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Di Sansebastiano, GP, Barozzi, F, Piro, G et al. (2 more authors) (2018) Trafficking routes to the plant vacuole: connecting alternative and classical pathways. Journal of Experimental Botany, 69 (1). pp. 79-90. ISSN 0022-0957

https://doi.org/10.1093/jxb/erx376

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Trafficking routes to the Plant Vacuole: 1 connecting alternative and classical pathways. 2 3 Gian Pietro Di Sansebastiano^{1*}, Fabrizio Barozzi¹, Gabriella Piro¹, Jurgen Denecke² and 4 Carine de Marcos Lousa^{2,3} * 5 6 1. DiSTeBA (Dipartimento di Scienze e Tecnologie Biologiche ed Ambientali), 7 ECOTEKNE, University of Salento, Campus 73100 Lecce, Italy; fabrizio.barozzi@unisalento.it and gabriella.piro@unisalento.it. 8 9 2. Centre Sciences, for Plant Leeds University, Leeds, LS29JT, UK; 10 j.denecke@leeds.ac.uk. 3. Leeds Beckett University, School of Applied and Clinical Sciences, Leeds, LS13HE, 11 12 UK 13 * corresp. authors: Gian Pietro di Sansebastiano gp.disansebastiano@unisalento.it, (+39 0832 14 29 8713) and Carine de Marcos Lousa c.de-marcos-lousa@leedsbeckett.ac.uk (+44 1138125639) 15 16 running title: Alternative pathways to the vacuole. 17 Highlights: Recent discoveries have found uncharacterised trafficking pathways to the plant 18 vacuole. Soon, these alternative routes might become classical routes. This review aims at 19 summarising our general understanding in this field. 20 21 Abstract 22 23 Due to the numerous roles plant vacuoles play in cell homeostasis, detoxification and protein 24 storage, the trafficking pathways to this organelle have been extensively studied. Recent 25 evidence however suggests that our vision of transport to the vacuole is not as simple as 26 previously imagined. Alternative routes have been identified and are being characterised. 27 Intricate interconnections between routes seem to occur in various cases, complicating the 28 interpretation of data. In this review, we aim to summarise the published evidence and linking

29 the emerging data with previous findings. We give the current state of information on 30 alternative and classical trafficking routes to the Plant vacuole.

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Key words: Alternative routes, Membrane protein, Multivesicular bodies, Protein sorting,
 Trafficking pathways, Vacuole, VSR,

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Abbreviations: VSR (Vacuolar Sorting Receptor), MVB (MultiVesicular Bodies), PVC
(PreVacuolar Compartment), LPVC (Late PreVacuolar Compartment), ER (endoplasmic
reticulum), AP (Adaptor Complex), PSV (Protein Storage Vacuole), DVs (Dense Vesicles),
PAC (Precursor Accumulating Vesicles), PB (Protein Bodies).

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40 Introduction:

Describing vacuolar sorting mechanisms is a difficult task especially because vacuolar organization is far from well understood. The topic is often associated with the trafficking of vacuolar sorting receptors but some vacuolar proteins, in particular membrane proteins, escape this association. This review summarizes recent advances in vacuolar sorting characterization, highlighting the knowledge gaps.

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47 1. CLASSICAL ROUTE TO THE VACUOLE: VSR as a model

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49 <u>1a. Vacuolar sorting receptors.</u>

50 Transport of soluble vacuolar cargo to the vacuole is commonly described using the 51 conventional pathway involving Vacuolar Sorting Receptor (VSR) (De Marcos Lousa et al., 52 2012). Plant VSRs are type I transmembrane proteins which appear to have evolved 53 independently from the widespread sortilin/vps10 class of receptors and the mammalian 54 mannose 6 phosphate receptor family (de Marcos Lousa and Denecke, 2016). VSRs are 55 typically found in plants including green algae as well as the supergroup of Stramenopiles, 56 Alveolates and Rhizaria (SAR). Similar to the other two classes, VSRs bind and release cargo 57 with their large luminal domains whilst their cytosolic C-terminus controls the trafficking of 58 the receptor to and from prevacuoles.

Although the C-terminal part of VSRs has been well studied and motifs important for trafficking of the receptor have been identified (see below), the characteristics of N-terminal luminal domain of VSRs are still unclear. The interaction between vacuolar cargo and the receptor is affected by calcium concentrations, oxidising conditions and pH *in vitro*. Experimental evidence to support their relevance *in vivo* however remains to be established. The luminal domain of VSRs has been shown to bind to a specific NPIR motif found in the N- 65 terminus of many soluble vacuolar cargo. In addition to this NPIR motif, different sorting 66 signals, such as C-terminal and internal motifs, were also found in various other types of 67 soluble cargo. Therefore, the VSR luminal domain can recognise a range of vacuolar sorting 68 signals, all of which have yet to be identified. To understand the mechanism of cargo-receptor 69 interaction, elucidation of the crystal structure of the luminal domain of VSR1 was attempted 70 after overexpression in bacteria (Luo et al., 2014). It revealed a folding mechanism between 71 two sub-domains, triggered by ligand binding. Despite identifying some important amino 72 acids, only a portion of the luminal domain has been crystallised, unfortunately missing the 73 real binding site of the NPIR motif. Therefore, further investigation is still needed to 74 understand the real mechanism allowing the VSR luminal domain to bind a diversity of 75 vacuolar cargoes. One possibility would be that various vacuolar cargo are transported by 76 different isoforms of VSRs. Indeed, seven isoforms have been identified in A.thaliana which 77 have been classified in three groups. While group 1 and 2 can complement each-other in 78 knockout mutants, group 3 appears to be different (Zouhar et al., 2010) and could possibly 79 represent receptors for new types of vacuolar cargo.

80 Efforts to understand the trafficking of vacuolar receptors, rather than the binding to 81 the cargo, have been much more conclusive. Many studies have led to the identification of two 82 major signals in the cytosolic tail of vacuolar sorting receptors the $Yxx\Phi$ motif and the 83 dileucine motif (Braulke and Bonifacino, 2009; de Marcos Lousa and Denecke, 2016). Surprisingly, despite the structural differences between plant, yeast and mammalian 84 85 homologous lysosomal/vacuolar receptors, these two motifs are well conserved across these 86 organisms (de Marcos Lousa et al., 2016). The $Yxx\Phi$ motif is mostly based on the presence 87 of a tyrosine residue and a hydrophobic residue in position +3 of the tyrosine, both of which 88 are essential for anterograde trafficking of lysosomal/vacuolar receptors to the prevacuolar 89 compartment (PVC) (daSilva et al., 2006). However, in plant VSRs, the hydrophobic residue 90 (in this case a leucine in the YMPL motif of plant receptors) has a dominant role in retrograde 91 trafficking to rescue VSRs from degradation in the vacuole (Foresti et al., 2010). Indeed, a 92 leucine mutant of VSR2 is still able to traffic to the late compartments (anterograde 93 trafficking), but is unable to recycle and thus reaches a more distal compartment (termed late 94 prevacuole or LPVC) as well as the central vacuole itself (Foresti et al., 2010). Although this 95 does not exclude a minor role in anterograde trafficking, it demonstrates that anterograde and 96 retrograde trafficking are controlled by different machineries that are connected by at least one 97 motif $Yxx\Phi$.

98 Until now, the function of the N-terminal (luminal) and C-terminal (tail) domains of VSRs 99 have been studied independently and the signal transduction between the two domains remains 100 elusive. It is not clear how the binding of cargo to the N-terminal domain of VSRs triggers the 101 trafficking cycle of VSRs from early to late compartments. Dimerisation of the receptors has 102 been proposed to be a prerequisite for the trafficking of VSRs but not for binding to the cargo 103 (Kim et al., 2010). This suggests that cargo binding might lead to a dimerization of the receptor 104 which would be the signal for VSRs to start trafficking. Although this represents an attractive 105 hypothesis, evidence shows that fluorescent fusions devoid of a luminal VSR domain can still 106 complete a full VSR transport cycle, indicating that the tail may exhibit an autonomous 107 function in trafficking. Therefore, it is still unclear whether VSRs continuously traffic between 108 early and late organelles, or if binding to vacuolar cargo is required prior to trafficking being 109 initiated. Despite this uncertainty, studying the C-terminal tail of VSR has shed light on 110 specific events of transport cycle that can now be mapped, as outlined below.

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113 **1b. Stage 1: early steps of transport to the vacuole**

The classical route to the vacuole involves binding of the soluble cargo in early compartments and release in late compartments. Upon cargo release, the receptors are recycled to early compartments for a new round of binding while vacuolar cargo proceeds to the vacuole.

At early stages, VSRs are transported from the ER to the Golgi in a COPII-dependent route, as
VSR trafficking can be inhibited by a GTP-restricted mutant of Sar1 (H71L) or overexpression
of the guanine nucleotide exchange factor Sec12, both indicative of a canonical COPII-

120 mediated ER to Golgi transport (Gershlick et al., 2014).

121 Despite this simple model being established and accepted, the compartment where VSRs bind 122 their cargo is still controversial. Due to the accumulation of proteins in ER protein bodies, it 123 was first assumed that receptors start their journey by binding their cargo in the ER. In 124 agreement with this hypothesis, a trapped VSR luminal domain fused to an ER retention signal 125 can also retain vacuolar cargo in the ER (Watanabe et al., 2004; daSilva et al., 2005; Niemes 126 *et al.*, 2010*a*). However, since ER retention signals are thought to be retrieval signals capturing 127 proteins from the Golgi cisternae (Pelham et al., 1988), VSR-ligand binding could either occur 128 in the ER, the Golgi or in both compartments. Recent experiments suggest that sorting occurs 129 mostly in the Golgi cisternae (Gershlick et al., 2014). When a vacuolar sorting signal and an

130 ER retention signal were placed on two different cargo molecules, the fusion proteins were

131 partially found in the ER and in the vacuole and the function of both signals was compromised. 132 This can only be explained by the presence of mutually exclusive binding to either vacuolar 133 and ER receptors (VSR or ERD2) in the same compartment. Most likely, the cis-Golgi would 134 be a good candidate as HDEL-cargo can also be detected in this compartment in electron 135 microscopy (Phillipson et al., 2001). However the results do not rule out that low affinity 136 ligand-VSR binding might be happening in the ER lumen (Künzl et al., 2016). A recent report 137 showing that glycosylation of the VSR luminal domain is crucial for cargo-receptor interaction 138 (Shen et al., 2014) adds to the growing list of conditions that affect ligand-binding, but it is 139 unclear how glycans contribute to the binding pocket of the receptor.

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142 **1c. Stage 2: Trafficking from post-golgi organelles.**

There is currently great uncertainty and disagreement in the field about how VSRs proceed after ligand-binding. Results obtained from VSR sorting mutants strongly suggest that ligandrelease takes place at the PVC, from which receptors recycle whilst cargo moves on to the LPVC which is a mature version of PVC depleted for VSRs (Foresti *et al.*, 2010). However, the route taken to and from the PVC is subject to debate. The involvement of the TGN (*trans*-Golgi network) and the PVC in vacuolar sorting have been discussed at various levels and two models have been proposed (discussed in Kang and Hwang, 2014).

150 One model suggests that VSRs are selectively recruited at the TGN via AP-1 and AP-151 4 complexes and this would depend on the presence of the $Yxx\Phi$ motif. This is supported by 152 various evidence including *ap-1* and *ap-4* knockouts affecting vacuolar sorting as well as the 153 VSR tyrosine mutant (in the $Yxx\Phi$ motif) being unable to traffic in the TGN (Foresti *et al.*, 154 2010). In addition, direct interaction between VSR tails and both AP-1 and AP-4 mu subunits 155 has been shown (Oliviusson et al., 2006; Gershlick et al., 2014; Nishimura et al., 2016). 156 Therefore, the first model suggests that VSR molecules are transported from the TGN to the 157 PVC via clathrin coated vesicles using AP-1/AP-4 adaptor complexes (Fuji et al., 2016). In the 158 PVC, VSR and cargo dissociate and VSR recycle to earlier compartments via the retromer 159 complex. Further supporting this model, Vps29 recycling mutants accumulate VSRs in the 160 PVC (Kang et al., 2012). The recycling stages of VSRs appear to be limiting steps of the 161 trafficking cycle, as VSRs accumulate in the PVC at steady state (daSilva et al., 2005; 162 Oliviusson et al., 2006; Shen et al., 2014).

163 The alternative model proposes that VSRs steady state is found at the TGN instead of 164 the PVC (Niemes *et al.*, 2010b). In this model, only the cargo proceeds to post TGN organelles 165 whilst the receptor is recycled at the TGN (Niemes *et al.*, 2010b; Künzl *et al.*, 2016). This 166 cargo transport is mediated by maturation of the TGN into the PVC and therefore excludes 167 active transport of vacuolar proteins (both cargo and receptor) from the TGN. To support this 168 model, retromer components such as sorting nexins were found to be located at the TGN 169 instead of the PVC in tobacco protoplasts (Niemes et al., 2010; Scheuring et al., 2011; Stierhof 170 et al., 2013). Additionally, using FRET-FLIM experiments with nanobody epitope interaction, VSRs were found to bind the cargo only in the ER and Golgi, but not in post-Golgi organelles 171 172 (Künzl et al., 2016). Despite its attractiveness, the model cannot explain the segregation of 173 secretory bulk flow of soluble proteins from that of soluble vacuolar proteins (Dorel et al., 174 1989; Denecke et al., 1990), and neither does it give a role for AP complexes in vacuolar 175 trafficking. Finally, the effect of selective VSR tail mutants in the $Yxx\Phi$ motif can also not be 176 explained using this model.

177 Discrepancy between these two models could reflect the use of various models 178 (knockout in *A.thaliana* vs overexpression in Tobacco protoplast...) but nevertheless requires 179 further investigation to establish the so-called vacuolar trafficking pathway.

180

181 **1d. Stage 3: fusion with the vacuole : LPVC and vacuolinos and other small vacuoles.**

182 Whether VSRs reach the PVC or not (model I or II respectively), vacuolar cargo do 183 reach the prevacuolar compartment and are delivered to the vacuole by fusion with this 184 compartment. The mechanism of fusion involves a cascade of Rab5 and Rab7 GTPases (Cui 185 et al., 2014; Singh et al., 2014). Interestingly, growing evidence shows that fluorescent 186 vacuolar cargo accumulates in discrete punctate structures prior to fusion with the vacuole. 187 Their visualisation can be enhanced using a Rab7NI mutant, demonstrating that fusion of these 188 structures to the vacuole is dependent on an active Rab7GTPase (Bottanelli et al., 2012). In 189 normal conditions, comparable structures have been seen upon expression of Aleurain-GFP 190 marker in A.thaliana roots (Fluckiger et al., 2003; Jaillais and Gaude, 2007; Gendre et al., 191 2011), Arabidospis protoplasts (Miao et al., 2008) as well as tobacco protoplasts (Scheuring et 192 al., 2012). Initially, these structures were described as colocalising with markers of the 193 PVC/MVBs such as VSR2 and SNX1 and sensitive to wortmanin and overexpression of 194 Ara7QL (Jaillais et al., 2007; Miao et al., 2008; Jia et al., 2013). However, by refining the 195 analysis using weak expression of similar markers, these structures were found to label the

196 LPVC (Foresti et al., 2010). In contrast to the classical PVC that is enriched in VSRs 197 (schematic 1), the LPVC is depleted in VSRs but enriched in Rab5 small GTPases. Weak 198 expression of organelle markers are essential to visualise the LPVC as their overexpression 199 lead to organelle fusion events similar to those observed upon treatment with wortmannin or 200 expression of constitutively active mutant Ara7QL (Bottanelli et al., 2012; Jia et al., 2013). 201 Most studies however use strong promoters to express and visualise these organelle markers, 202 which results in mislabelling organelles. Therefore, establishing lines that express PVC and 203 LPVC markers at low levels will allow distinction between these two organelles (PVC and 204 LPVCs) in current models, leading to meaningful conclusions on vacuolar sorting pathways. 205

206 The existence of this new organelle is not trivial as it sheds light on the late steps of vacuolar 207 delivery. The LPVC is formed by selective retrieval of VSRs from the PVC and accumulation 208 of cargo molecules. Consistent with this hypothesis, a VSR recycling defective mutant in the 209 $Yxx\Phi$ motif of VSRs (L615A) is now found to accumulate in the LPVC instead of the PVC 210 (Foresti et al., 2010). Interestingly, the presence of PVC and LPVC organelles is comparable 211 to early endosome (EE) and late endosomes (LE) described for the mammalian lysosomal field 212 and would be consistent with a cascade of Rab5-Rab7 progressing from the PVC to the LPVC 213 before fusing to the vacuole. This model is not without challenges as it is unclear how 214 membranes would be recycled from the central vacuole and how new PVCs would be 215 replenished after they mature into LPVCs. The mechanisms of vacuolar fusion seem to be more 216 complex than expected and the role of the LPVC as an intermediate organelle between the PVC 217 and the vacuole needs to be further evaluated.

218 Other types of punctate structures accumulating vacuolar cargo have been described in 219 petunia petal epidermis. These structures accumulating Aleu-GFP are completely separated 220 from the anthocyanins-rich central vacuole and do not share markers with the tonoplast 221 (Verweij et al., 2008; Faraco et al., 2017). Due to their resemblance with small vacuoles, the 222 name "vacuolinos" has been proposed (Faraco et al., 2017). Further investigation has shown 223 that the trafficking of tonoplast localised PH1-PH5 pumps transit through the vacuolinos in a 224 SNARE dependent pathway (Faraco et al., 2014; 2017). In contrast, before reaching the 225 vacuole, a-, d- and g- TIPs from Arabidopsis or Petunia accumulate in similar structures which 226 are distinct from vacuolinos and CV. These observations, together with additional data using a 227 collection of mutants affecting biogenesis and fusion of vacuolinos, have led the authors to 228 propose the existence of multiple vacuoles in a single cell (Faraco et al., 2017). This hypothesis is supported by the identification of individual markers for each type of vacuole (vacuolinos,
CV and PSV). Although vacuolinos are confined to Petunia petal epidermis, the co-existence
of different types of vacuoles in a single cell has been speculated by many and represents a
future path worth investigating.

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235 <u>2. GOLGI to VACUOLE TRAFFICKING PATHWAY (Golgi-DEPENDENT ROUTE).</u> 236

The classical view described above, with VSR as a model, is still considered as the only or major route for delivering vacuolar proteins. But this has been somewhat challenged by a growing number of reports describing alternative routes to the vacuole. In the following paragraphs, we will give an overview of various alternative pathways that are starting to emerge for vacuolar transport routes.

242

243 2a. The case of AP-3

244 AP-3 is an adaptor complex similar to AP-1 and AP-4. In yeast, the AP-3 dependent pathway 245 to the vacuole was first described 20 years ago. It is known as the ALP (alkaline phosphatase 246 pathway) pathway, as opposed to the classical CPY (carboxypeptidase) pathway (Valls *et al.*, 247 1990; van Voorst et al., 1996; Cowles et al., 1997; Jørgensen et al., 1999). Despite using 248 similar proteins, the two pathways have been shown to be independent as the inhibition of the 249 ALP pathway affects ALP transport without affecting the transport of CPY (Cowles et al., 250 1997). In mammalian cells, the AP-3 pathway has also been very well described and is involved 251 in transport to the lysosome or related organelles, such as the melanosome and platelet dense 252 granules or lytic granules. Mutation in the AP-3 complex leads to relocation of lysosomal 253 proteins and genetic disorder (Dell'Angelica et al., 1997; Nakatsu et al., 2004; Assoum et al., 254 2016).

In both yeast and mammals, AP-3 has an established role in transport of specific vacuolar/lysosomal proteins directly from the Golgi, therefore bypassing the post-golgi organelles (Rous *et al.*, 2002; Reusch *et al.*, 2002; Bowers and Stevens, 2005; Feraru *et al.*, 2010). Yet, in plants, a role for AP-3 in vacuolar sorting is only starting to emerge.

In Arabidopsis, the localisation of AP-3 is still unclear. AP-3 β subunit was found to be mostly cytosolic with discrete punctate structures, rarely localising with endomembranes (Feraru *et al.*, 2010). Although these structures have not been identified, Lee et al (2007) have 262 demonstrated that AP-3 interacts with two TGN proteins, VTI12 and EPSIN2. Therefore it 263 would appear that AP-3 could be localising partially at the TGN, similarly to yeast and 264 mammals where AP-3 and AP-1 colocalise on the same membranes but on distinct regions of 265 trans-Golgi network or recycling endosomes (Cowles et al., 1997; Odorizzi et al., 1998; Peden 266 et al., 2004). Likewise, we would expect AP-3 to localise and act at the level of the TGN in 267 plants, similarly to AP-1 and AP-4. Yet, this hypothesis is questioned by the finding that in 268 AP-3 β mutants, SUC4 (a sucrose transporter) was arrested in the Golgi rather than in the TGN 269 (Wolfenstetter et al., 2012), suggesting that in plants, AP-3 could also be involved in a direct 270 route from the Golgi to the Vacuole.

Despite this uncertainty on AP-3 localisation in plants, the role of AP-3 in vacuolar transport is established as an alternative pathway to the classical AP-1/AP-4 pathway. Various evidence suggests that transported substrates are different for these two routes.

274 While AP-3 does not seem to interact with VSR2, as shown with a yeast two hybrid experiment 275 (Gershlick et al., 2014), AP-3 β knock-out mutant mistarget membrane proteins such as 276 vacuolar invertase, PIN1, PIN2, BRI1, plasma membrane aquaporin and ATPases or 277 membrane proteins essential for lytic vacuole biogenesis (Feraru et al., 2010; Zwiewka et al., 278 2011; Pertl-Obermeyer et al., 2016). While storage protein delivery is not affected in this 279 mutant' seeds, the transition from PSV to lytic vacuole was compromised with enlargement of 280 RabF2b/Ara7 positive compartments (Feraru et al., 2010). Therefore, it appears that AP-3 281 could act in parallel to the classical pathway with a double function: the rapid delivery of 282 essential proteins for the biogenesis of the vacuole (mostly membrane proteins) and the recycling of plasma membrane proteins such as PINs. An interplay between the AP-1/AP-4 283 284 route and the AP-3 route cannot be excluded, as it has already been shown in mammalian cells 285 (Hirst *et al.*, 2012). In agreement with this, signals such as $Yxx\Phi$ motif and dileucine motifs 286 involved in the classical pathway, seem to also be recognised by the AP-3 pathway in 287 mammals. Although this has not yet been tested in plants yet, similar evidence could explain 288 an overlap between the two pathways in plants. Nevertheless, other unidentified signals should 289 be present on cargo proteins to selectively recruit membrane protein cargos to AP-3 290 subdomains, separate from the AP-1/AP-4 subdomains. Finally, a putative receptor for 291 unconventional soluble vacuolar cargo using the AP-3 pathway still awaits identification.

292

293 **2b.** Transport from Golgi to the vacuole: Dense Vesicles

294 Several pathways connecting the ER or even the Golgi directly to the vacuole seem to usually 295 share a common trait: they all use electron dense vesicles. This characteristic has given its 296 name to Dense Vesicles (DVs) as seen by electron microscopy in pea cotyledons (Hohl et al., 297 1996), and this was later confirmed with density gradients (Hinz et al., 1999a). Dense vesicles 298 are slightly bigger than clathrin coated vesicles (average of 130 nm compared to around 60 nm 299 (Dhonukshe et al., 2007) and appear to mature from the side of the cis-Golgi to the trans-Golgi 300 where they bud off. They accumulate specific storage proteins, such as prolamins and globulins 301 (vicilin and legumin), and sucrose binding protein (SBP) (Craig et al., 1979; Hohl et al., 1996; 302 Wenzel et al., 2005; Robinson et al., 2005). In addition, they seem to be devoid of BP80/VSRs 303 but contain RMRs, putative vacuolar receptors (Hinz et al., 1999a, 2007; Hillmer et al., 2001). 304 The mechanism by which DVs fuse to the PSV (protein storage vacuole) remains elusive 305 (Vitale and Raikhel, 1999). It was suggested that DVs fuse directly with the PSV (Herman and 306 Larkins, 1999a; Liu et al., 2013). However DVs in rice endosperm were found to fuse to 307 different types of prevacuolar compartments before fusing with the PSVs (Shen et al., 2011). 308 These prevacuolar compartments contain RMRs due to the fusion with DVs, but are not 309 labelled with VSRs. Moreover, as in the classical pathway, fusion of DVs with PSVs depend 310 on Rab5 proteins (Fukuda et al., 2013; Liu et al., 2013). In agreement with this, Wang and 311 collaborators have reported that, in late stages of bean cotyledon development, globulin 8s is 312 found in DVs and also in novel forms of partitioned MVBs with one side packed with storage 313 proteins and the other packed with internal vesicles (Wang et al., 2012). Again, these 314 partitioned MVBs were labelled with Rha1, but the authors have not investigated the role of 315 this protein.

316 In the light of this evidence, DVs represent an alternative pathway for proteins destined for the 317 vacuole. Although the fate of DVs still requires further investigation, the similarities between 318 DVs and LPVCs are intriguing. Indeed, the LPVC was defined in tobacco transgenics as 319 enriched in Soluble vacuolar proteins, depleted in vacuolar receptors and labelled by Rab5 320 GTPases, characteristics similar to DVs (Foresti et al., 2010). Growing evidence also show an 321 increasing interconnection between MVBs and DVs in rice (Shen et al., 2011; Liu et al., 2013). 322 Hence, the link between LPVC and DVs could represent a new point of convergence leading 323 to the merge of the lytic and storage protein trafficking pathways before fusion to the vacuole 324 (Figure 1). Various reports give indication in favour of this statement. Indeed, while DVs have 325 been reported to pack storage proteins at level of the Cis-Golgi, they were reported as partially 326 coated with clathrin after progressing to the trans-Golgi network (von Lüpke et al., 2008).

Additionally, Aleurain, which predominantly binds to VSR and traffics through the classical pathway, could also be detected in DVs (Hinz *et al.*, 2007). All this evidence suggests that pathways to the vacuole are flexible and interconnected and views on a strict segregation between lytic and storage vacuolar trafficking pathways might have to be reconsidered (Jiang *et al.*, 2002).

332

333 3. ER - VACUOLE TRAFFICKING PATHWAY (Golgi-independent route)

Both AP-3 and dense vesicles routes are described as Golgi-dependent pathways to the vacuole. In parallel, more evidence is pointing to the existence of Golgi-independent routes for unconventional vacuolar cargo.

337

338 **3a. Direct ER to Vacuole trafficking**

339 Several direct trafficking events between the ER and the vacuoles have been studied in detail340 but they are generally not considered as part of a unique molecular mechanism.

341 One of the mechanisms that is involved in the direct transport of storage protein precursors 342 from the ER to PSV, i.e. by-passing the Golgi, involves precursor-accumulating (PAC) 343 vesicles. PAC vesicles have been described during the maturation of C. maxima seeds but were 344 also described in other plants such as O. sativa (Hara-Nishimura et al., 1998). In this organism, 345 PAC vesicles were reported to contain storage proteins, such as glutelin and α-globulin, as well as an ER-resident protein such as BIP (Takahashi et al., 2005; Pelham, 1990; Vitale and 346 347 Denecke, 1999). For this reason, and their larger size compared to Golgi-derived dense 348 vesicles, PAC vesicles were suggested to derive directly from the ER and transport proteins 349 directly to the vacuole directly. The presence of VSR molecules and other hyperglycosylated 350 proteins in PAC vesicles, however, has questioned this hypothesis, indicating that they might 351 not by-pass the Golgi where glycosylations occur (Shimada et al., 2002). In addition, the Golgi-352 mediated vacuolar transport of a BiP deletion mutant lacking the HDEL motif suggests that the 353 presence of BiP in PAC vesicles is not sufficient evidence to prove a direct trafficking from 354 ER membranes (Pimpl et al., 2006). The origin of PAC vesicles and the involvement of the 355 Golgi in this pathway is therefore still unclear.

Nevertheless, other types of ER to vacuole transport have been reported. One of them involves protein bodies (PBs). PBs differ in shape and size from the electron-dense core PAC vesicles. Yet, their content is very similar as PBs have been reported to accumulate storage proteins and ER proteins. Two types of PBs have been described. In *O. sativa*, glutelin is stored 360 in PB type II (PB-II) and transported to the vacuole, while prolamin is deposited in PB type I 361 (PB-I), a sub-domain of the ER. Calreticulin, a protein with an ER-retention signal at the C-362 terminus, (Pelham, 1990; Vitale and Denecke, 1999) has been found in both PB types with a 363 small portion also reported in PSVs in rice callus and mesophyll cells (Torres et al., 2001). 364 This finding has prompted the authors to suggest an alternative pathway from the ER directly 365 to the vacuole via PBs. However in tobacco leaf protoplasts, calreticulin has been shown to 366 follow a classical COPI and COPII route (Phillipson et al., 2001; Pimpl et al., 2006). These 367 apparent discrepancies could be explained in terms of cell maturation: although in early stages 368 (seed development) calreticulin could be accumulating in PB and transported to the vacuole in 369 a Golgi-independent pathway, such protein would follow a more classical route in established 370 and mature cells. It was recently hypothesized that in leaves, PBs do not detach from the ER 371 but rather dynamically interact with the ER to exchange proteins (Saberianfar et al., 2016). 372 Another factor could be cell type: while glutelin could be sorted to PSV by-passing Golgi 373 cisternae in rice (Torres et al., 2001), a Golgi-dependent sorting was described in castor beans 374 (Jolliffe et al., 2004) and pea (Hinz et al., 1999b). Such differences may reflect the high 375 flexibility of the alternative trafficking pathways from the ER to the vacuole, adjusting the 376 routes with the needs of cell types.

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379 **3b.** Autophagic related processes

380 Autophagy is the main process for organelle degradation in most eukaryotes and hence 381 plays a major role in cell homeostasis (Michaeli et al., 2016/2; Liu and Bassham, 2012). In 382 addition, autophagy related mechanisms appear to also be involved in a number of trafficking 383 events, such as the direct ER-vacuole trafficking (Robinson *et al.*, 1998; Herman and Larkins, 384 1999a; Michaeli et al., 2014). Indeed, PBs have been reported to become surrounded by 385 autophagic membrane in the cytosol after their release from the ER (Herman and Larkins 386 1999). This autophagosome then fuses with the tonoplast, releasing PBs in the vacuole. Early 387 evidence of the presence of PBs engulfed in vacuoles comes from electron microscopy 388 observations of storage protein delivery by the ERvt pathway (Levanony et al., 1992; Coleman 389 et al., 1996). Interestingly, prolamins can be delivered to vacuole via the Golgi-dependent 390 pathway in early stages of development, and then switch to autophagy mediated delivery in 391 later stages when accumulation in PBs is increased (Levanony et al., 1992). This again shows 392 the flexibility and interconnection between pathways depending on the cell status.

393 Autophagy has also been proposed for the delivery of other types of cargos and vesicles 394 originating from the ER such as rubber and anthocyanins (Pourcel et al., 2010/1; Herman and 395 Schmidt, 2004; Chanoca et al., 2015). Autophagy of ER-derived compartments can also be 396 induced by stress or overexpression of proteins (Bassham et al., 2006). In stress induced events, 397 Atg8, the main protein involved in classical autophagy processes, has been shown to be 398 recruited to ER membrane and to the vacuole (Liu et al., 2012). Despite this observation, the 399 role of the main autophagy regulators such as Atg8 in the process of ER-vacuole trafficking is 400 questionable as knock out mutants of Atg proteins appear not to disturb seed formation in 401 Arabidopsis (Liu and Bassham, 2012). In addition, Atg8 is not present with prolamin-402 containing PBs engulfed in maize seeds vacuoles (Reyes et al., 2011). Therefore, it seems that 403 despite the existence of autophagy like processes involved in vacuolar trafficking, the main 404 autophagy regulators do not seem to play a role. New regulators of this pathway hence await 405 identification.

406

407 **3c. Anthocyanins trafficking and other metabolites**

408 Other interesting observations derived from staining of neutral red-stained bodies 409 (NRSBs) include large bodies found inside plant vacuoles that are stained by the supravital dye 410 neutral red. In anthocyanin accumulating cells, NRSBs appear much bigger than in other cells, 411 suggesting a relationship with AVIs (anthocyanin vesicular inclusions), other anthocyanin 412 accumulating bodies (Pourcel et al., 2010). Anthocyanins have been proposed to be 413 synthesized on the cytosolic side of the ER and further transported to the vacuole, which then 414 confers typical petal colors (Saslowsky and Winkel-Shirley, 2001; Winkel-Shirley, 2002). 415 However, the transport of anthocyanins to the vacuole is not yet understood. TT19, an 416 Arabidopsis glutathione S-transferase ligand transporter, seem to play a specific role in the 417 transport of anthocyanins to vacuoles. Indeed, the inhibition of TT19 lowers the amount of 418 total anthocyanins (Poustka et al., 2007; Sun et al., 2012). Therefore it has been postulated that 419 TT19 induces the solubility of cytoplasmic anthocyanins, which otherwise aggregate and are 420 engulfed by microautophagy in the vacuole (Chanoca et al., 2015). This mechanism appears 421 to be Atg-dependent as Atg mutants are defective in the accumulation of anthocyanins, with 422 fewer numbers NRSBs and AVIs reported (Pourcel et al., 2010). NRSBs and AVIs disappear 423 in *Exo70B1-2* double mutants demonstrating that Exo70B1-2 is also implicated in the transport 424 of anthocyanins from the ER to the vacuole (Kulich et al., 2013) (Kulich and Žárský, 2014). 425 NRSBs and AVIs are nevertheless not the only mechanism of anthocyanin transport to the 426 vacuole. In Vitis vinifera and Zea mays, anthocyanins accumulate initially in small tubular or

vesicular bodies that become larger through vesicular fusion or vacuolar autophagy (Irani and
Grotewold, 2005; Zhang *et al.*, 2006; Conn *et al.*, 2010; Gomez *et al.*, 2011). These bodies and
tubes are composed of ER membranes or ER-derived vesicles and are localized to tonoplast
invaginations deep inside the vacuole (Poustka *et al.*, 2007; Gomez *et al.*, 2011). This suggests
that they may be the plant version of autophagic tubes previously described in yeast (Müller *et al.*, 2000).

433

434 Apart from anthocyanins, other secondary metabolites and hormones are also reported 435 to be directly sorted to the vacuole from the ER. This is the case for compounds such as 436 phenylpropanoid/flavonoids and cyanogenic glucosides (Ralston et al., 2005), alkaloids 437 (sanguinarine) and indole alkaloids (vinblastine) (Alcantara et al., 2005), phytohormones, like 438 salicylic acid (Yoshimoto et al., 2009), abscisic acid glucosyl ester (ABA-GE) and its activator 439 (AtBG1, a β-glucosidase (Lee *et al.*, 2006; Burla *et al.*, 2013), and auxin (Kulich and Žárský, 440 2014). However, these pathways are difficult to observe as they may involve cooperation of 441 multiple transport mechanisms as suggested for flavonoids (Zhao, 2015). Membrane 442 transporters, glutathione S-transferase conjugation and vesicle trafficking may be cooperating 443 for the vacuolar sequestration of flavonoids. In fact, the only known protein involved in the 444 membrane fusion of flavonoid-containing vesicles with vacuoles is the Golgi-localized 445 membrane protein GFS9 (Ichino et al., 2014; Zhao, 2015). Therefore, more work is required 446 to understand how these secondary metabolites are transported to the vacuole (Kulich and 447 Žárský, 2014).

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449

450 **3d. Other uncharacterized vacuolar pathways.**

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In addition to the above described unconventional trafficking to the vacuole, many more routes have been reported but still require clarification or remain controversial. In the following paragraph, we give a summary of the findings to date.

455

456

457 *The Chitinase A case*

In contrast to Aleurain which contains a typical N-terminal NPIR motif, Chitinase is an enzymethat carries a C-terminal vacuolar sorting determinant (CtVSD). This determinant does not

460 have a consensus sequence, but relies on 4-7 amino acids with hydrophobic characteristics. 461 Chimeric proteins fused with this C-terminal signal are transported to the vacuole showing that 462 it acts as a VSD. Other proteins such as barley lectin and phaseolin also contain a CtVSD. It 463 has been shown that VSR affinity for this type of protein is very low, and instead another 464 putative vacuolar receptor (RMR: Receptor Membrane RING-H2) has been proposed (Ahmed 465 et al., 2000; Park et al., 2007). A fusion protein GFPChi is in part retained in the ER and also 466 found in uncharacterised punctate structures different from those labelled by Aleu-RFP in 467 tobacco (Stigliano et al., 2013) and tomato (Di Sansebastiano et al., 2014) protoplasts.

468 Altogether these observations suggest that Chitinase and Aleurain might use different routes 469 to the vacuole (Stigliano et al., 2013). Various reports have shown differences in Chitinase and 470 Aleurain sorting: engineered glycosylated GFPChi appears to be sensitive to EndoH treatment 471 whereas the glycosylated AleuGFPgl133 is not (Stigliano et al., 2013). SNAREs appear to 472 control vacuolar sorting and modulate targeting of these markers differentially (Uemura end 473 Ueda 2014). Indeed, VTI12 and SYP51 has been reported to affect more specifically GFPChi 474 trafficking, while VTI11 and SYP52 seem to be involved in AleuGFP transport (Sanmartin et 475 al., 2007; De Benedictis et al., 2013). Finally, Sar1HL, an inhibitor of COPII trafficking, seem 476 to increase the fluorescence of Chitinase in the vacuole while Aleurain trafficking is prevented. 477 Taken together this evidence suggests that Aleurain and Chitinase might traffic through 478 different routes. Nevertheless, other reports have shown that RFPChi transport is still 479 dependent from components of the classical route such as Rab11, Rha1, Ara6 and Rab7 480 (Bottanelli et al., 2011). RFPChi was found to strongly label the ER, with only weak labelling 481 of the central vacuole (Bottanelli et al, 2011). Although these observations might only be the 482 result of differential fluorescent fusion (GFP vs RFP), a plausible explanation is that Chitinase 483 could be trafficking through various routes depending on the cell status and vacuole identity, 484 as suggested above (Fluckiger et al., 2003). Indeed, Chitinase can also be found in dense 485 vesicles, budding off from the Golgi, or in ER bodies in seeds and developing cotyledons 486 respectively (G. Hinz unpublished data). Both Aleurain and Chitinase can also be found 487 colocalising in BFA bodies or in prevacuolar compartments upon treatment with auxin and/or 488 acetylcholine (ACh) (Stigilano et al., 2013; Di Sansebastiano et al., 2014). Auxin and ACh 489 treatments do not alter sorting pathways like BFA treatments (Stigliano et al., 2013) but simply 490 change the sorting specificity, emphasizing compartments characterized by PIN1 and PIN7 491 (Kleine-Vehn et al., 2006; Geldner, 2009). These observations again suggest a close 492 connection between pathways.

493

494 495

496 *Cardosines*

497 Even if the trafficking of Chitinase may appear exceptional, an increasing number of 498 proteins may soon be reported as trafficking through alternative pathways. Cardosin A, a 499 vacuolar aspartic proteinase, is characterized by two domains: a plant specific insert (PSI) 500 domain and a C-terminal region. Both domains act as vacuolar sorting determinants (VSDs) 501 but each of them is involved in distinct routes to the vacuole (Tormakangas et al., 2001). A 502 working model for Cardosin A trafficking suggests that the C-terminus mediates a COPII-503 dependent ER-to-Golgi pathway to the vacuole while the PSI domain mediates either a COPII-504 dependent or COPII-independent vacuolar trafficking pathway in a non-glycosylated or 505 glycosylated form, respectively. Again, the relevance of the PSI-mediated pathway depends on 506 the type of tissue and the metabolic activity of the organs (Pereira et al., 2008, 2013).

507

508 Membrane proteins examples

Although most studies have concentrated on the sorting of storage and lytic proteins to the vacuole, membrane proteins have also been studied and found to use various routes. As already described above, VSRs and RMR proteins traffic via different pathways (classical or DVs).

513 AtRMR1 and -2. AtRMR2 homodimers and AtRMR2/AtRMR1 heterodimers have 514 been recently shown to assemble in the ER and bind different vacuolar cargos (Occhialini et 515 al., 2016). Two different pathways sort AtRMRs to the TGN, either a Golgi-dependent or 516 Golgi-independent pathway (Occhialini et al., 2016). Comparative studies emphasizing 517 common characteristics between lysosomes and vacuoles also point out that the percentage of 518 N-glycoproteome is much higher in lysosomal/PM membrane than in the tonoplast (Pedrazzini 519 et al., 2016; Pompa et al., 2017). Based on this observation, the authors propose that the major 520 trafficking pathway to the tonoplast might be bypassing the Golgi apparatus.

521 Other reports on more membrane proteins again support the presence of multiple pathways to 522 the tonoplast. α -TIP, the SNARE VAMP3 and CBL6 were all found to be COPII independent 523 in tobacco epidermis, suggesting a direct ER-vacuole transport (Bottanelli *et al.*, 2011). 524 However, while α -TIP trafficking is sensitive to Rab mutants (Rha1, ara6 and Rab7), Vam3 is 525 only sensitive to Rab7 mutant and CBL6 is not affected by any of these mutants. Moreover, additional evidence comes from the fact that BFA affects the sorting of TIP1;1, but not of TIP3;1 (α-TIP) and TIP2;1 in *A. thaliana* hypocotyls (Rivera-Serrano et al. 2012).

PIN proteins also traffic through different pathways: PIN2 (as well as AUX1) recycling appears to be BFA insensitive whereas PIN1 and 3 appear to be BFA sensitive and dependent on the GNOM pathway (Geldner *et al.*, 2003; Kleine-Vehn *et al.*, 2006; Ding *et al.*, 2011). The inhibition caused by this molecule also defines a link between the BFA-insensitive pathway and PIN2 recycling (Rivera-Serrano *et al.*, 2012). However, the BFA treatment disrupts most of the pathways exhibiting these markers (Kleine-Vehn *et al.*, 2006; Drakakaki *et al.*, 2009; Ding *et al.*, 2011).

Golgi-mediated trafficking may play a role in controlling and modifying another kind of compartment formed directly from the ER membranes, the dark-induced protein (DIP) vesicles. These compartments are characterized by the presence of DIP aquaporin (specifically α -TIP; (Neuhaus and Rogers, 1998) and RMR-like proteins, and are formed with the direct contribution of the ER and the Golgi (Jiang *et al.*, 2000, 2001). DIP vesicles are the main system for transporting crystalloid elements to PSVs (Vitale and Hinz, 2005).

541 A small amount of DIP aquaporin is present in the PSV tonoplast. In contrast, α - and γ -542 aquaporin are typically targeted to CVs and are absent from DIP vesicles (Jiang *et al.*, 2000). 543 DIP vesicles are surrounded by a double membrane that fuses with PSVs, delivering the inner 544 membrane that forms an independent compartment inside PSVs. DIP vesicles probably 545 transport specific membrane proteins and hydrolytic enzymes (Isayenkov, 2014).

546

547 Clearly, more evidence is still needed to decipher interconnections between vacuolar 548 pathways. Nevertheless, the obvious existence of alternative transport routes for these 549 membrane proteins suggests that some classes of soluble vacuolar cargo molecules could also 550 be using such alternative pathways. This hypothesis however does not exclude the existence of 551 a merging point with the classical routes at various stages (Bottanelli *et al.*, 2011).

552

553 Non-vesicular ER-Vacuole transport

554

A Golgi-independent tonoplast biogenesis model has been proposed in which the smooth ER is involved. This ER sub-domain has a distinctive lipid composition that accumulates proteins and lipids destined for the tonoplast (Viotti *et al.*, 2013). After reaching a certain size, the smooth ER curves (Knorr *et al.*, 2012) and eventually fuses with the pre559 existing vacuolar network. When post-Golgi trafficking is blocked by BFA, provacuoles 560 appear multi-lamellar, suggesting that a component delivered by the TGN is necessary for the 561 separation of the provacuole from the ER or for fusion with the vacuolar network (Viotti *et al.*, 562 2013). The analogy with the GERL model (Golgi-associated ER from which lysosome 563 apparently form) (Marty, 1999) first described in the late 70s (Marty, 1978) is evident. GERL 564 models proposes that despite the formation of provacuoles in the vicinity of Golgi trans faces, 565 the Golgi apparatus itself appears to be bypassed in the transport. The novelty of more recent 566 research arises from evidence that trafficking can now be shown to fully bypass the Golgi, and 567 merge with endocytosis and phagocytosis later.

568

569 Whilst models need to be adjusted and fine-tuned, it is now obvious that direct transport from 570 the ER to vacuoles represent a large portion of the transport to the vacuole. The Golgi 571 contribution in this process is still unclear, but if it occurs, it certainly differs from the classic 572 Golgi-dependent model in ways that are slowly emerging.

- 573
- 574

575 **Conclusions**

576 Golgi-independent vacuolar trafficking is not exceptional but a fundamental process, which is 577 still poorly understood, and affects the very interpretation of cell compartmentalization starting 578 from vacuoles characterization. It is evident that their compartmental diversity is not due to a 579 maturation process similar to that observed in Golgi cisternae. Vacuoles receive cargo 580 molecules and membranes from multiple sources and acquire their functional specificity 581 depending on the contribution of different donors. The ER is the most important of these donors 582 but the plasma membrane and Golgi apparatus are also involved.

583 ER export has a central role in controlling the biogenesis of intermediate compartments, 584 including endosomes. In the absence of specific pathways activated by growth, stress, 585 starvation and/or other specific processes, post-Golgi organelles such as the TGN and the 586 LPVC may represent hubs where trafficking events could merge. Clearly, the trafficking 587 pathways are more complex and interconnected than previously thought. In addition, direct 588 routes involving post-translational modifications mediating transport from the cytosol to 589 membranes of the secretory pathway such as the tonoplast need to be explored in more depth 590 (Batistic et al., 2012). Future studies will probably contribute to the idea that "unconventional 591 trafficking" routes will soon become conventional.

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596 **Figure 1:**

- 597 Possible routes from the Endoplasmic Reticulum (bottom) to the Vacuole (top). Depicted are
- 598 multiples routes that can be adopted by various storage or lytic proteins showing classical and
- 599 unconventional sorting to the vacuole.

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VACUOLE

