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1 **Datamining and functional environmental genomics reassess the phylogenetics and**
2 **functional diversity of fungal monosaccharide transporters**

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22 **Key words:** Fungi, sugar transporters, environmental genomics, metatranscriptomics

23

24 **Abstract**

25 Sugar transporters are essential components of carbon metabolism and have been extensively
26 studied to control sugar uptake by yeasts and filamentous fungi used in fermentation
27 processes. Based on published information on characterized fungal sugar porters, we show
28 that this protein family encompasses phylogenetically distinct clades. While several clades
29 encompass transporters that seemingly specialized on specific “sugar-related” molecules (e.g.
30 *myo*-inositol, charged sugar analogs), others include mostly either mono- or
31 di/oligosaccharide low-specificity transporters. To address the issue of substrate specificity of
32 sugar transporters, that protein primary sequences do not fully reveal, we screened “multi-
33 species” soil eukaryotic cDNA libraries for mannose transporters, a sugar that had never been
34 used to select transporters. We obtained 19 environmental transporters, mostly from
35 *Basidiomycota* and *Ascomycota*. Among them, one belonged to the unusual “fucose H⁺
36 symporter” family, which is only known in *Fungi* for a rhamnose transporter in *Aspergillus*
37 *niger*. Functional analysis of the 19 transporters by expression in yeast and for two of them in
38 *Xenopus laevis* oocytes for electrophysiological measurements indicated that most of them
39 showed a preference for D-mannose over other tested D-C6 (glucose, fructose, galactose) or
40 D-C5 (xylose) sugars. For the several glucose and fructose-negative transporters, growth of
41 the corresponding recombinant yeast strains was prevented on mannose in the presence of one
42 of these sugars that may act by competition for the binding site. Our results highlight the
43 potential of environmental genomics to figure out the functional diversity of key fungal
44 protein families and that can be explored in a context of biotechnology.

45 **Key Points**

- 46 - Most fungal sugar transporters accept several sugars as substrates
- 47 - Transporters, belonging to 2 protein families, were isolated from soil cDNA libraries
- 48 - Environmental transporters featured novel substrate specificities

49 **Introduction**

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2 50 In osmotrophic microorganisms such as *Fungi*, sugar transporters inserted in the cell
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4 51 membrane are at the frontline for the provision of external soluble sugars to fuel primary
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6 52 carbon metabolism (Gonçalves et al. 2016). These transporters are confronted to, and may
7
8 53 cope with, rapid shifts in both external concentrations and chemical diversity of available
9
10 54 substrates. To adjust fluxes in responses to these shifts, fungi have evolved a series of
11
12 55 transcriptional and post-transcriptional mechanisms that modulate synthesis and turnover of
13
14 56 such membrane proteins (Özcan and Johnston 1999; Horák 2013). Additionally, these
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16 57 transporters have evolved intrinsic characteristics, namely substrate ranges and affinities that
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18 58 specialize them on a specific set of sugars in a specific range of concentrations.
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24 59 In nature, sugars are represented as soluble free mono or disaccharides that accumulate in
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26 60 specific plant exudates such as flower nectar, plant sap, fruit pulp, rhizodeposits or milk
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28 61 (Hutsch et al. 2002). However, most sugars are stored as polysaccharides constitutive of the
29
30 62 plant biomass (e.g. cellulose, hemicelluloses, starch) (Popper and Tuohy 2010; Schädel et al.
31
32 63 2010). Plant biomass degradation by extracellular hydrolytic enzymes continuously generates
33
34 64 a diversity of mostly C5 (e.g. xylose, arabinose) or C6 (e.g. glucose, galactose, mannose)
35
36 65 monosaccharides as well as oligosaccharides (e.g. maltose, xylobiose, cellobiose,
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38 66 mannobiose, regarding di-saccharides) that are substrates for sugar transporters (Gunina and
39
40 67 Kuzyakov 2015). Consequently, sugar transporter-encoding gene families are among the most
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42 68 diversified gene families in fungal genomes with up to 86 different members in the case of the
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44 69 mold *Aspergillus niger* (Peng et al. 2018).
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51 70 In yeasts and filamentous fungi, playing key roles in carbon metabolism, fermentation
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53 71 processes, and biotechnology to achieve high conversion rates of complex substrates (e.g.
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55 72 plant biomass, dairy effluents), sugar transporters have been the focus of numerous studies
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57 73 and literature reviews (e.g. Bisson et al. 2016; Hara et al. 2017). Most noticeably, is the
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74 characterization of the substrate specificity of most of the sugar transporters in the model and
75 industrial yeast *Saccharomyces cerevisiae* (e.g. Bisson et al. 2016). For this species, mutant
76 and recombinant strains unable to use either mono- or disaccharides (Wieczorke et al. 1999;
77 Marques et al. 2017) have been selected and extensively used to characterize transporters
78 from other fungal species by functional complementation. This has also been the case for
79 several degradation products from cellulose, hemicellulose or pectin that *S. cerevisiae* cannot
80 naturally metabolize, such as xylose, cellobiose, xylobiose, cellobionic acid or galacturonic
81 acid (e.g. Galazka et al. 2010; Li et al. 2015; Sloothaak et al. 2016; Zhang et al. 2017; Protzko
82 et al. 2018).

83 From a structural point of view, sugar transporters are described within the Major
84 Facilitator Superfamily (MFS) referenced in the Transported Classification Database (TCDB,
85 Saier et al. 2016) as TC 2.A.1. Almost all fungal sugar transporters described so far belong to
86 the so-called Sugar Porter (SP) family (TC 2.A.1.1). More marginally, sugar acquisition
87 through specific members of the Drug:H⁺ Antiporter-1 family (DHA1, TC 2.A.1.2) has been
88 reported (essentially for fructose) in *Saccharomycotina* yeasts (Leandro et al. 2011;
89 Gonçalves et al. 2016), as well as through a “Fucose: H⁺ Symporter” (FHS) family member
90 (TC 2.A.1.7) in the case of L-rhamnose in *A. niger* (Sloothaak et al. 2016). Putative SWEET
91 transporters (TC 2.A.123; Chen et al. 2010; Takanaga and Frommer, 2010) have also been
92 identified in the genome of chytrid fungi (Hu et al. 2016). In what concerns the SP family, it
93 is found in all domains of life and virtually in all eukaryotic species examined. The 3-
94 dimensional structures of several bacterial, plant and animal members of this family have
95 been resolved (e.g. Deng et al. 2014; Wisedchaisri et al. 2014; Paulsen et al. 2019) along with
96 the identification of key amino acid residues interacting with the transported sugars (e.g.
97 Young et al. 2014; Zhang et al. 2015). Furthermore, it was shown that very limited changes in
98 the fungal SP primary sequences, obtained through directed or random mutagenesis, can alter

99 transport features in terms of substrate range, affinity or transport inhibition by non-
100 transported competitive substrates (e.g. Reznicek et al. 2015; Li et al. 2016; Trichez et al.
101 2019). Despite this apparent wealth of knowledge regarding fungal sugar transporters, their
102 true phylogenetic and functional diversity within the kingdom Fungi remains underexplored.
103 Indeed, functional data available for fungal sugar transporters suffer from several potential
104 biases. On the one hand, (i) these data have been acquired from a limited number of fungal
105 species not necessarily representative of the phylogenetic and functional diversity of this
106 taxonomic group. On the other hand, (ii) a large number of the characterized transporters had
107 been selected either based on their phylogenetic proximity to already characterized
108 transporters or based on their capacity to transport a restricted number of sugars (often
109 glucose, xylose or fructose in the case of monosaccharide transporters).

110 To overcome the taxonomic bias, in the present study, we selected transporters by the
111 functional complementation of a *S. cerevisiae* yeast mutant defective in monosaccharide
112 transport using metatranscriptomic libraries made from polyadenylated mRNA extracted from
113 a broadleaf (*Fagus sylvatica*) and an evergreen (*Picea abies*) forest soils. Fungal communities
114 present in these soils encompass several hundreds of taxa distributed among several main
115 orders belonging to *Basidiomycota*, *Ascomycota* and *Mucoromycota* (Damon et al. 2010).
116 These taxa encompass nutritional strategies featuring either soil or litter saprotrophs, white or
117 brown rots, plant or animal pathogens and mycorrhizal mutualists. Regarding the sugars used
118 as "baits" to select sugar transporters, we concentrated our efforts on D-mannose. In the
119 literature, this monosaccharide had never been specifically used to select transporters
120 although it is widespread and abundant in natura as a component of plant biomass (mannans)
121 or as a component of glycoproteins as for example in the fungal cell wall mannoproteins
122 (including yeasts; see Lipke and Ovalle, 1998). Noticeably, gymnosperm cell walls are
123 specifically enriched in mannans that represent on average 31% of the needle's hemicellulose

124 biomass (Schädel et al. 2010). It could therefore be hypothesized that fungal species that
125 specifically thrive in gymnosperm (e.g. *P. abies*) forest may express mannose-specific
126 transporters. Furthermore, in a context of biotechnology, the characterization of transporters
127 that efficiently transport mannose but no other monosaccharides could be used to engineer
128 yeast strains for an efficient use of this plant-derived sugar in a context where other sugars are
129 present.

130 Our objectives were thus (i) to update our current knowledge on fungal sugar
131 transporter functional diversification through the establishment of an exhaustive database of
132 characterized members of this fungal protein family and subsequent phylogenetic analysis of
133 the corresponding proteins, and (ii) to search for novel members possibly defining novel
134 substrate preferences (such as mannose) through an environmental genomics approach.

135 **Materials and methods**

136 *Soil sampling, RNA extraction and cDNA library construction*

137 Two organic matter-rich composite soil samples were collected in July 2007 in a beech (*F.*
138 *sylvatica*) and in a spruce (*P. abies*) forest (Damon et al. 2010; 2011; 2012) located in central
139 France (Breuil-Chenue site, 47°18'10''N, 4°4'44''E). More details about forests, soil
140 characteristics and sampling strategy are given in Damon et al. (2010). Total RNA was
141 extracted from 104 g of each frozen soil samples as previously described (Damon et al. 2010)
142 and eukaryotic cDNAs were synthesized from 3 µg of total soil RNA using the Mint-2 cDNA
143 synthesis kit (Evrogen, Moscow, Russia). After size-fractionation by 2-dimensional agarose
144 gel electrophoresis (Yadav et al. 2014), the recovered 1-3 kb cDNA fractions were PCR-
145 amplified (26 cycles using the Mint-2 cDNA synthesis kit) and cloned downstream of the *S.*
146 *cerevisiae* PMA1 promoter in the pDR196 yeast–*Escherichia coli* shuttle vector (Rentsch et
147 al. 1995) into which a kanamycin resistance gene and *SfiIA* and *SfiIB* cloning sites had been
148 introduced. For each soil cDNA library, recombinant plasmids were introduced into electro-
149 competent *E. coli* cells (MegaX DH10B™ T1R Electrocomp™ cells, Invitrogen, Thermo
150 Fisher Scientific, Illkirch, France) and at least 2 10⁶ kanamycin resistant bacterial colonies
151 growing on agar medium were collected and pooled to constitute two soil cDNA plasmid
152 libraries after alkaline lysis extraction (Sambrook and Russell 2001).

153 *Yeast strains, media, and culture methods*

154 Environmental cDNAs encoding sugar transporters were selected for their capacity to restore
155 growth on mannose or xylose of yeast mutant strains deleted of their monosaccharide
156 transporters. For mannose, we used the EBY.VW4000 *S. cerevisiae* mutant strain (*MATa*
157 *leu2-3, 112 ura3-52 trp1-289 his3-Δ1 MAL2-8c SUC2 Δhxt1-17 Δgal2 stlΔ::loxP agt1Δ::loxP*
158 *mph2Δ::loxP mph3Δ::loxP*) unable to use mannose, but also glucose, fructose and galactose
159 as carbon sources (Wieczorke et al. 1999). For xylose, we used the EBY.X1-2 *S. cerevisiae*

160 strain which is the EBY.VW4000 strain in which had been introduced plasmids p414-TEF.X1
161 and p25G.X2 containing the *XYL1* and *XYL2* genes from *Scheffersomyces stipitis*, respectively
162 (Young et al. 2011). These two genes code for a xylose reductase (*XYL1*) and a xylitol
163 dehydrogenase (*XYL2*), which are the two enzymes activities, absent from *S. cerevisiae*,
164 needed for the use of xylose as a carbon source. The EBY.VW4000 strain was grown at 30°C
165 in liquid or on solid yeast nitrogen base medium (YNB, 6.7 g.l⁻¹ without amino acids, pH 5.9)
166 supplemented with (in g.l⁻¹) adenine, 0.01; arginine, histidine and methionine, 0.02; lysine,
167 tryptophan and uracil, 0.04; threonine and tyrosine, 0.05; isoleucine, leucine and
168 phenylalanine, 0.06; valine, 0.15 and maltose, 20. Selection of EBY.VW4000 transformants
169 expressing monosaccharide transporters was performed on solid YNB medium lacking uracil
170 and supplemented with amino acids and mannose as sole carbon source. Concerning the
171 EBY.X1-2 strain, it was grown at 30°C in liquid or on solid YNB medium lacking leucine and
172 tryptophan and supplemented with 20 g.l⁻¹ maltose. Selection of EBY.X1-2 transformants
173 expressing xylose transporters was performed on solid YNB medium lacking uracil, leucine
174 and tryptophan and supplemented with xylose as sole carbon source. The wild-type *S.*
175 *cerevisiae* CEN.PK2-1C and its mutant derivatives (EBY.VW4000 and EBY.X1-2) were
176 complemented with the empty pDR196-*SfiIA/B* plasmid to use them as positive and negative
177 controls during growth rate measurements on different monosaccharides, respectively.

178 *Selection of fungal sugar transporters by functional yeast complementation*

179 Both soil cDNA plasmid libraries (from spruce and beech forest soils) were used to transform
180 *S. cerevisiae* using a standard lithium acetate protocol (Rose and Broach 1990). Concerning
181 the functional screening on mannose, EBY.VW4000 transformed yeast cells were selected
182 directly on a solid yeast nitrogen base (YNB) minimal medium supplemented with mannose
183 (0.2 or 0.5%) and amino acids but lacking uracil. In the case of xylose-transporter screening,
184 EBY.X1-2 transformed yeast cells were first plated on a solid YNB minimal medium

185 supplemented with 2% maltose and amino acids but lacking uracil, leucine and tryptophan.
186 Then, after 3 days of growth, uracil prototrophic yeast colonies were collected, washed by
187 centrifugation and resuspended in sterile water before being plated on solid YNB minimal
188 medium supplemented with 2% xylose and amino acids but lacking uracil, leucine and
189 tryptophan. Plasmids from the yeast transformants were extracted using the Zymoprep Yeast
190 Plasmid Miniprep I (Zymo Research, Irvine, CA, U.S.A.) and used to transform One Shot
191 TOP10 chemically competent *E. coli* (Invitrogen) to kanamycin resistance. After plasmid
192 extraction (NucleoSpin Plasmid kit; Macherey Nagel, Hoerd, France), inserts were Sanger
193 sequenced using primer PMA (5'-CTCTCTTTTATACACACATTC-3') and additional
194 internal primers. The different fungal sugar transporters retrieved from spruce and beech soil
195 cDNA libraries were annotated spS1 to spS12 and spB1 to spB7, respectively. Both yeast
196 mutant strains (EBY.VW4000 and EBY.X1-2) were further transformed with all of these
197 different environmental fungal sugar porters to study their capacity to transport different C6
198 and C5 monosaccharides. Sequences of environmental transporters that support the findings
199 of this study have been submitted to the EMBL database with accession codes LR862110-
200 LR862128.

201 *Phenotypic characterization of yeast transformants and growth rate measurements*

202 The monosaccharide utilization profile of EBY.VW4000 transformants was performed using
203 drop-test assays on solid YNB minimal medium (Rose and Broach 1990) and
204 electrophysiology assays (Damon et al. 2011). Only mannose, fructose and glucose could be
205 tested using drop-test assays as other sugar sources are either not assimilated or naturally
206 transported by the EBY.VW4000 mutant strain. Due to the complexity of the methodological
207 approach, electrophysiological analyses were only performed with potential mannose specific
208 transporters (spS1 and spS2), found by screening of EBY.VW4000 cells, to test the transport
209 of sugar constitutive of cellulose and hemicelluloses (cellobiose, glucuronic acid, glucose,

210 fucose, galactose, rhamnose, arabinose, mannose, fructose and xylose). Additionally, maltose
211 and two disaccharides abundantly found in plant tissues (mannobiose and sucrose) were also
212 tested using these electrophysiological assays. Procedures used to characterize by voltage-
213 clamp recordings the sugar transporters spS1 and spS2 expressed in *Xenopus laevis* oocytes
214 are detailed in Online Resource 1.

215 Growth rates of the transformed EBY.VW4000 yeast strains were measured in triplicate using
216 a Bioscreen C system (Growth Curves USA, Piscataway, NJ) equipped with a wide-band
217 filter (420 to 580 nm) recommended for optical density (OD) measurements (Young et al.
218 2011). A 1 μl inoculum of fully-grown cultures diluted to $5 \cdot 10^6$ cells. ml^{-1} , was added to each
219 well filled with 250 μl of YNB minimal medium supplemented with amino acids but lacking
220 uracil and with 0.1%, 0.5% or 1% (w/v) of carbon source (either maltose, D-glucose, D-
221 fructose, D-mannose or D-galactose). The experiment was run 4 days at 30°C using a medium
222 amplitude and normal intermittent shaking (10s) and OD measurement every 10 min.

223 Inhibition of mannose transport by other non-assimilated carbon sources (either glucose or
224 fructose) was assessed in media containing 0, 0.1, 0.5 or 1% mannose and supplemented with
225 either 0 or 1% of either glucose or fructose. Growth rates of EBY.X1-2 transformants in
226 presence of xylose as carbon source were tested in liquid YNB minimal medium
227 supplemented with 1% xylose as described by Colabardini et al. (2014). Yeast transformants
228 were first grown on plates containing solid YNB minimal medium supplemented with 2%
229 xylose. After 21 days of incubation at 30°C, colonies were transferred in 3 ml of YNB
230 minimal medium supplemented with 1% maltose. After 24 h of culture at 180 rpm and 30°C,
231 $1.5 \cdot 10^6$ yeast cells were washed with water and transferred in 3 ml of YNB minimal medium
232 supplemented with 1% xylose. Yeast-cell growth was estimated once every 2-3 days during a
233 period of 21 days by measuring the absorption at 600 nm.

234 Exponential growth rates were analyzed using R (version 3.5.3) and the package
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2 235 Growthcurver (Sprouffs et al. 2016). Growth data were fitted to a standard logistic equation
3
4 236 and the Area Under the Curve (AUC) parameter was estimated with a 95% confidence
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7 237 interval to be able to detect any significant change between each condition (P value < 0.05).
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9 238 *Phylogenetic analyses*

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11 239 Environmental transporter sequences were compared to closest reference sequences retrieved
12
13 240 from public databases as well as to all sequences of fungal sugar transporters that have been
14
15 241 functionally characterized. Sequences highly similar to the selected environmental sugar
16
17 242 transporters were identified by BLASTp searches in the GenBank database. For the
18
19 243 taxonomic assignment of environmental sequences, the ten best BLAST hits were selected.
20
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22 244 Amino acid sequences were aligned using MUSCLE (Edgar 2004). Maximum-likelihood
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24 245 (ML) phylogenetic trees were generated with PhyML v.3.0 (Guindon et al. 2010) using the
25
26 246 LG substitution model (Le and Gascuel 2008) as implemented in SeaView v.4 (Gouy et al.
27
28 247 2010). Robustness of tree topologies was assessed by bootstrap analysis (1000 replicates).
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31 248 Tree was drawn using FigTree v.1.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).
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249 **Results**

250 *Phylogenetic and functional diversity of characterized fungal sugar porters (SPs)*

251 From more than 70 literature references, we identified 123 fungal sugar transporters,
252 belonging to the SP family (TC 2.A.1.1) that had been functionally characterized (Online
253 Resource 2). A majority (109) of these genes originated from 30 *Ascomycota* species with an
254 overrepresentation of *Saccharomycotina* yeasts (15 species), among which *S. cerevisiae* is
255 represented by 22 genes. The database included nevertheless two transporters from the
256 *Glomeromycotina* (2 species) and 12 from the *Basidiomycota* (7 species).

257 In a majority of cases functional characterization consisted in the expression of the
258 corresponding fungal genes in a *S. cerevisiae* mutant deleted of its endogenous transporter
259 genes followed by growth tests of the corresponding recombinant strain on one or several
260 sugars that could no longer be assimilated by the yeast mutant (Young et al. 2011; Online
261 Resource 2). Based on this often-fragmentary functional information in terms of number and
262 diversity of tested substrates, we classified the transporters as monosaccharide (M) or
263 oligosaccharide (O) transporters. Monosaccharide transporters encompassed those capable of
264 transporting C5 or C6 monosaccharides but also structurally related molecules such as polyols
265 (e.g. glycerol, mannitol, *myo*-inositol or sorbitol), gluconic, galacturonic or quinic acids.
266 Oligosaccharides tested as potential substrates were mostly disaccharides (e.g. sucrose,
267 cellobiose, xylobiose, maltose or lactose) and more rarely tri- (e.g. cello- or maltotriose) or
268 tetraoses (cellotetraose). In five cases, transporters had been shown to transport both mono-
269 and oligosaccharides (MO transporters). This is the case of the *Kluyveromyces lactis* *LAC12*
270 that transports both lactose and galactose Riley et al. 1987; Baruffini et al. 2006), but also of
271 the *AGT1*, *MPH2* and *MPH3* “maltose transporters” of *S. cerevisiae* whose deletions were
272 needed to suppress monosaccharide transport in the EBY.VW4000 mutant strain (Wieczorke
273 et al. 1999). Besides their substrate (sugars) specificities, fungal SPs have also been shown to

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274 function as either facilitators (e.g. Jordan et al. 2016) or H⁺ symporters (e.g. Dos Reis et al.
275 2013) co-transporting a proton along with a sugar molecule. Since the transport mode was
276 very rarely assessed for published transporters, this information was not analyzed further.

277 Despite the fact that almost all "M" transporters had not been tested on
278 oligosaccharides and inversely regarding "O" transporters on monosaccharides (Online
279 Resource 2), this simple classification was well supported in a global phylogenetic analysis of
280 the characterized transporter sequences that grouped almost all "O" and "M" transporters in
281 distinct and well-supported clades (bootstrap values >80%; Fig. 1). The very few exceptions
282 to this rule may require additional functional data to further refine their true substrate
283 specificity prior to speculate about occasional reversal of "O" transporters to transport
284 monosaccharides. At least in the case of monosaccharide "M" transporters, sequences
285 originating from a single species, belonging to *Ascomycota* (e.g. the *Saccharomycotina* yeast
286 *Yarrowia lipolytica* or the *Pezizomycotina A. nidulans*) or to *Basidiomycota* (e.g. the
287 *Agaricomycotina Laccaria bicolor*) were often distributed in different clades suggesting that
288 divergences between these sequences occurred at least prior to the divergence between
289 *Ascomycota* and *Basidiomycota*. Besides specialization towards mono or oligosaccharides,
290 functional data available for most transporters (Online Resource 2) are however insufficient to
291 attribute a more specific specialization in terms of transported substrates to most clades
292 identified in the global phylogenetic tree. Nevertheless, we observed that six of the seven
293 *myo*-inositol transporters included in the tree, originating from three *Ascomycota* and one
294 *Basidiomycota* species respectively, grouped together to form a homogeneous clade (clade
295 VII, Fig. 1). This is also the case for (i) four transporters, from four filamentous *Ascomycota*
296 species, known to transport charged, acidic molecules, either quinic acid, galacturonic acid or
297 4-deoxy-L-erythro-5-hexoseulose uronate, a constituent of alginate (clade IX) or (ii) two
298 glycerol transporters from the yeasts *S. cerevisiae* and *Debaryomyces hansenii* (clade XI).

299 Regarding monosaccharide transporters, 52 of them had been tested on at least the four
1
2 300 C6 sugars D-glucose, D-galactose, D-mannose and D-fructose that share the same molecular
3
4 301 formula (C₆H₁₂O₆). While 25 of them (48%) transported all four sugars and 42 of them (81%)
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7 302 glucose, only five of them were apparently specific for one of these four sugars, three for
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9 303 fructose, one for mannose, one for galactose and none for glucose (Online Resource 2).
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11 304 Regarding xylose transporters, widely studied in the context of plant biomass utilization, of
12
13 305 the 24 xylose transporters studied for their capacity to transport at least one C6
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15 306 monosaccharide, only one of them (*XltB* from *A. niger* tested on mannose, glucose, galactose
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17 307 and fructose) was seemingly specific for xylose (Sloothaak et al. 2016). This analysis suggests
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19 308 that strict specificity towards one of the most common sugar constitutive of plant biomass is a
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21 309 rare, if not inexistent, feature among fungal SPs.
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26 310 Focusing on the transport of mannose, we observed a close association between
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28 311 mannose and glucose transport (Online Resource 2). Indeed, of the 47 published mannose
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30 312 transporters tested on glucose, only two (both from the yeast *Y. lipolytica*) could not transport
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32 313 glucose. Conversely, of the 49 published glucose transporters tested on mannose, only five
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34 314 (from *S. cerevisiae*, *Neurospora crassa* and *Piriformospora indica*) could not transport
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36 315 mannose.
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41 316 *Phylogenetic diversity of sugar transporters isolated from soil cDNA libraries*

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43 317 The screening of two forest soil metatranscriptomic cDNA libraries for the functional
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45 318 complementation of the growth defect of the EBYVW4000 yeast mutant on mannose-
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47 319 containing media led to the isolation of 15 different cDNAs; 11 from the spruce (*P. abies*, spS
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49 320 genes and proteins) library and 4 from the beech (*F. sylvatica*, spB genes and proteins) one. A
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51 321 similar screening on xylose-containing media using the same yeast strain expressing the *S.*
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53 322 *stipitis* xylose catabolic pathway led to the isolation of 4 cDNAs; 1 from the spruce library
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55 323 and 4 from the beech one. Eighteen of these 19 transporters were unambiguously attributed to
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324 the SP family (TCDB #2.A.1.1). In blast searches against the curated SwissProt or TCDB
325 databases, their best hits all belonged to this family and they were all predicted to have 12
326 transmembrane domains that displayed characteristic signature sequences for this SP family
327 (Online Resource 3). Conversely, the spB4 transporter, that also possessed 12 putative
328 transmembrane domains, displayed high similarity values to members of the so-called
329 “Fucose: H⁺ Symporter” (FHS) family (TC 2.A.1.7). Members of this FHS protein family
330 have been experimentally shown to transport different monosaccharides in *Bacteria*, including
331 L-fucose in the case of the *E. coli FucP* transporter (Gunn et al. 1994). Although members of
332 this family have been predicted in the proteomes of many (but not all) fully sequenced fungal
333 species, only the *RhtA* gene from *A. niger* has been demonstrated to encode a L-rhamnose
334 transporter (Sloothaak et al. 2016).

335 A phylogenetic analysis that incorporated all 19 transporters and their 10 most similar
336 sequences identified in blast searches against the generalist GenBank nr database suggested
337 that all these 19 environmental sequences most likely originated from *Fungi*. Ten of them
338 could originate from *Ascomycota* and eight from *Basidiomycota* (Fig. 2). Regarding the
339 divergent spB4, although most likely of fungal origin, its exact taxonomic placement could
340 not be precisely ascertained as similar sequences originated from *Basidiomycota* but also
341 *Chytridiomycota* (namely *Gonapodya prolifera*, belonging to the *Monoblepharidomycetes*;
342 Fig. 2). BLASTp searches for spB4 homologs in fully sequenced fungal genomes showed that
343 homologous sequences were absent in numerous fungal species and extremely rare in specific
344 taxonomic groups such as the *Saccharomycotina* yeasts where a single sequence was
345 identified in the genome of *S. stipitis*. A preliminary phylogenetic analysis using sequences
346 from different fungal phyla, as well as from *Bacteria*, placed the spB4 environmental
347 sequence, with other sequences from *Chytridiomycota*, *Ascomycota* and *Basidiomycota* in a
348 clade (Online Resource 4) associated to a second clade encompassing bacterial sequences, as

349 well as a sequence from the *Mucoromycotina Mucor circinelloides*. Sequences identified in
1
2 350 the genomes of fungal species extensively studied for sugar transport (*Aspergillus* sp., *N.*
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4 351 *crassa*, *Trichoderma reesei*, *S. stipitis*, but also *Tuber melanosporum*; Online Resource 1),
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6
7 352 including the *RhtA* rhamnose transporter from *A. niger*, grouped together to form another
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9 353 distinct clade (Online Resource 4).

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12 354 When all environmental sequences were incorporated in the phylogenetic tree that
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14 355 encompassed nearly all characterized fungal SPs, we observed that all of them (except the
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16 356 divergent spB4 sequence used to root the tree) fell in clades of monosaccharide "M"
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19 357 transporters (Fig. 1). Furthermore, more than half (11) of the environmental sequences fell in
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21 358 a single clade (clade III, Fig. 1) that encompassed exclusively characterized proteins from
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23 359 *Ascomycota* species although five of the environmental sequences attributed to this clade were
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25 360 predicted to be from *Basidiomycota* (spS1, S2, S7, B2 and B7; Fig. 2).

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27 361 *Monosaccharide utilization profiles of sugar transporters isolated from soil cDNA libraries*

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29 362 Substrate range and preferences for D-monosaccharides was assessed by measuring the
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31 363 growth of the recombinant EBYVW4000 yeast strain constitutively expressing each of the
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33 364 environmental transporters on different concentrations of either fructose, galactose, glucose
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35 365 and mannose as the sole C sources in both liquid (Fig. 3) and solid (Online Resource 5)
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37 366 media. Additionally, growth of the recombinant EBY.X1-2 yeast strain expressing each of the
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39 367 environmental transporters in combination with the *S. stipitis* xylose assimilation pathway
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41 368 was assessed on a medium containing 10 g.l⁻¹ of xylose as sole carbon source (Online
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43 369 Resource 6). Regarding the use of C6 sugars a great variability was observed among
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45 370 environmental transporters. While for each transporter, mannose was always the best sugar, or
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47 371 among the best, in terms of final biomass yield at the end of the culture period (4 days), this
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49 372 yield was particularly low for several transporters (namely spB4, spS2 and spS7) on all of the
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51 373 tested concentrations of the different sugars. This may be the result of improper expression of
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374 these proteins in yeast (as already reported for sugar transporters by e.g. Dreyer et al. 1999;
375 Wieczorke et al. 2003) or may suggest that in vivo, in their respective fungal species, these
376 transporters may preferentially transport other sugars.

377 While several transporters could be categorized as relatively generalists (e.g. spB2,
378 spS4, spS8, spS9 or spS11), leading to comparable growth rates on all four C6 sugars tested,
379 others had a more restricted substrate range. Noticeably, five environmental transporters
380 (spB3, spB4, spS1, spS2 and spS7) did not allow growth of the recombinant yeasts on all
381 three tested concentrations of glucose (particularly well visible in drop tests on solid media,
382 Online Resource 5). This proportion of "glucose negative" environmental transporters among
383 "mannose positive" ones (26%) is significantly higher (Chi2 test, $P < 0.01$) than the proportion
384 observed among published transporters (two in 47; 4%). Among these five SPs, the
385 phylogenetically related spS2 and spS7 ones (Fig. 2) were seemingly mannose specific in
386 both liquid and solid cultures. However, both spS2 and spS7 were among the transporters for
387 which the final biomass yield was always low irrespective of the monosaccharide added to the
388 culture medium. Altogether, clustering of environmental transporters according to their
389 substrate range, deduced from the growth of the recombinant EBYVW4000 strain on different
390 concentrations of the four C6 monosaccharides (Fig. 3) demonstrated an absence of
391 correspondence between substrate preferences and phylogenetic proximity of the primary
392 sequences (Fig. 1 and 2).

393 As already reported in the literature, growth on xylose of recombinant yeast strains
394 expressing a heterologous xylose catabolic pathway is intrinsically low (Tran Nguyen Hoang
395 et al. 2018). We could nevertheless show that 18 out of the 19 environmental transporters
396 supported growth of this strain on xylose (Online Resource 6). Furthermore, all of these
397 proteins harbored the amino-acid motif "G-G/F-XXX-G" (where X represents a variable, but
398 usually non-polar, amino acid residue) in the first predicted transmembrane domain (Online

399 Resource 3). According to Young et al. (2014), this motif represents a signature for xylose
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2 400 transport in SPs. Only the transporter spB4 belonging to FHS family did not support xylose
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4 401 assimilation at all and did not present this xylose specific amino-acid motif (Online Resource
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7 402 3).

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9 403 To further analyze substrate range and specificity of the environmental transporters,
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11 404 we hypothesized that they could function as symporters and two of them (spS1 and spS2
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13 405 featuring different substrate specificities in growth tests) were expressed in *X. laevis* oocytes
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15 406 to measure electrophysiological responses in presence of mono- or disaccharides including
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17 407 several sources (e.g. L-C5 or L-C6 monosaccharides, cellobiose or mannobiose) that are not
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19 408 assimilated by the wild-type *S. cerevisiae*. The selected transporters were spS1, which
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22 409 supported good growth on mannose, moderate growth on fructose, galactose and xylose and
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25 410 no growth on glucose and spS2 supporting poor growth on all tested C6 sugars (Fig. 3).
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28 411 Transport of mannose was confirmed for both selected transporters as expected from the yeast
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31 412 complementation assay (spS1, n=24, N=7; spS2 n=16, N=7; where n is the number of studied
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33 413 oocytes from N different batches) in test solutions complemented with 10 mM mannose at pH
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36 414 5.5 (Fig. 4). When applying hyperpolarizing voltage pulses, negative currents of up to several
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39 415 100 nA were induced dependent on the applied potential, thus indicating that both spS1 and
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41 416 spS2 indeed functioned as sugar/ion co-transporters (Fig. 4A,B). Current induction by
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43 417 mannose was not observed in water-injected control oocytes (n=4, N=3) and was reversible in
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45 418 transporter-expressing oocytes, as perfusion with control solution reduced the substrate
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48 419 specific currents (reversibility was tested for all recorded currents). These sugar-specific
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51 420 negative currents would correspond to cation influx (or anion efflux). The observed currents
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53 421 could be shown to be dependent on external pH (i.e. H⁺ concentration) as no currents were
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56 422 induced with mannose at pH 7.5 (n=3, N=2; Fig. 4C) indicating influx of protons and thus H⁺-
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58 423 mannose symport. Several sugar transporters have been described to function as H⁺-sugar
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424 symporters (Bush 1990; 1993; Wolf et al. 1991; Boorer et al. 1996; Lemoine et al. 1996; Zhou
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2 425 et al. 1997; Rottmann et al. 2016). Amplitudes of current induction varied between oocytes
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4 426 probably because of different expression levels in oocytes and oocyte batches. Interestingly,
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7 427 both transporters differed clearly with respect to transport of glucose (Fig. 4C). In agreement
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10 428 with growth measurements, the transporter spS1 did not transport glucose (n=10, N=4;
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12 429 Fig. 4C) whereas spS2 mediated undoubtedly glucose transport (n=6, N=5; Fig. 4B,C). In
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14 430 contrast, fructose was never transported by spS2 (n=6, N=5; Fig. 4C) but partly by spS1 (n=5,
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16 431 N=3; Fig. 4A,C). However, first experiments suggested that spS1 did not transport fructose
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19 432 (n=4, N=3) most probably by an inhibitory effect of the non-transported glucose due to the
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22 433 sequential arrangement of the tests. This result suggests that glucose might bind to the spS1
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24 434 transporter without inducing currents, thus hindering transport of other substrates. The
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27 435 observed differences for the transport of glucose and fructose for the two tested mannose
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29 436 transporters spS1 and spS2 underline the specificity of such transport systems. Interestingly,
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32 437 both mannose transporters mediated currents in oocytes only for D-mannose but not for L-
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34 438 mannose (Fig. 4C; spS1 n=3, spS2 n=4) pointing to highly specific structural requirements
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36 439 needed for binding or transport. Further tests of substrates with either D- or L-configuration
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39 440 were pooled and confirmed the structural substrate specificity. The “L-pool” with L-
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41 441 arabinose, L-rhamnose, and L-fucose did not induce any current (spS1 n=5, spS2 n=1). The
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44 442 “D-pool” with D-galactose, D-xylose, and D-glucuronic acid provoked unfortunately
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46 443 endogenous currents also in control oocytes, so that these three substrates had to be tested
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49 444 separately. In fact, D-glucuronic acid destabilized oocytes, even control ones, and could not
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51 445 be tested. However, in agreement with growth measurements, D-galactose and D-xylose
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54 446 induced currents for both transporters (n=3, each; Fig. 4C). In agreement with the
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56 447 phylogenetic placement of the spS1 and S1 transporters among monosaccharide (M)
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58 448 transporters (Fig. 1), four tested disaccharides (maltose (n=5, each), sucrose (spS1 n=3, spS2
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2 449 n=4), mannobiose (n=4 each), and cellobiose (n=4 each)) did not activate any currents in
3 450 oocytes expressing the two transporters.

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5 451 Glucose inhibition of transport of other monosaccharides by SPs that do not transport
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7 452 glucose, as suggested here in the oocyte experiment for spS1, has been repeatedly reported in
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9 453 the literature (Subtil and Boles 2012; Farwick et al. 2014). We evaluated this phenomenon, as
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11 454 well as potential inhibition by fructose, for five environmental transporters (spS1, spS2, spS7,
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13 455 spB3 and spB6) that did not support significant growth on any concentration of both glucose
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15 456 and fructose. For all five cases, we observed that in the presence of 10 g.l⁻¹ of either glucose
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17 457 or fructose in the culture medium, the EBYVW4000 strain expressing the corresponding
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19 458 transporters failed to grow on either low (1 g.l⁻¹), medium (5 g.l⁻¹) or high (10 g.l⁻¹)
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21 459 concentrations of mannose (Online Resource 7).
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460 Discussion

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2 461 The compilation of possibly all fungal SPs characterized thus far and their inclusion in a
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4 462 phylogenetic context support earlier observations, made on more fragmentary datasets, of a
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7 463 clear separation between mono- and oligosaccharide SPs in the Fungi (e.g. Peng et al. 2018)
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10 464 However, the present analysis did not address the issue of potentially multiple origins of
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12 465 either mono- or oligosaccharide clades of SPs in the *Fungi*. The presence, in several of the
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14 466 clades, of transporters from both the *Basidiomycota* and *Ascomycota* and even from the
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17 467 *Glomeromycotina* suggests that the corresponding clades originated early during the
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19 468 diversification of the *Fungi*. Alternatively, this distribution of transporters across the
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22 469 phylogenetic tree could also be the results of horizontal gene transfers between species
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24 470 belonging to different clades as demonstrated for other transporter genes (Slot et al. 2007;
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27 471 Coelho et al. 2013).

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29 472 Confrontation of the functional database to the SP phylogenetic tree suggested that
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31 473 few clades of "monosaccharide transporters" may feature functional specialization on specific
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34 474 substrates structurally related to monosaccharides, such as *myo*-inositol, acidic sugar
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36 475 derivatives or glycerol. This phylogenetic information could thus be used for the functional
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39 476 annotation of similar transporters from sequenced fungal genomes. As for the other clades of
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41 477 monosaccharide transporters, they encompass sequences that transport bona fide
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44 478 monosaccharides (either C5 or C6 sugars), but also sugar alcohols without any clear
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46 479 correspondence between clade identity and the exact nature of the transported molecules.
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49 480 While for several yeast species (e.g. *S. cerevisiae* or *Schizosaccharomyces pombe*), most of
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51 481 their monosaccharide SP genes seemed to originate from recent duplication events and belong
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53 482 to the same clade, other species (e.g. *A. nidulans*, *N. crassa*, or *Y. lipolytica*) seem to rely on
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56 483 different highly divergent SPs, belonging to different clades for their supply of
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485 A comprehensive analysis of the substrate range of monosaccharide transporters
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2 486 indicates that a large majority of the studied transporters accepts several sugars as substrates
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4 487 and that specificity towards one or two molecules seems to be an exception (Online Resource
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7 488 1). In this respect, occasional claims of a substrate-specific transporter often reflect the fact
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9 489 that a very limited number of potential substrates have been studied (e.g. Wang et al. 2016). It
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11 490 could however be argued that overexpression of a sugar transporter in the yeast *S. cerevisiae*,
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13 491 the most widely used approach to characterize such transporters from fungi (Young et al.
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15 492 2011), may overestimate the substrate range of the corresponding transporter. Overexpression
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17 493 may indeed allow significant influx of otherwise poorly transported substrates (Dreyer et al.
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19 494 1999) that would not normally support cell multiplication. These experimental artifacts can be
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21 495 partly solved using the more labor-intensive expression of transporters in *X. laevis* oocytes for
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23 496 electrophysiological measurements that also allows the evaluation of molecules that are not
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25 497 normally assimilated by *S. cerevisiae* (e.g. C5 or L-sugars) as potential substrates. Using this
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27 498 approach with two environmental SPs originally selected on mannose, we confirmed yeast
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29 499 growth assay observations by showing that both spS1 and spS2 transport mannose, xylose and
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31 500 galactose, and that they differ in their specificity towards fructose and glucose. Corresponding
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33 501 to the yeast assays, we also observed that one of them accepted fructose, the other one glucose
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35 502 as a substrate. Furthermore, we demonstrated that both transporters did not accept L-
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37 503 monosaccharides and di-saccharides as substrates.
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46 504 Although not being specific towards one or two potential substrates, many transporters
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48 505 are neither truly generalists and clearly do not transport several "common" monosaccharides.
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51 506 Overrepresentation of glucose-transporting monosaccharide transporters may reflect the
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53 507 widespread occurrence of this sugar in nature (albeit often as monomer of polysaccharides)
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55 508 and its centrality in carbon metabolism (Gunina and Kuzyakov 2015). Alternatively, it could
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57 509 also be hypothesized that overrepresentation of glucose-transporting transporters in databases
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510 may reflect a scientific bias as numerous fungal transporters were precisely selected for their
511 capacity to transport glucose. For the specific case of mannose, the high prevalence of
512 glucose-transporting porters that can also transport mannose could be explained by the
513 observation that, at least in yeast, genes encoding enzymes necessary for its use as a carbon
514 source (hexokinases and mannose-6-phosphate isomerases) are expressed in both glucose and
515 mannose-containing media. This suggests that these two sugars can be assimilated
516 simultaneously, with however a preference for glucose over mannose.

517 By selecting transporters from metatranscriptomes based on their capacity to transport
518 mannose, we tested the hypothesis that "mannose specific" transporters, or at least
519 transporters that preferentially transport mannose over glucose may be present in soil
520 organisms occasionally confronted to carbon sources with particularly high mannose content
521 (e.g. gymnosperm plant biomass or fungal necromass) (Lipke and Ovalle 1998; Schädel et al.
522 2010)). As previously observed in the case of oligopeptides (Damon et al. 2011), the
523 screening of environmental cDNA libraries for sugar transporters yielded genes from only
524 *Fungi*, although genes from other eukaryotic organisms were present among the studied
525 metatranscriptomes (Damon et al. 2012). Furthermore, all but one of the selected genes
526 encoded proteins that belonged to the SP family, suggesting that other sugar transporters
527 reported in fungal genomes may play a minor role in sugar assimilation by fungi. From a
528 taxonomic perspective, eight of the environmental transporters likely originated from
529 *Basidiomycota*, thus doubling the number of characterized sugar transporters from this fungal
530 phylum published thus far (Online Resource 1). From a phylogenetic perspective,
531 environmental SPs were distributed in several of the distinct clades that form this protein
532 family. However, more than half of them (11), from both *Basidiomycota* and *Ascomycota*, fell
533 in a single clade (clade III in Fig. 1) that, thus far, encompassed only published *Ascomycota*
534 sequences. This uneven distribution of environmental SPs across the global phylogenetic tree

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535 of this fungal protein family could originate from a preferential functional expression of these
536 structurally related proteins in yeast. It could also suggest that *Fungi* preferentially use SPs
537 from a limited number of clades for their supply in monosaccharides. This latter hypothesis
538 could be addressed in model organisms by measuring the relative expression levels and
539 contribution to monosaccharide utilization of endogenous sugar porter encoding genes
540 belonging to different evolutionary lineages. Finally, screening of soil metatranscriptomes
541 also yielded a highly divergent fungal sugar transporter sequence (spB4) that belonged to the
542 poorly studied “Fucose: H⁺ Symporter” (FHS) family (TC 2.A.1.7). In *Fungi*, only one
543 member of this FHS family able to transport monosaccharides was reported so far. In *A.*
544 *niger*, the related *RhtA* transports L-rhamnose and marginally D-fructose (Sloothaak et al.
545 2016). Since both rhamnose and fucose are deoxy sugars that occur in nature in the unusual
546 levorotary (L-) conformation, it could be hypothesized that fungal FHS family members are
547 specialized on these substrates and marginally accept other sugars as in the case of spB4 that
548 confers poor growth of recombinant *S. cerevisiae* on mannose and all other tested sugars. This
549 hypothesis could be tested by expression of this protein, as well as other homologous ones
550 found in fungal genomes, in *X. laevis* oocytes as performed for the spS1 and spS2 SPs.
551 Overall, our observations that result from the analysis of "environmental" sequences further
552 illustrate the power of functional genomics for quickly accessing the true diversity of specific
553 eukaryotic protein families (Damon et al. 2011; Marmeisse et al. 2017).

554 From a functional perspective, the analysis of environmental fungal sequences
555 reevaluates the known functional diversity of fungal SPs. It revealed the existence of
556 phylogenetically distinct transporters that allow mannose, but not glucose transport. This
557 lends support to the hypothesis that the presence of sugars other than glucose in the
558 environment may have led to the independent evolution of sugar transporters that
559 preferentially use mannose (and eventually other monosaccharides) over glucose.

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560 Furthermore, as an excess of glucose seemingly inhibits these transporters, this observation
561 further suggests that indeed they may only be operational in environments depleted of this
562 sugar.

563 "Other than glucose" (e.g. xylose) monosaccharide transporters have been searched for
564 the independent, simultaneous and non-competitive entry of glucose and other sugars in
565 fungal (e.g. yeast) cells for their simultaneous co-fermentation. Alternatively, these
566 transporters can also be used for the specific utilization of the "other than glucose"
567 monosaccharide as carbon source in a context where glucose is also present. One limitation to
568 this strategy is that transporters that do not transport glucose are often inhibited by this sugar
569 (Farwick et al. 2014; Li et al. 2016) which, possibly, clogs the entry pore of the protein. We
570 showed that this phenomenon may also affect mannose transport by mannose porters that do
571 not support glucose transport. Furthermore, we also show that this phenomenon is not
572 glucose-specific but can also be generated by other non-transported sugars such as fructose.
573 Several of the selected environmental transporters could thus be used for the co-fermentation
574 of mannose and other sugars or the specific use of mannose in the presence of other sugars,
575 providing that their inhibition by competing substrates could be relieved (Farwick et al. 2014).
576 In the case of xylose transporters, mutagenesis and directed evolution, which resulted in a
577 limited number of changes in the primary sequence, have been successfully employed to
578 render glucose-insensitive the corresponding transporters (Farwick et al. 2014; Li et al. 2016).

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1
2 580 The EBY.VW4000 *S. cerevisiae* mutant strain used to select environmental transporters was
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4
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6
7 582 Microbien program and the INRA métaprogramme M2E (project Metascreen).
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11
12 584 **Author contribution**

13
14 585 FB, PL and RM conceived and designed research. FB, LV, CG-G, SDZ, DM, JD and PL
15
16
17 586 conducted experiments. LF-T co-lead with PL the first part of the experiments performed by
18
19 587 FB. CG-G and SDZ performed and interpreted electrophysiological measurements. ML
20
21
22 588 contributed new reagents and analytical tools. FB, LV, SDZ, DM, DA, PL and RM analyzed
23
24 589 data. SDZ, PL and RM wrote the manuscript. All authors read and approved the manuscript.
25

26 590 **Conflict of interest**

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28
29 591 The authors declare that they have no conflict of interest
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31 592 **Ethical approval**

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34 593 Experiments using oocytes from *Xenopus* frogs have been performed accordingly to the
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36 594 French national rules for animal maintenance and experiments (agreement A34172044).
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802 **Legends of the Figures**

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2 803 **Fig. 1** Phylogenetic diversity of 104 functionally characterized fungal sugar transporters
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4 804 belonging to the Sugar Porter (SP) family. The maximum likelihood (PhyML) tree was rooted
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7 805 using the environmental spB4 protein that belongs to the “Fucose H⁺ symporter” family.
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9 806 Only bootstrap values (1000 replicates) above 80% are indicated and proteins were grouped in
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11 807 13 clades (I to XIII). Colors refer to the taxonomic origin of the proteins, red, *Ascomycota*;
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14 808 blue, *Basidiomycota* and black, *Glomeromycotina*. Proteins were named according to the
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16 809 species they come from and the category of molecules they transport; M, monosaccharides
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19 810 and related molecules; I, *myo*-inositol; O, di and oligosaccharides; S, sucrose; MO, both mono
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22 811 and disaccharides. Full correspondence between protein names, species names, amino acid
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24 812 sequences and accession numbers are given in Online Resource 3. Asterisks highlight
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26 813 environmental sequences selected from soil cDNA libraries. For legibility, we excluded from
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29 814 the final phylogenetic analysis several characterized sequences from the yeasts
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32 815 *Saccharomyces* sp. that in preliminary analyses were all closely related to the sequences from
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34 816 these species retained for the final analysis.

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36 817 **Fig. 2** Putative taxonomic origins of the 19 environmental sugar transporter proteins retrieved
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39 818 from soil metatranscriptomic cDNA libraries. The phylogenetic (PhyML) tree encompasses
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41 819 all 19 environmental sequences (asterisks) and their 10 best hits following BLASTp searches
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44 820 in the GenBank database (144 reference sequences in total). Colors refer to the taxonomic
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46 821 origin of the proteins, red, *Ascomycota*; blue, *Basidiomycota* and black, *Chytridiomycota*
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48 822 (*Monoblepharidomycetes*). Only bootstrap values (1000 replicates) above 80% are indicated.

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51 823 **Fig. 3** Growth of recombinant *S. cerevisiae* EBYVW4000 strain expressing each of the 19
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53 824 environmental transporter proteins (spS1-12; spB1-7) in liquid media containing 3
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55 825 concentrations (1; 0.5 or 0.1%) of 4 D(+)-monosaccharides (glu, glucose; gal, galactose, fru,
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58 826 fructose and man, mannose). “Area under the curves” were measured after four days’ growth
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1 827 in microplates and used to draw a heatmap where sugar transporters clustered according to the
2 828 growth profile of the recombinant yeast strains. Panels on the right illustrate the growth
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4 829 profiles on the different sugar concentrations (as well as on 1% maltose used as a positive
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7 830 growth control) for recombinant yeasts expressing 3 genes, each representative of one of the
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9 831 three main clusters observed in the heat map (spS1 for cluster 1, spS2 for cluster 2 and spS11
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11 832 for cluster 3).

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14 833 **Fig. 4** Mannose sugar porters spS1 and spS2 induce sugar-specific pH-dependent currents
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16 834 when heterologously expressed in *Xenopus laevis* oocytes. (A,B) Representative examples of
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19 835 mannose-induced currents in oocytes expressing spS1 (A) or spS2 (B), respectively, recorded
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22 836 by two-electrode voltage-clamp in presence of 10 mM mannose at pH 5.5. To a similar but
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24 837 slightly minor extent, also other substrates are transported, as fructose by spS1 (A), or glucose
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27 838 by spS2 (B). (C) Mean current amplitudes induced by different sugar substrates in oocytes
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29 839 expressing spS1 or spS2. Current amplitudes induced by different substrates have been
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31 840 determined at -100 mV after subtracting initially endogenous background currents recorded in
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34 841 control solution without the added substrate. Mannose-induced currents measured at pH 5.5
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36 842 (“mann” S1 n=24, N=7; S2 n=16, N=7) are shown to be pH-dependent as no current induction
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39 843 was observed at pH 7.5 (“mann 7,5” S1 and S2 n=3, N=2) and to be conformation-dependent
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41 844 (“Lmann” S1 n=3, S2 n=4). Glucose was transported by spS2 (“gluc” S1 n=10, N=4; S2 n=6,
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44 845 N=5), fructose by spS1 (“fruct” S1 n=5, N=3; S2 n=6, N=5). Galactose (“gal” S1 and S2 n=3)
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46 846 and xylose (“xyl” S1 and S2 n=3) induced currents by both transporters.
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Fig. 1

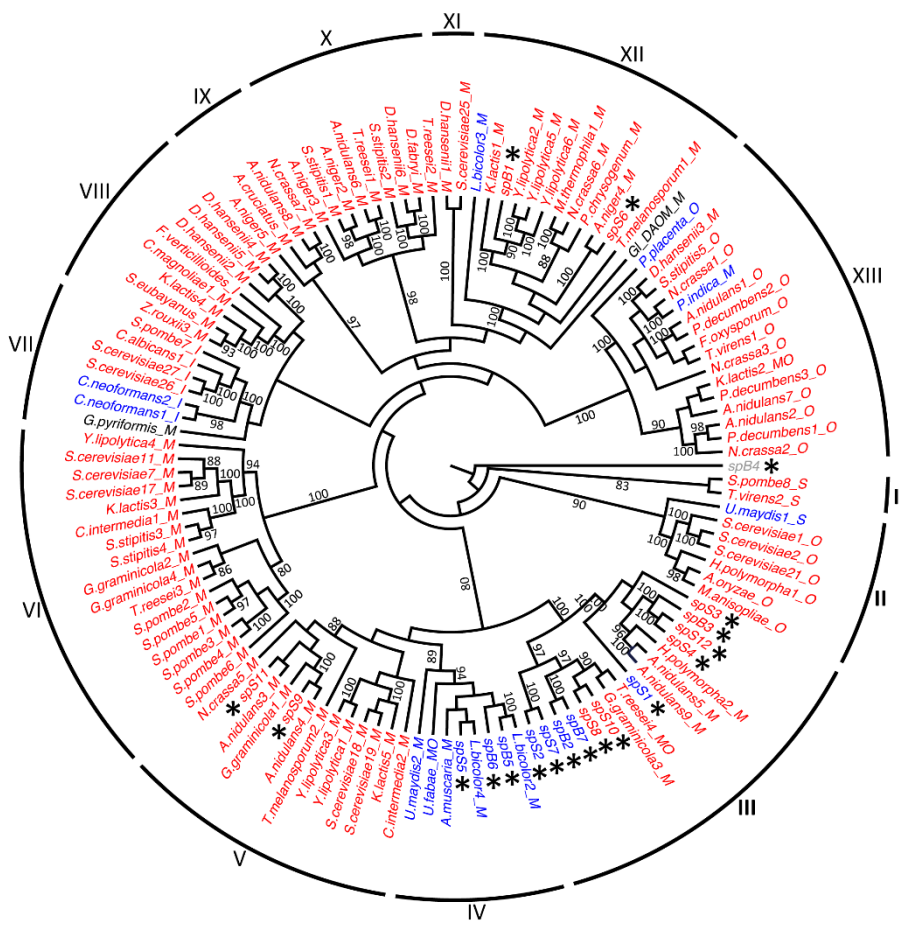


Fig. 2

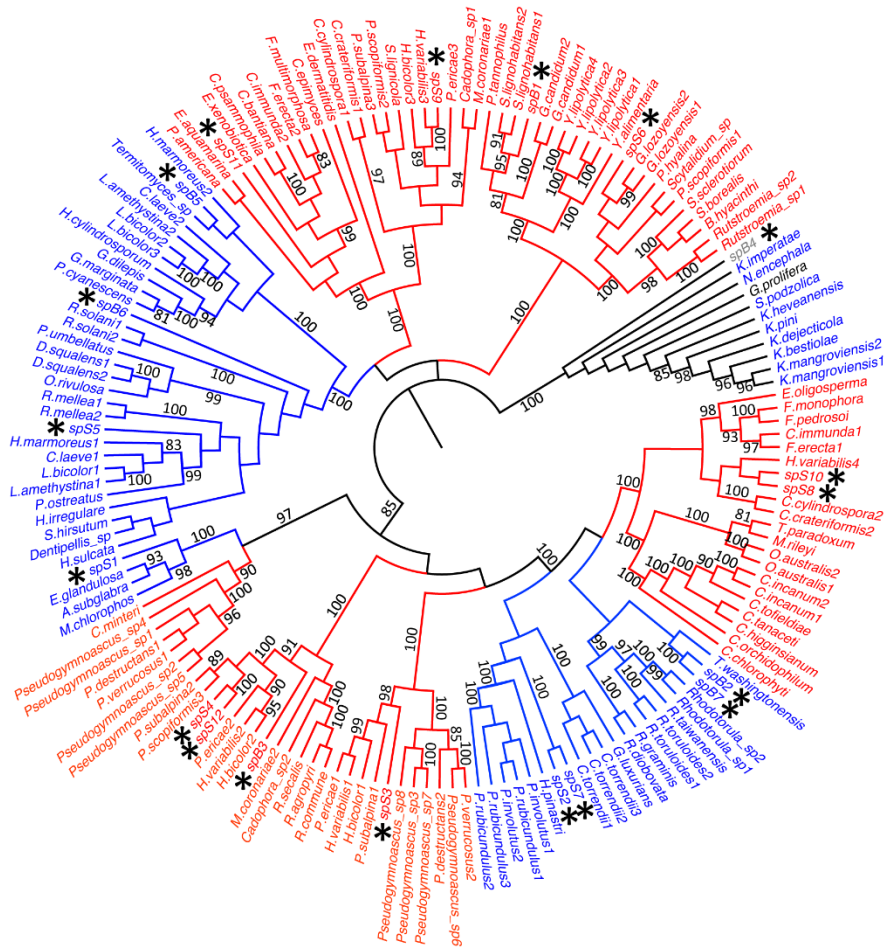


Fig. 3

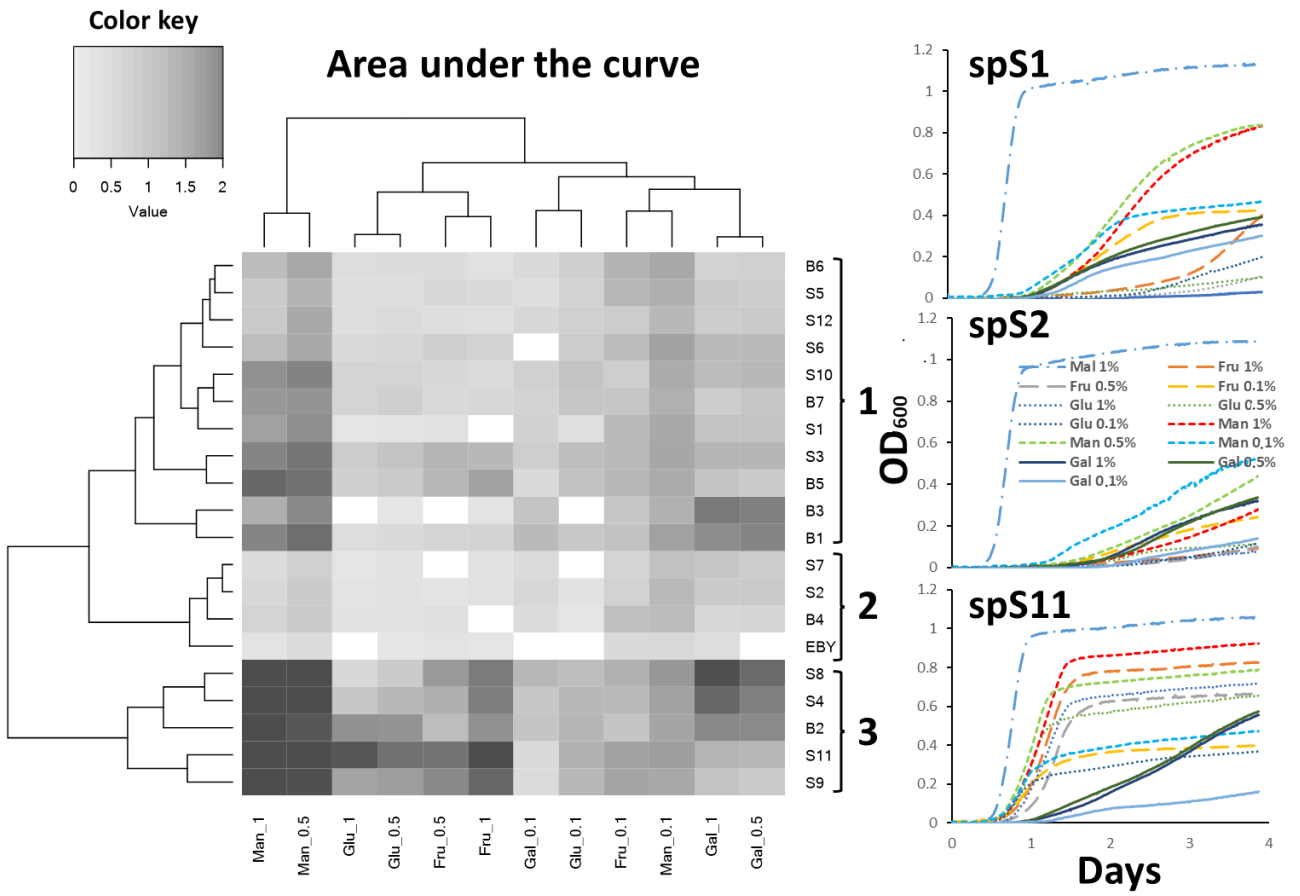
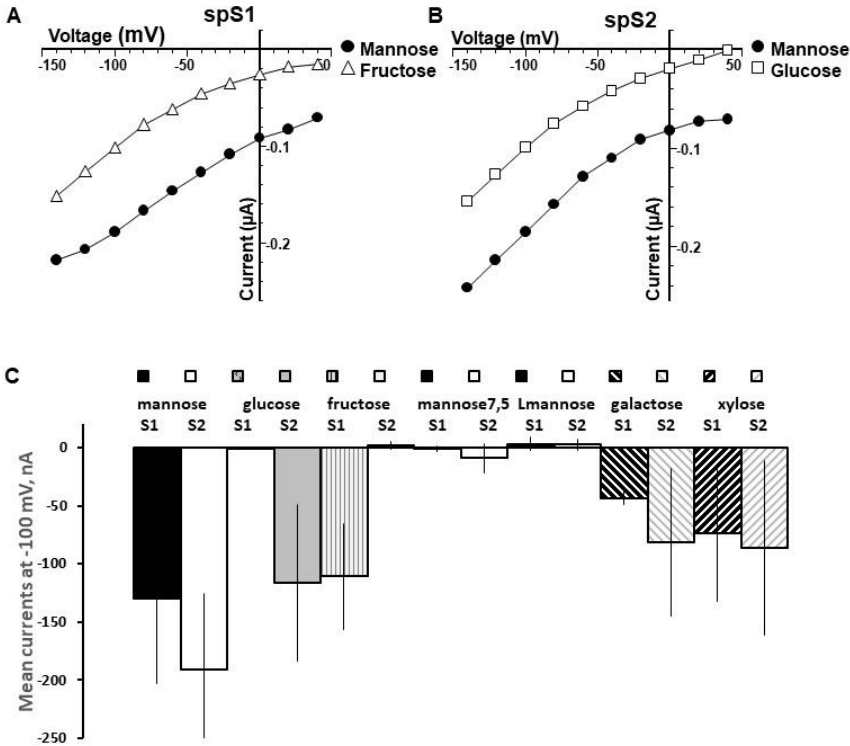


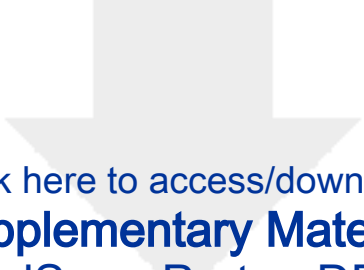
Fig. 4





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