer, M.J., Geuze, H.J. and Raposo, G. (2002) The biogenesis and functions of exosomes. *Traffic* 3, 321–330.
- [4] Lakkaraju, A. and Rodriguez-Boulan, E. (2008) Itinerant exosomes: emerging roles in cell and tissue polarity. *Trends Cell Biol.* 18, 199–209.
- [5] Simons, M. and Raposo, G. (2009) Exosomes: vesicular carriers for intercellular communication. *Curr. Opin. Cell Biol.* 21, 575–581.
- [6] Pap, E., Pallinger, E., Pásztói, M. and Falus, A. (2009) Highlights of a new type of intercellular communication: microvesicle-based information transfer. *Inflamm. Res.* 58, 1–8.
- [7] Olver, C. and Vidal, M. (2007) Proteomic analysis of secreted exosomes. *Subcell. Biochem.* 43, 99–131.
- [8] Théry, C., Boussac, M., Véron, P., Ricciardi-Castagnoli, P., Raposo, G., Garin, J. and Amigorena, S. (2001) Proteomic analysis of dendritic cell-derived exosomes: a secreted subcellular compartment distinct from apoptotic vesicles. *J. Immunol.* 166, 7309–7318.
- [9] Greco, V., Hannus, M. and Eaton, S. (2001) Argosomes: a potential vehicle for the spread of morphogens through epithelia. *Cell* 106, 633–645.
- [10] Entchev, E.V. and González-Gaitán, M.A. (2002) Morphogen gradient formation and vesicular trafficking. *Traffic* 3, 98–109.
- [11] Nevot, M., Deroncelle, V., Messner, P., Guinea, J. and Mercade, E. (2006) Characterization of outer membrane vesicles released by the psychrotolerant bacterium *Pseudoalteromonas antarctica* NF3. *Environ. Microbiol.* 8, 1523–1533.
- [12] An, Q., Ehlers, K., Kogel, K.H., van Bel, A.J.E. and Hüchelhoven, R. (2006) Multivesicular compartments proliferate in susceptible and resistant MLA12-barley leaves in response to infection by the biotrophic powdery mildew fungus. *New Phytol.* 172, 563–576.
- [13] An, Q., van Bel, A.J.E. and Hüchelhoven, R. (2007) Do plant cells secrete exosomes derived from multivesicular bodies? *Plant Signal. Behav.* 2, 4–7.
- [14] Regente, M., Corti Monzón, G. and de la Canal, L. (2008) Phospholipids are present in extracellular fluids of imbibing sunflower seeds and are modulated by hormonal treatments. *J. Exp. Bot.* 59, 553–562.
- [15] Gonorazky, G., Laxalt, A.M., Testerink, C., Munnik, T. and de la Canal, L. (2008) Phosphatidylinositol-4-phosphate accumulates extracellularly upon xylanase treatment in tomato cell suspensions. *Plant Cell Environ.* 31, 1051–1062.
- [16] Mears, R., Craven, R.A., Hanrahan, S., Totty, N., Upton, C., Young, S.L., Patel, P., Selby, P. and Banks, R.E. (2004) Proteomic analysis of melanoma-derived exosomes by two-dimensional polyacrylamide gel electrophoresis and mass spectrometry. *Proteomics* 4, 4019–4031.
- [17] Dubertret, B., Skourides, P., Norris, D.J., Noireaux, V., Brivanlou, A.H. and Libchaber, A. (2002) In vivo imaging of quantum dots encapsulated in phospholipid micelles. *Science* 298, 1759–1762.
- [18] Laemmli, U.K. (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* 227, 680–685.
- [19] Pérez-Reinado, E., Ramírez-Boo, M., Garrido, J.J., Jorrín, J.V. and Moreno, A. (2007) Towards a global analysis of porcine alveolar macrophages proteins through two-dimensional electrophoresis and mass spectrometry. *Dev. Comp. Immunol.* 31, 1220–1232.
- [20] Nakagawa, R., Yasokawa, D., Okumura, Y. and Nagashima, K. (2000) Cloning and sequence analysis of cDNA coding for a lectin from *Helianthus tuberosus* callus and its jasmonate-induced expression. *Biosci. Biotechnol. Biochem.* 64, 1247–1254.
- [21] Nicolas, C., Nicolas, G. and Rodriguez, D. (1998) Transcripts of a gene, encoding a small GTP-binding protein from *Fagus sylvatica*, are induced by ABA and accumulated in the embryonic axis of dormant seeds. *Plant Mol. Biol.* 36, 487–491.
- [22] Molendijk, A.J., Ruperti, B. and Palme, K. (2004) Small GTPases in vesicle trafficking. *Curr. Opin. Plant Biol.* 7, 694–700.
- [23] Nielsen, E., Cheung, A.Y. and Ueda, T. (2008) The regulatory RAB and ARF GTPases for vesicular trafficking. *Plant Physiol.* 147, 1516–1526.
- [24] Woollard, A.A.D. and Moore, I. (2008) The functions of Rab GTPases in plant membrane traffic. *Curr. Opin. Plant Biol.* 11, 610–619.
- [25] Savina, A., Vidal, M. and Colombo, M.I. (2002) The exosome pathway in K562 cells is regulated by Rab11. *J. Cell Sci.* 115, 2505–2515.
- [26] Lu, C., Zainal, Z., Tucker, G.A. and Lycett, G.W. (2001) Developmental abnormalities and reduced fruit softening in tomato plants expressing an antisense Rab11 GTPase gene. *Plant Cell* 13, 1819–1833.
- [27] Elola, M.T., Wolfenstein-Todel, C., Troncoso, M.F., Vasta, G.R. and Rabinovich, G.A. (2007) Galectins: matricellular glycan-binding proteins linking cell adhesion, migration, and survival. *Cell Mol. Life Sci.* 64, 1679–1700.
- [28] Rabinovich, G.A., Liu, F.T., Hirashima, M. and Anderson, A. (2007) An emerging role for galectins in tuning the immune response: lessons from experimental models of inflammatory disease, autoimmunity and cancer. *Scand. J. Immunol.* 66, 143–158.
- [29] Denzer, K., Kleijmeer, M.J., Heijnen, H.F., Stoorvogel, W. and Geuze, H.J. (2000) Exosome: from internal vesicle of the multivesicular body to intercellular signaling device. *J. Cell Sci.* 113, 3365–3374.
- [30] Casadevall, A., Nosanchuk, J.D., Williamson, P. and Rodrigues, M.L. (2009) Vesicular transport across the fungal cell wall. *Trends Microbiol.* 17, 158–162.