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Supporting materials

FIG. S1. SDS-polyacrylamide gel electrophoresis of GFPP. Proteins were denatured at 100°C for 10 min in 0.1% SDS and 1% 2-mercaptoethanol before being loaded in a 4% (wt/vol) stacking gel and separated in a 15% (wt/vol) separation gel. The gel was stained with Coomassie bright blue R250. The molecular weight markers from Thermo Scientific are shown at the left side of the panel.

kDa Marker GFPP

200		1000	
150	-	1.000	
$\begin{array}{c} 120 \\ 100 \end{array}$		trinadi Inipade	
85 70 60	4		
50	-	660	
40			
30 25		ninsi Mash	
20			
15	-		
10			

FIG. S2. Multiple amino acid sequence alignment of GFPP from different organisms. Multiple alignments were performed with the ClustalW program using the BioEdit sequence alignment software. The corresponding nucleotide sequences encoding *M. alpina* GFPP has been deposited in the GenBank/EMBL database with Accession No. 1825641. Accession numbers for the other protein sequences above are: Human GFPP (AAH32308.1|), Mouse GFPP (AAI10553.1), *Dictyostelium discoideum* GFPP (XP_638295.1), *Medicago truncatula* (XP_003626575.1), *Bacteroides fragilis* GFPP (KFX74805.1), *Arabidopsis thaliana* GFPP (NP_563620.1), *Pisum sativum* UDPsugar pyrophosphorylase (BAD66876.1), *Leishmania major* UDP-sugar pyrophosphorylase (ABY79093.1), and human UDP-N-acetylglucosamine pyrophosphorylase (NP003106). The motif was boxed and other residues are marked with asterisks. GFPP M.alpina GFPP Mouse GFPP Human GFPP D. discoideum GFPP Medicago GFPP/FUK B.fragilis GFPP/FUK Arabidopsis USP Pisum sativum USP Leishmania major UDP-GlcNAc Human

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NSNNQAAPHPTGIDDLSQV QAVHA NLKH QRD KHPATAIPRTQA DPWD VYTAGTA SRKCZEN ISBCV/GL PQRAK H/D DFQS MAS PRATL SLRRSEB RCK	98 74 83 94 114 102 79 96 93 79
IG SG TCLV VV REHIPAD	158 136 144 175 188 167 169 153 156 139
EKIN Y HLLET PPERFITSATCID. SONTPEPSEPKPFTI ALMESTOICSTERY HELT WYTHDROHPROSALLLKCE FERKE- EKIA Y DEPSN REGL TCADIEL SVG SEYLARD PG HALHESSTOICSTERY HELT WYTHDROHPROSALLLKCE FERKE- EKIA Y DEPSN REGL TCADIEL SVG SEYLARD PG HALHESSTOICSTERY HELTSSOHROLEYRSCH FERF EKIA Y DEPLN REGL TCADIEL SUG FERIND PG HALHESSTOICSTERY HELTSV MENDER EKIA Y DEPLN REGL TCADIEL SUG FERIND PG HALHESSTOICSTERY HELT WY MENDER I ALMESCA GAF DES LT TIGUT PC HASYMIPDIASITITUTIED AS SEMI HALT VH NONYA SSLUNDLEXE- HERT HELT MENDER HERT REGLESSTOR FERIND PC HASYMIPDIASITITUTIED AS SEMI HALT VH NONYA SS	257 226 234 263 275 256 255 244 228 227
V KSVPRVI YPDPNDSAN	339 322 330 339 349 344 329 321 324 297
VOGRH, KOHLOAGVS DVIVILA KAYF, SANDAL AND	421 409 417 428 431 435 411 420 424 363
P YIEW VLAPEA THPCST VD-SC PRDA IPKSCVPTIC ORE VTFTFSLKDD IRRITPASTATSLS DEEAIASLDRLY IF RVPVSRI P VOIS SC G-PEISIGENCI S-SS IAKT VPAYSLCS SY AIN GH KYSTNYFG ODLIKKSKTLEDI ALGPCCFLSCD VM N VEIS SC G-PD S GENCI SG SY LITKALPAPSY VCSD SWN-RC KYATH VG ODLIKKSKTLEDI ALGPCCFLSCD VM N VEIS SC G-GFHRSLCI VGASIS DHOYCARDON ODCOCO COQOCI SSNYS IEIPSNSFIOTLSI SO STOTEGSCFLSCD VM N VEIS SC G-GFHRSLCI VGASIS DHOYCARDON ODCOCO COQOCI SSNYS IEIPSNSFIOTLSI SO STOTEGS	519 498 507 526 525 533 503 510 523 431
PHQAHPLTGATVEAPSAG SLWNAP/FEBARTAQ-SURLAUDRUDRI NCLIGAPAE/VCNPD/GREPGADITGVIB_INAARKAREYE AT KLPSCRNKIN SLWNAP/FEBARTAQ-SURLAUDRUDRI NCLIGAPAE/VCN	608 584 593 626 612 630 591 598 618 505

Fig. S3. Phylogenetic tree of amino acid hydroxylases from different organisms. The tree was constructed using the neighbor-joining method with ClustalW NJplot. The horizontal branch length is proportional to the amino acid substitution rate per site.



Figure S4. LC-MS chromatographs of GFPP reaction with the addition of MgCl₂ (C, D), MnCl₂ (E, F), KCl (G, H), CuCl₂ (I, J), CoCl₂ (K, L), FeCl₂ (M, N), CaCl₂ (O, P), ZnCl₂ (Q, R), NiSO₄ (S, T), and HgCl₂(U, V); LC-MS chromatographs of GFPP reaction with the addition of MgCl₂ and EDTA (W, X); Extracted ion chromatogram (XIC) of L-fucose-1-phosphate standard (A, m/z 243.03); XIC of GDP-L-fucose standard (B, m/z 588.08); XIC of L-fucose-1-phosphate (C, E, G, I, K, M, O, Q, S, U and W; m/z 243.03); XIC of the GDP-L-fucose (D, F, H, J, L, N, P, R, T, V and X; m/z 588.08).



Figure S5. The kinetic parameters of GFPP for L-fucose-1-phosphate.



Time (min)	Flow rate	В%
(11111)	(1111/11111)	
0	0.1	80
5	0.1	80
21	0.1	56
22	0.2	40
26	0.2	40
27	0.2	80
34	0.2	80
35	0.1	80

Table S2. Gradient elution of the chromatographic separation

Samples	Dry cell	GDP-L-fucose	Specific GDP-
	weight	concentration	L-fucose
	(g/L)	(mg/L)	content
			(mg / g cell)
Control	11.76±0.32	2.50±0.0047	0.21±0.0015
1day fucose (10 nM)	12.36±0.27	2.64 ± 0.0052	0.21 ± 0.0019
3days fucose (10 nM)	11.67±0.37	3.76±0.0053	$0.32{\pm}0.0014$
3days Mg ²⁺ (10 nM)	12.34±0.29	3.12 ± 0.0046	0.25 ± 0.0016
3 days fucose (1 nM) and Mg^{2+} (10 nM)	12.30 ± 0.32	2.68 ± 0.0049	$0.22{\pm}0.0015$
3 days fucose (5 nM) and Mg^{2+} (10 nM)	11.43±0.33	$2.92{\pm}0.0044$	$0.26{\pm}0.0013$
3 days fucose (10 nM) and $Mg^{2+}(10 nM)$	12.31 ± 0.37	7.02 ± 0.0049	$0.57{\pm}0.0013$
3 days fucose (20 nM) and $Mg^{2+}(10 nM)$	12.53±0.29	8.15 ± 0.0051	$0.65 {\pm} 0.0018$
3 days fucose (30 nM) and $Mg^{2+}(10 nM)$	12.62±0.35	8.58 ± 0.0052	$0.68 {\pm} 0.0015$

Table S3. Summary of GDP-L-fucose content in M. alpina.