

Table S1. Annotation (Sma3s and Blast2GOPro softwares) and mean expression levels (FPKM) of putative tyrosine decarboxylase transcripts (CNAG olive genome database, OE6.OLIVEFAT) in ripening fruits (22-25 weeks after flowering) of seven olive cultivars (Dokkar, Menya, Piñonera, Picual, Klon, Fishomi and Abou kanani).

Transcript	<i>OE6A000744</i>	<i>OE6A082511</i>	<i>OE6A073377</i>	<i>OE6A011752</i>	<i>OE6A094428</i>
Gene name	<i>OeAAS</i>	<i>OeTDC1</i>	<i>OeTDC2</i>	-	-
Sma3s annotation	Pyridoxal phosphate-dependent decarboxylase	Putative tyrosine decarboxylase	Putative tyrosine decarboxylase	Pyridoxal phosphate-dependent decarboxylase	Tryptophan decarboxylase
Blast2GOPro annotation	Tyrosine decarboxylase 1	Tyrosine DOPA decarboxylase 1-like	Tyrosine DOPA decarboxylase 1-like	Tyrosine DOPA decarboxylase 1-like	Tyrosine DOPA decarboxylase 1-like
Mean expression	592	1011	253	0	4

Table S2. Protein sequences used for the phylogenetic analysis shown in Figure 3.

Protein	Plant species	GenBank Accession
OeTyrDC1	<i>Olea europaea</i>	PP534480
OeTyrDC2	<i>Olea europaea</i>	PP590793
AcTyrDC	<i>Ananas comosus</i>	OAY76026
AcTyrDC	<i>Aristplochchia contorta</i>	ABJ16446
AmTyrDC	<i>Argemone mexicana</i>	ACJ76782
AtPAAS	<i>Arabidopsis thaliana</i>	Q8RY79
AtTyDC2	<i>Arabidopsis thaliana</i>	NP_001078461
BdTyDC	<i>Brachypodium distachyon</i>	XP_3569907.1
CaTrpDC1	<i>Camptotheca acuminata</i>	AAB39708
CaTrpDC1	<i>Capsicum annuum</i>	ACN62127
CaTrpDC2	<i>Camptotheca acuminata</i>	AAB39709
CaTyrDC2	<i>Capsicum annuum</i>	XP_016541857.1
CrTrpDC	<i>Catharanthus roseus</i>	P17770
CrTyrDC1	<i>Cistrus reshni</i>	ACX29990
CsTyrDC	<i>Citrus sinensis</i>	XP_024953754.2
GmTyrDC2	<i>Glycine max</i>	XP_006576967.1
KnAAS	<i>Klebsormidium nitens</i>	GAQ86385.1
LaTyrDC1	<i>Lycoris aurea</i>	AYH64864
LrTyrDC2	<i>Lycoris radiata</i>	QXF78538.1
MdTyrDC	<i>Malus domestica</i>	XP_008358473
NnTyrDC	<i>Nelumbo nucifera</i>	XP_010245170
NtTyrDC	<i>Nicotiana tabacum</i>	XP_016449301.1
OeAAS	<i>Olea europaea</i>	QJA07379.1
OpTrpDC	<i>Ophiorrhiza pumila</i>	BAC41515.1
OsTrpDC	<i>Oryza sativa</i>	XP_015648701.1
OsTyrDC	<i>Oryza sativa</i>	015633932.1
PbTyrDC	<i>Pyrus bretschneideri</i>	XP_009364243
PcAAS	<i>Petrosilum crispum</i>	Q06086.1
PcTyrDC4	<i>Petroselinum crispum</i>	AAA33863
PhAAS	<i>Petunia hybrida</i>	ABB72475.1
PpTyrDC	<i>Prunus persica</i>	XP_007213045.2
PsTyrDC2	<i>Papaver somniferum</i>	P54769
PsTyrDC	<i>Papaver somniferum</i>	AAC61842.1 1
PtTyrDC	<i>Populus trichocarpa</i>	QBL52493.1
RcTyrDC	<i>Rhodiola crenulata</i>	AFN89854.1
RgTyDC1	<i>Rehmannia glutinosa</i>	ULR57004
RgTyDC2	<i>Rehmannia glutinosa</i>	UKS50408
RgTyDC3	<i>Rehmannia glutinosa</i>	ULR57005
RgTyDC4	<i>Rehmannia glutinosa</i>	ULR57006
RhAAS	<i>Rosa hybrid</i>	ABB04522.1
RrAAS	<i>Rhodiola rosea</i>	AUI41112.1
RsTyrDC	<i>Rhodiola sachalinensis</i>	ABF06560
SiTyrDC	<i>Sesamun indicum</i>	XP_011096642.1
SfTyrDC	<i>Solanum tuberosa</i>	AHI16968.1
TaTDC	<i>Triticum aestivum</i>	CDM81842
TcTyrDC	<i>Theobroma cacao</i>	EOX96928
TfTyrDC	<i>Thalictrum flavum</i>	AAG60665
TtTyr-DOPADC	<i>Thralictrum thalictroides</i>	KAAF5198316
ZmTyrDC	<i>Zea mays</i>	ACG46884.1
ZmTyrDC AAS	<i>Zostera marina</i>	KMZ74011.1

Table S3. Oligonucleotides used for RT-qPCR expression analysis of *OeTDC1* (GenBank PP534480) and *OeTDC2* (GenBank PP590793).

Name	Sequence (5'-3')
q <i>OeTDC1</i> -F	ACCCTTACAGAAAACAGGCA
q <i>OeTDC1</i> -R	TTTTTGTCATCTTCATCTTC
q <i>OeTDC2</i> -F	ACCCTTACAGAAAACAGGCA
q <i>OeTDC2</i> -R	CGCAAACATAAAATGGACAAAAGCA
q <i>OeEF1α</i> -F	TGCTCTATCTGGATTGCCATT
q <i>OeEF1α</i> -R	TCAAATGCCACCATGACTTC
q <i>OeGAPDH</i> -F	TGAGATGCTGCACAATGGTT
q <i>OeGAPDH</i> -R	CACGATAGGCTTACGCAACA
q <i>OePP2A</i> -F	CTCGCCTGAAAACGAAAGAC
q <i>OePP2A</i> -R	CACAAAGCAGACCAAAACCA

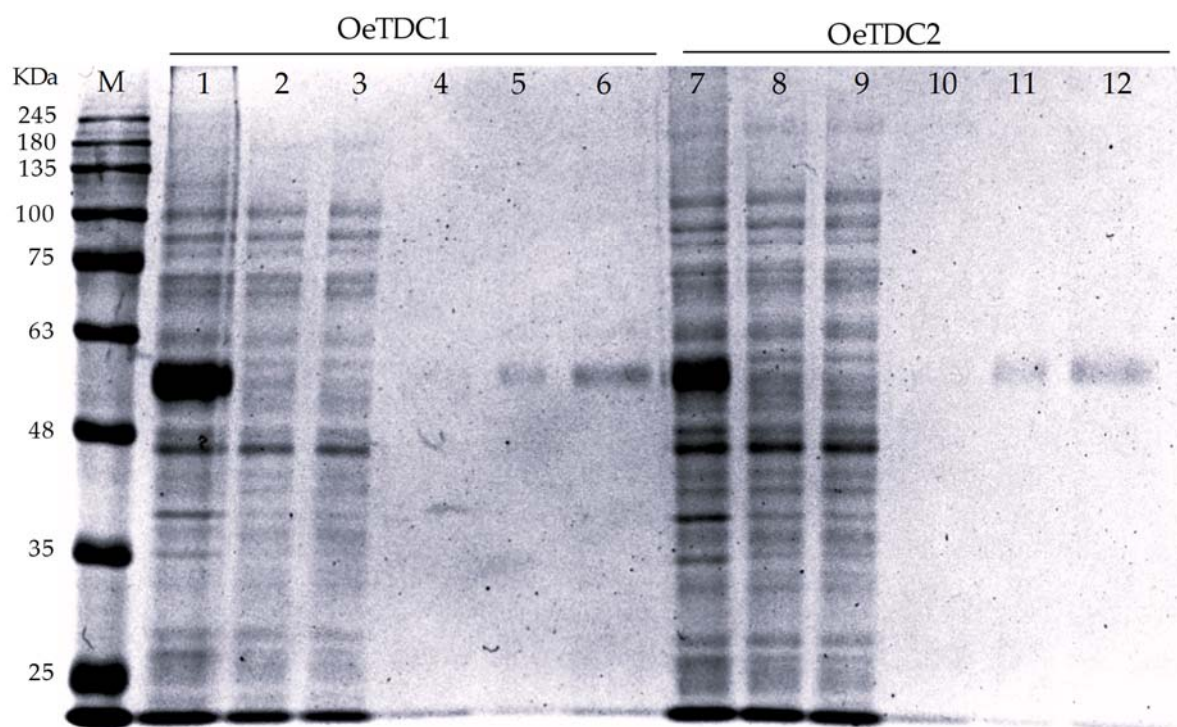


Figure S1. SDS-PAGE followed by a Coomassie blue staining of representative purifications of olive TDC recombinant proteins. M: molecular weight protein ladder; 1, *OeTDC1* induced sample; 2, BL21(DE3) pIZ227 *OeTDC1* control sample; 3, total *OeTDC1* induced sample eluted from Ni-Sepharose column; 4, Ni-Sepharose *OeTDC1* elution, fraction 1 (0.5 mL); 5, Ni-Sepharose *OeTDC1* elution, fraction 2 (2.5 mL); 6, Ni-Sepharose *OeTDC1* elution, re-eluted fraction 2; 7, *OeTDC2* induced sample; 8, BL21(DE3) pIZ227 *OeTDC2* control sample; 9, total *OeTDC2* induced sample eluted from Ni-Sepharose column; 10, Ni-Sepharose *OeTDC2* elution, fraction 1 (0.5 mL); 11, Ni-Sepharose *OeTDC2* elution, fraction 2 (2.5 mL); 12, Ni-Sepharose *OeTDC2* elution, re-eluted fraction 2.

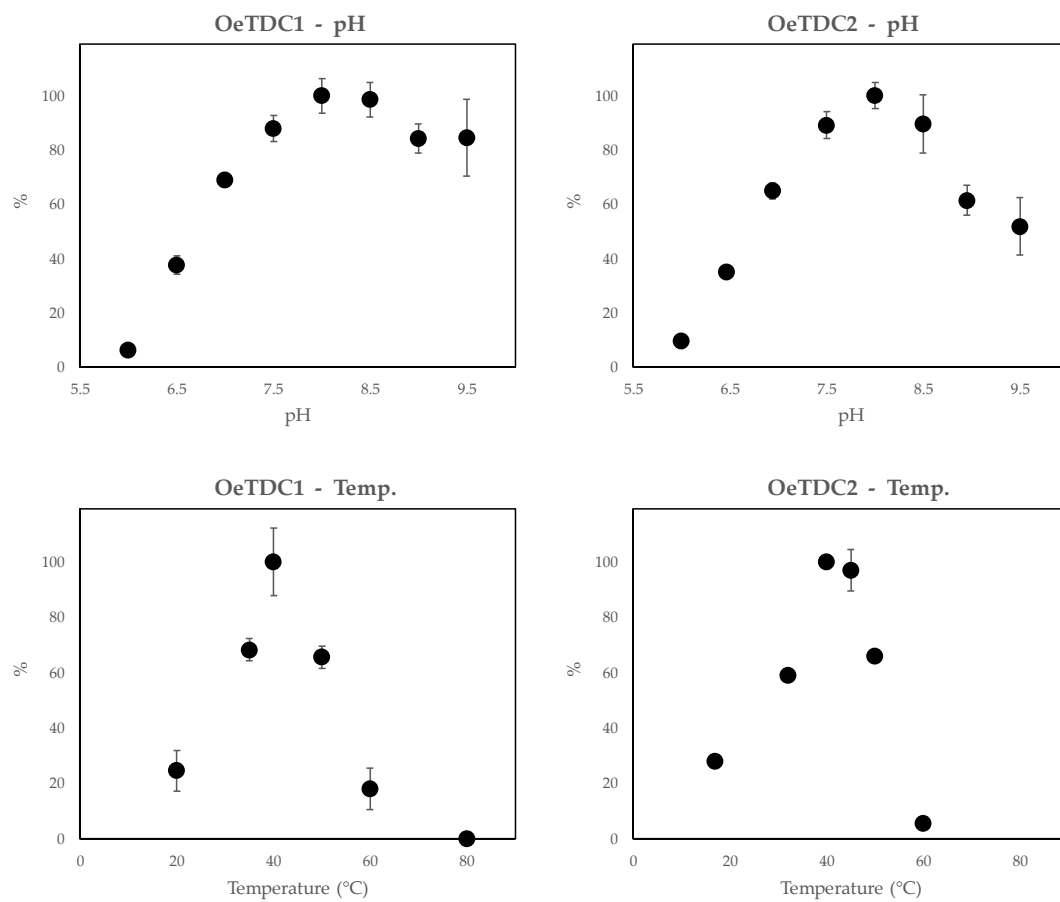


Figure S2. Effect of pH and temperature in the reaction medium for *OeTDC1* and *OeTDC2* using tyrosine as substrate.

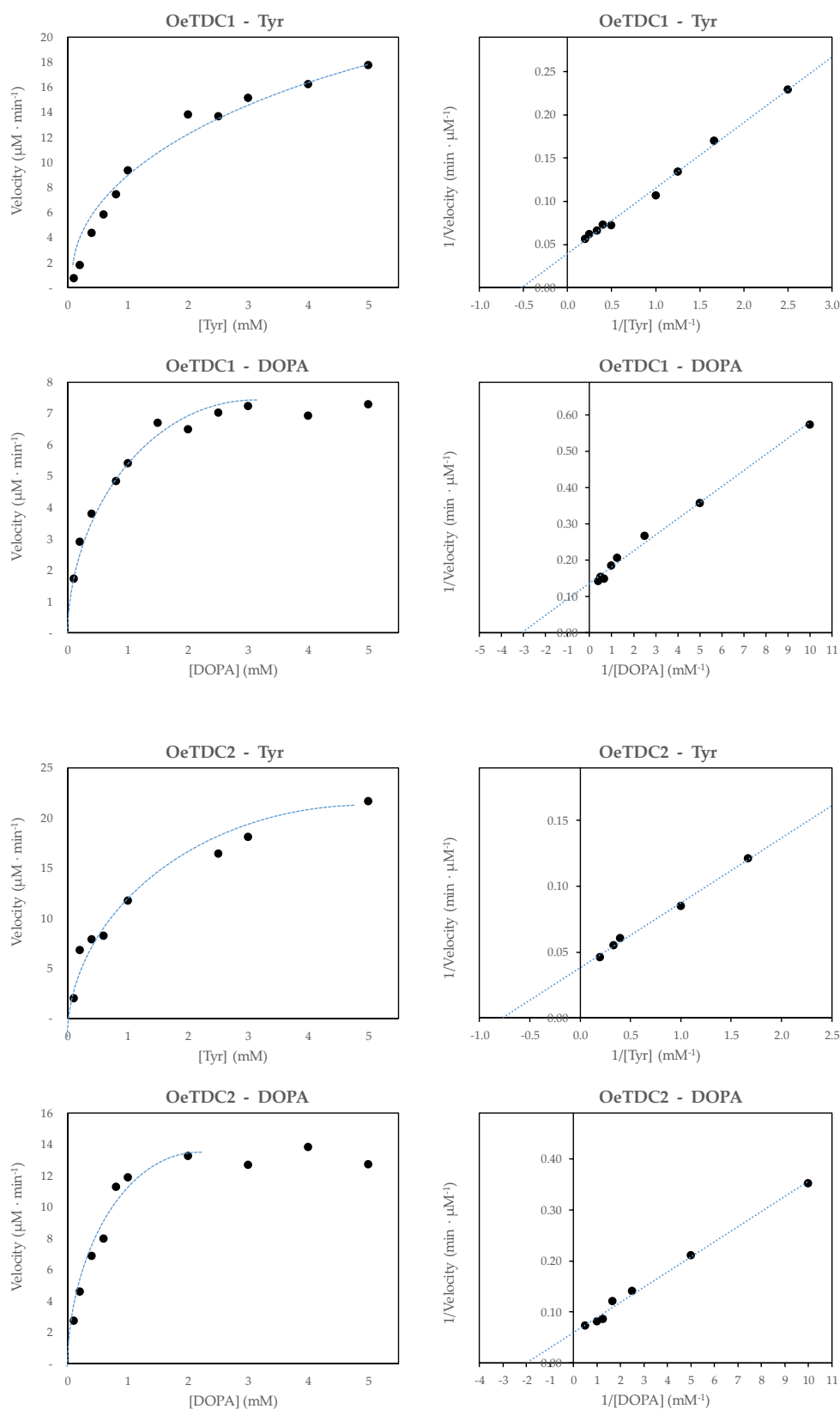


Figure S3. Determination of catalytic properties of *OeTDC1* and *OeTDC2* for tyrosine and DOPA. Olive TDCs were incubated at different concentrations of tyrosine or DOPA for 15 min at 40 °C. Activity was determined by analyzing the amount of reaction product by HPLC.

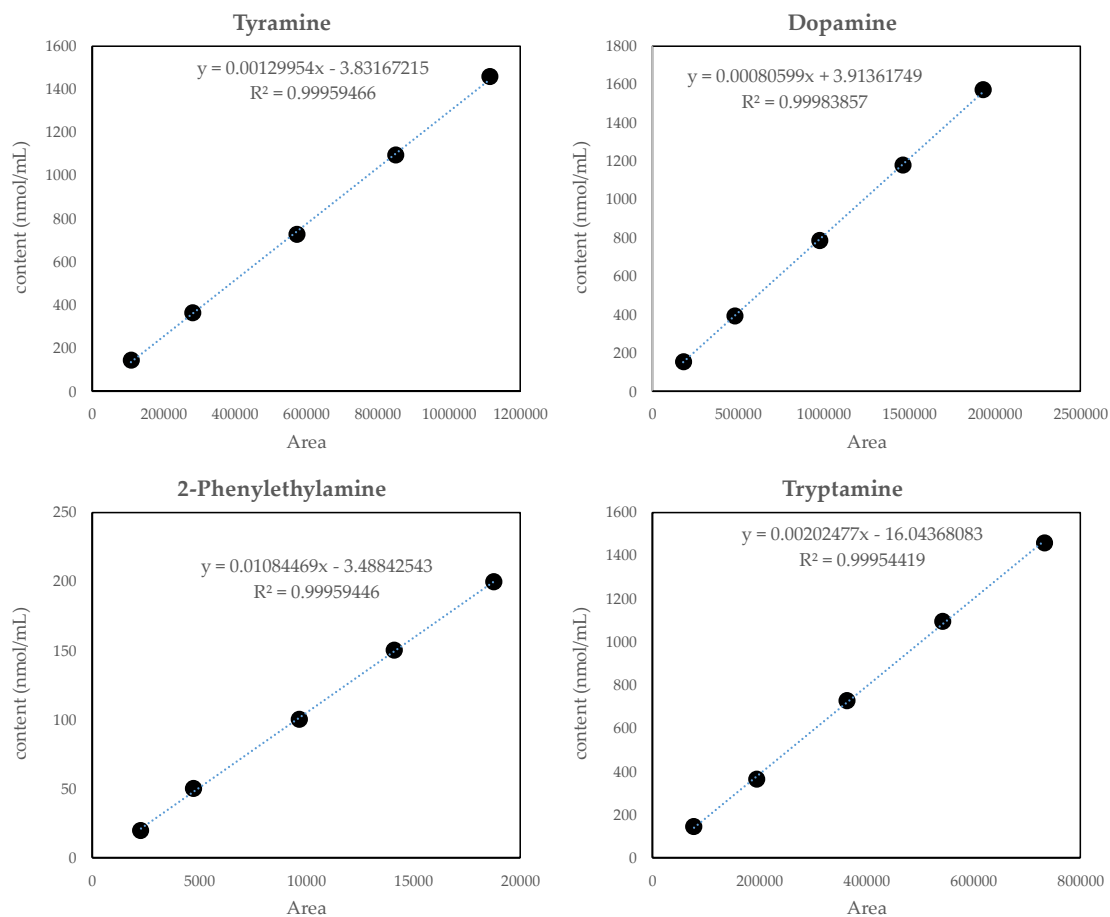


Figure S4. Calibration curves for the possible reaction products of *Oe*TDC1 and *Oe*TDC2. Tyramine and dopamine were monitored at 280 nm, 2-phenylethylamine at 258 nm, and tryptamine at 276 nm.