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Supporting information for article:

Crown ether-mediated crystal structures of the glycosyltransferase *Pa*GT3 from *Phytolacca americana*

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Capsaicin



Resveratrol



m-Hydroxyl benzoic acid



Kaempferol



Apigenin

trans-p-Coumaric acid

ю

Daidzein



Aureusidin



Cyanidin



Betanidin



6-hydroxyflavone



Artepillin C

Figure S1

Structures of representative compounds glycosylated by *Pa*GT3 (Noguchi *et al.*, 2009; Ozaki *et al.*, 2012; Iwakiri *et al.*, 2013; Shimoda *et al.*, 2014).







Figure S2

a. Structure of *Pa*GT3 crystallized in presence of 15-crown-5. b. σ -A weighted $2mF_o$ - DF_c electron density map observed for 15-crown-5 ether at 1 σ . c. Residues of *Pa*GT3 around 15-crown-5 ether. The residues from molecule A and B are coloured light-green and yellow, respectively. Crown ether binds in such a way that the molecules of *Pa*GT3 are packed with nearly 2 fold rotation symmetry, hence residues are labelled only once.

PaGT3		$\xrightarrow{\beta_1}$	α1	$\beta 2$ $\beta 2$	α2 0000000000
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	1 MGAEPQQI MTTTTTKKE MSMSDINKNS MSQTTTNN MENKTETTVRRF MEHRKE MG <mark>N</mark> FAN R KE	10 HVLVIPFPIMAE ELIFIPAPGI HVAVLAFPFS RIILFPVPFC HVLAVPYPSC HVVMIPYPVC	20 IGHMIPTLDIARLF GHMVPHLDLTROJ GHLASALFFAKLI THAAPLLAVVRRI IGHIPFRQFCKRI GHINPLFKLAKLI GHINPLFKLAKLI	40 AARNVRATIITT LLRGATVTVVT TNHDKNLYITVF AAAAPHAVFSFF YSKGFSITIFHT HFKGLKTTLALT HLRGFHITFVNT	50 PLNAHTFTKAIE PKNSSYLDALRS CIKFPGMPFADS STSQSNASIFHD NFNKPKTSNYPH TFVFNSINPDLS EYNHKRLLKSRG
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	60 MGKKNGSPTII LHSPEHFKT.LI YIKSVLASQ.PQ SMHTMQCNI.KS FTFFFILDNDPQI GPISIATIS PKAFDGFTDFNFF	β3 70 HLELFKFPAQL LPFPSHPCIF QIQLIDLPEVE VDISDGVPEG DERISNLPTHG DGYDHG DGYDHG	η1 22 TT 80 SGVES SPPPQE	00 200000 90 ILEQALGSS LT EK .LQQLPLEAIVH LLKSPEFY LT F VFAGRPQED I EL PLAGMRIP II NE .GFETADS I D Y GDVSQDVP TL CQ	3 2000000 2000 FFKGVGLLREQ <mark>L MFDALSRLHDPL LESLIPHVKATI FTRAAPESFRQG HGADELRRELEL LKDFKTSGSKT SVRKNFLKPYCE</mark>
PaGT3 PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	α4 20202020 EAYLEKTRPN VDFLSRQPPSDLF KTILSNKVVG MVMAVAETGR LMLASEDEE ADITQKHQTSDNF LLTRLNHSTNVFF	β4 120 CLVADMFF DAILGSSFLS LVLDFFC VSCLVADAFI VSCLVADAFI VSCLVADAFI VTCLVSDCCM	α5 QQQQQQ 130 14 Q PWATDSAAKENTE SPWINKVADAPSIE VSMIDVGNEFGIE WFAADMAAEMCVA VFAQSVADSUNIE PWALDVAREFGIV ISPTIQAAEDPELF	β5 CRLVFHGTSFFSL SISFSISF SYLFLTSN.VGF WLPFWTAGPNSL RLVLMTSSLFNF YATPFFTQPCAVN NVLYFSSSACSL	α6 2020202020 160 CALEVVRLYEPH SIMVSLKNRQI SIMVJIDEIREK HAHVSLPQFDEL VVYLSYINNG. LNVMHFRSFVER
PaGT3 PaGT3 UDP89C1 UGT1IG1 VvGT1 UDP76G1 UDP74F2 UGT85H2	TT 170 KNVSSDEE EEVFDDSD GYLDPD GILPFKDESYLTN	β6 TT 180 .LFSLPLFPF LPINAF .REDELLNFI DKTRLE SLQLPI IGCLETKVUWI	$\begin{array}{c} \beta7 & \eta2 & \alpha7 \\ \bullet & 000 & 000 \\ 190 \\ 100 $	20 200 WKHEKAEGKTRL DRSFF ACFNKDGGYTAY GIVFGNLNSLFS DIKSAYSNWQILK FFSVSGSYPAYF FIRTTNPNDIML	α8 210 210 KLTKESELK NDLETATTE YKLAERFRD RMLHRMGQVLPK EILGKMIKQTKA EMVLQQFINFEK EFEIEVADRVNK
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	$\begin{array}{c c} \beta 8 & \eta 3 \\ \hline 220 & 2002 \\ SYGUVINSFYDU \\ SYGUVINSFYDU \\ TKGIVNTF5DU \\ SSGVIWNSFKDU \\ SSGVIWNSFKDU \\ ADFVLVNSF0DU \\ DTTLLNTFNEL$	COO COO COO COO COO COO COO COO	β9 240 25 240 25 25 25 25 25 25 25 25 25 25	η4 ο 260 SLCNRSTEDK.A LPFKAGV LDLKGQ TPPPVVP LTASSSS YLDQRIKSDTGY LKQTPQIH.QLD	270 QRGKQTSIDEHE DRGGQSSIPPAK PNPKLDQAQHDL NTTG LLDHDRT DLNLFESKDDSF SLDSNLWKEDTE
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	α10 280 280 CLKWLNSK.KKNS VSAWLDSCPEDNS ILKWLDEQPDKS CLOWLKER.KPTS VFOWLDQO.PPS CLNWLDTR.PCOS CLNWLESK.EPGS	β10 z 9 0 VFLCFGSTP VFLCFGSMGV VYISFGTVT VLVSFGSTS VVVNFGSTT VVVNFGSTT	COLOCOLOGICO COLOCOLOGICO COLOCOLOGICO COLOCICA CALCIA POLYEIAMA RETAEQIALAAA VSFGPSQIREIALO TPPPAEVVALSEA SEVDEKDFLEIARG QLINVQMELAS VMTPEQILEFAWG	β11 310 32 LEASGQEFIWVV LEASSVFIWAV LKHSGVRFIWS LEASRVPFIWS LOSKQSFLWVV VSN.,FSFLWVV LANCKKSFLWII	Q RNNNNNDD RDAAKKVNSSDN N RPGFVKG R RPDLV
PaGT3 PaGT3 UDF89C1 UGT71G1 UDP76G1 UDP74F2 UGT85H2	TT 0.00 330 340 DDDDSWLPRGF0 SVEEDVIPAGFE DKARVHLPEGFLE STWVEPLPDGFL SSEEEKLPSGFLE IGGSVIFSSET	2	α13 <u>2000000</u> 9 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	β13 AIGAFVTHCGWN AVGSYLTHLGWG AIGGFVSHCGWN AVGAFVTHCGWN AIGCFLTHCGWN SIGGFLTHCGWN	α14 STLEGTTAGVPM SVLEGMVGGVML SILESMWFGVPI SILESVGGVPL STLESVCGVPM STTESICAGVPM

PaGT3	β14 →	α15 22222222222 400	β15 410	η5 200 420	α16 2000000 430	5 222222 22 440
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	VTWPIFA LAWPMQA LTWPIYA ICRPFFGI IFSDFGLI VAMPQWTI LCWPFFA	YNEKLVNQI HERNTILIVDK 201 LNAFRLVE 001 LNGRMVEDV 001 LNARYMSDV 002 MNAKYIQDV 002 TDCRFICNE	LK <mark>IGV</mark> PVGAN LR AAVRV GEN WGVGLGLRVI LEIGVRIEG LKVGVYLEN(WK <mark>AGV</mark> RVKTH WE <mark>IGM</mark> ELDTN	IKWSRETSIEL IRDS)YRKGSC 	VIKKDATEKA VPUSDKLARI VVVAAEEIEKG VFTKSGLMSC .WERGEIANA IAKREEIEFS .VKRELAKL	IREIMVGDEAE IAESAREDL IKDIMDKDS FDQIISQEKGK IRRVMVDEGE IKEVMEGERSK INEVIAGDKGK
PaGT3	α1 2000000 450	7 2000000000 460	α1 2000000 470	8 2000000 480		
PaGT3 UDP89C1 UGT71G1 VvGT1 UDP76G1 UDP74F2 UGT85H2	ERRSRAKI PERVTLMI IVHKKVQI KLRENLR YIRQNAR EMKKNVKI KMKQKAMI	K LKE MAWKAVEE K LRE KAMEAIKE SMKEMSRNAVVO A LRE TA DRAVGP V LKOKA DVSIMK K WRD LAVKSINE SLKKKAEENTRP	GGSSYSDLS GGSSYKNLDE GGSSLISVGH KGSSTENFI GGSSYESLES GGSTDTNID GGCSYMNLNH	LIEELRGYHA LVAEMCL LVDDITG LVDLVSKPKE LVSYISSLL. FVSRVQSK VIKDVLLKQN		

Figure S3 Multiple sequence alignment of *Pa*GT3 with some UGTs with known crystal structures. The PSPG motif is indicated in a green box.



(a)

(b)



(c)

Figure S4

a. Surface view of acceptor binding site in *Pa*GT3 (green), UGT89C1 (light-blue), and *Vv*GT1 (light-brown) show that the acceptor binding pocket in *Pa*GT3 is larger than the other two UGTs. The sugar-acceptor, quercetin, in UGT89C1 and *Vv*GT1 are shown in light-blue and light-brown, respectively. b. Longer loops in *Pa*GT3 increased the volume of acceptor binding pocket. The corresponding loops are shorter in UGT89C1 (light-blue) and *Vv*GT1 (light-blue) and *Vv*GT1 (light-blue). Quercetin in UGT89C1 and *Vv*GT1 are shown in light-blue and light-brown, respectively.



Figure S5 Pictures of *Pa*GT3 crystals in (a) the absence and (b) the presence of 18-crown-6 ether.



Figure S6

a. Top to bottom: F_o - F_c omit map contoured at 3 σ after removing sodium ion, 18-crown-6 ether, and both sodium ion/18-crown-6 ether from the structure of *Pa*GT3 with 18-crown-6 ether. b. Top to bottom: F_o - F_c omit map contoured at 3 σ after removing sodium ion, 15-crown-5 ether, and both sodium ion/15-crown-5 ether from the structure of *Pa*GT3 with 15-crown-5 ether.