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PoPPO1 : QSLIAVSFSLTAFNFSSSSIKTNELVLSQVSLGSSRACRARSQVPAKIKTEKNQYEPNAL-HKSNLLRRNMLLGLGGLVCPAATLGLTFSSIALFAVILLFAAVKCFEAKDDTIIPRGMK : 132
PoPPO2 : VASIEFIATSTTN-TTATSAEEN-ELESFASQIAYKTRPHVLEI-RISCNPAKRDCC-----NENEQHVLCRRNMLLGLGGLVCPAATLGLTFVAFASIAKE-TAEATQCS-PISELEFNVRVNV-CC : 119
PoPPO3 : -NVALISESLTATE-ATATNIGKN-NSLGRSLSVSSSSQTRRIARISQPAASND-NOESSCTQN-FANNLLRRNMLLGLGGLVCPAATLGLGAS-NTFAFAELVENKVVNTT-CVAGFEER-CC : 123
PoPPO4 : EEFEL-----LTTTHLPIIS-TFFERASQISLRSQC'TREASF-RISQPAIKMNDENPKIHEDKTIANKLLRRNMLLGLGGLVCPAATLGLSPTTAAEITAEINACG--FALFELCKGLHN-CC : 119
PoPPO5 : AALFELSTNAATISAA-TTATIS-ELFELRQIHFCKRSHLETRISQPAKACQNPFRMTHDG-NANNLLRRNMLLGLGGLVCPAATLGLCAFASFAEITAEINAKSDE--FALFESNIDRSN-CC : 128
IbPPO : AEFETSEFCRAKTFELASATISSPLFESQELATARKTHHRF-RISQPAENKSCF-----LRRVVLGLGGLVCPAATLGLN-NTFAFAEITAEINAKSDEVFEPKLEFFLWVES-CC : 116

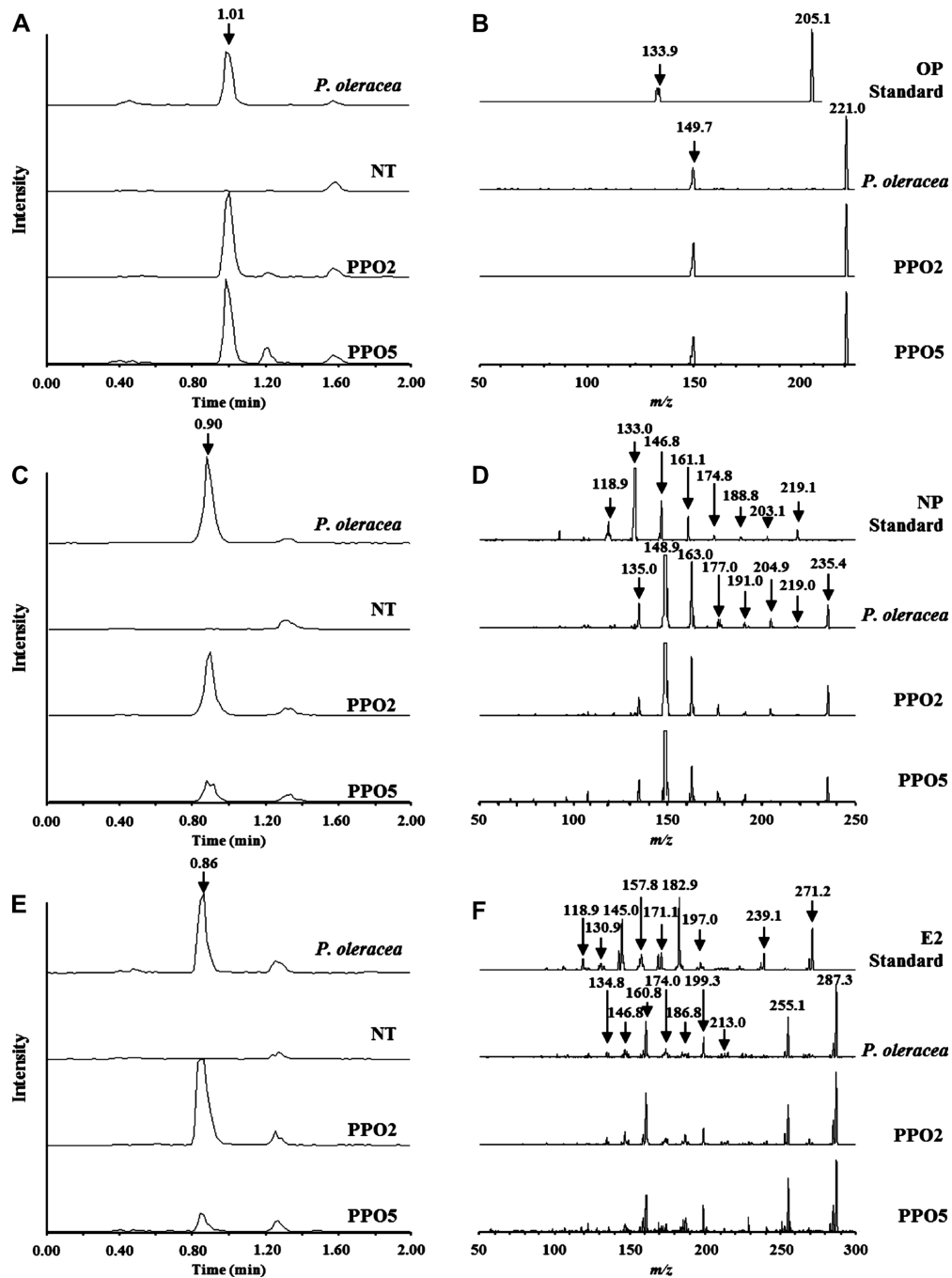
PoPPO1 : EF---LFKESVNLDFRNYWSEFVVEFAHRYSE--CAAKGREAVRRRRIPELLFRSFAACARHCAVCNCAWHIAATTINDHRICVHGSWLFHFFHAYLFFEFERIGSLVNPESFAIFVWNLHEDGM : 261
PoPPO2 : EF---MNNLIDRF-SNSRFTDIEPAHMDT--RYPQKRRSSIALPESFPRSTVCAANVHCAYCNCAWHVVEFPR--LDCVHGSWLFHFFHAYLVYFERTISLNLPTFAIFVWNLHEDGM : 243
PoPPO3 : LFFEFYKQDIEVFNKWPFFFAHVRRIHLLPAKKAQASRPAARAFELIIEEENKVAQVYKCGDSEKHDKIQIRIYVHGSWLFHFFHAYLFFEFERIGSLVNPESFAIFVWNLHEDGM : 257
PoPPO4 : EF---VAQNIDITL-EPTLAKVVEFAHSDN--EYKSNRQSLRRAHLLDLEERSQCAVHCAYCDSGNVVEFNP--LDCVHGSWLFHFFHAYLVYFERTISLNLPTFAIFVWNLHEDGM : 243
PoPPO5 : EF---VATNIDIT--FSASSTVEVEFAHVA--EYKSNRQSLRRAHLLDLEERSQCAVHCAYCDSGNVVEFNP--LDCVHGSWLFHFFHAYLVYFERTISLNLPTFAIFVWNLHEDGM : 251
IbPPO : EF---IATNIDITVSKPKVTSFSAARISFAHMDK--EYKAKERRRRLRRAHLLDLEERNVCAVHCAYCNCAWHVVEFNP--LDCVHGSWLFHFFHAYLVYFERTISLNLPTFAIFVWNLHEDGM : 241

PoPPO1 : YVSLVFCIGLSNLEVDYDTEREKS-LIDLCGLLEIKKEDNKIFEENQLEFYNRHHVHVAR-FKEAELFMGGRVARDKVSINSHETLRVPHVPHVHVEI--FEREYSILMSEYSGRDELFAVHH : 391
PoPPO2 : THAAHALD--KSLYDVPVSEFEMVALISLSDIDH-----VFKICQKTNLIVMMRQVSNAKNSGLFMGQRVAG--LTSKRFSELPVPHGPHVHVEI--RKTENPELMDNYSFAREDIFVAHH : 364
PoPPO3 : YVTHISEGGVSNLYANRSEFIEPRVILG-CGLPTK-----FVEEGKDKNLSMMQCSR-FKTNKLFMGGRVAGDEADIGLGVHLLPRNIVHNCN--E-GNGNGLMDNYSFAREDIFVAHH : 379
PoPPO4 : GMHAALDR--NSELYDSEDFGCEPVLVINDGEDTIL-----MSTLLLTANLIVMMRQVSNAKIARLELQQRVAG--GSEFGGSELENVPHGPHVHVEI--RNCENPELMDNYSFAREDIFVAHH : 365
PoPPO5 : RVSISLNT--SEELYDRRFAACEPTVILINDGSDLS-----TSDNALNANLIVMMRQVSNASTIERLELQQRVAGD-ASEFGGSELENVPHGPHVHVEI--RNCENPELMDNYSFAREDIFVAHH : 374
IbPPO : LHQIRNGL--NSELYDRNLCSELE-LVMLLGAIDTIL-----VIDLERISNMLALMKS-VTAAGIAELFLKRFVADLFVNRGGSELENVPHGPHVHVEI--RNCENPELMDNYSFAREDIFVAHH : 366

PoPPO1 : ANVDRNWTWAGLGG---RRRLEAFELNHEIFVDKRRKVVIVVIVLLEPRLGKRVTSQLEWLLHHPVVD-----HKPLIFEFV-----KRLFLGSGGCTRPFEE-NRV----- : 499
PoPPO2 : GNVDRNWSVMTIGPK---NRNKRSEFISSEVYDENARAVIVVEVLDLRLGKRVVPLVLEWRSKRETRARRVAVENKVK-LAVAPLST--MDVPTAEERPEL-KVIRTPHMPKRSRIRRAAL : 490
PoPPO3 : GNVDRNWSVMTIGPK---NRNKRSEFISSEVYDENARAVIVVEVLDLRLGKRVVPLVLEWRSKRETRARRVAVENKVK-LAVAPLST--MDVPTAEERPEL-KVIRTPHMPKRSRIRRAAL : 503
PoPPO4 : GNVDRNWSVMTIGAN---RVELESRWNASVYDENARAVIVVEVLDLRLGKRVVPLVLEWRSKRETRARRVAVENKVK-LAVAPLST--MDVPTAEERPEL-KVIRTPHMPKRSRIRRAAL : 492
IbPPO : ANVDRNWTWAGLGG---RRRLEAFELNHEIFVDENKCAVAVVVDLLEKRLCYNIVVIVLLEWLLSRFTSEASRVTLTSTIPTKIANRKLPSKPSSSSNLTPRRLD-SAITIILKPEEERSRERK : 505
PoPPO1 : DSEFLDIEKVCNASKNLEFVVLGDSNHRKTEDGKTRSAICVQSCDFEPCPHECHKTEEIFFTYLPSPVAVNVCNENVDVAFQCNLSELDLGLDLEHLL- : 611
PoPPO2 : DSEFLDIEKVCNASKNLEFVVLGDSNHRKTEDGKTRSAICVQSCDFEPCPHECHKTEEIFFTYLPSPVAVNVCNENVDVAFQCNLSELDLGLDLEHLL- : 597
PoPPO3 : DREELVLEKLELSTQIEFVVLGDSNHRKTEEIFFTYLPSPVAVNVCNENVDVAFQCNLSELDLGLDLEHLL- : 607
PoPPO4 : LGEELVVE-VEICSLVWVFLVYVNDDEIVPLKTI--VKTEAGSADVPHKHKHKEH-RMKTTIEHIGTLLLELCAIDGCVNIVLPSGKE-VTKIETVREVAS : 600
PoPPO5 : GGEELVVE-VEICSLVWVFLVYVNDDEIVPSKNNR--AFVEHGSADVPHKHKHKEH-RMKTTIEHIGTLLLELCAIDGCVNIVLPSGKE-VTKIETVREVAS : 614
IbPPO : AFEELVREGIEVAITQVAFVLYVINDDEFEAGRE---RAEAGSADVPHKHTGS---KIRTSEIGCNELFELGDFHCAVITLADVGG-DVTEENHIVGGS : 588

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Supplemental Figure 1. The amino acid sequences alignment of *PoPPO* genes. Compared with *IbPPO* (GeneBank accession number: AY822711). *PPO*'s two highly conserved copper-binding domains (CuA and CuB) and conserved histidine residues are shown (stars).



Supplemental Figure 2. Analysis of OP, NP and E2 metabolites by LC/PDA/MS/MS. (A) MS chromatogram at m/z 221.0. Peak at which retention times is 1.01 min, is OP metabolites. (B) Product ion spectra of OP standard (precursor ion m/z 205.1) and OP metabolites produced by portulaca, PPO2 and PPO5 (precursor ion m/z 221.0). (C) MS chromatogram at m/z 235.0. Peak at which retention times is 0.90 min, is NP metabolites. (D) Product ion spectra of NP standard (precursor ion m/z 219.1) and NP metabolites produced by portulaca, PPO2 and PPO5 (precursor ion m/z 235.0). (E) MS chromatogram at m/z 287.0. Peak at which retention times is 0.86 min, is E2 metabolites. (F) Product ion spectra of E2 standard produced by portulaca, PPO2 and PPO5 (precursor ion m/z 271.1) and E2 metabolites (precursor ion m/z 287.1).

Supplemental Table 1. Oligonucleotides used in this work

Name of oligonucleotides	Sequences (5' to 3')	Comments
<i>NotI</i> -oligo dT primer	aactggaagaattcggcgccaggaatttttttttttttt	for RACE
CuA1	ggctcttctcccg/ctt/gc/gcat/ca/cgata/tctat/cttg/ctac	for RACE
PoPPO1-5RACE-R	gtccagtagctccttgacatagatcttgac	for RACE
PoPPO2-5RACE-R	agtccttgaagtctgttcttgggtcct	for RACE
PoPPO3-5RACE-R	gcctggacactgggtgtacatcgaccatag	for RACE
PoPPO4-5RACE-R	gatgcatctaaccaatcagatcggtaaat	for RACE
PoPPO5-3RACE-F	ticayinywsitggytnttc	for RACE
PoPPO5-3RACE-R	caiabnbiccacawbckrtc	for RACE
PoPPO5-5RACE-F	gcbhtnccntwytggaaytg	for RACE
PoPPO5-5RACE-R	ccacatbckrtcbacrtdgmrtg	for RACE
PoPPO5 full length 1F	aaagccgtgccactcaag	for RACE
PoPPO5 full length 2F	gccgtgccactcaagatc	for RACE
ExactSTART primer 2-1	tagacttagaaattaatcagactcactatagtc	for RACE
Oligo dT primer	aactggaagaattcggcgccaggaatttttttttttttt	for RACE
poppo1 5'UTR-F	atctagaatccttcccactatcataactata	RT-PCR (tissues of portulaca)
poppo1 R	gtccagtagctccttgacatagatcttgac	RT-PCR (tissues of portulaca)
poppo2 5'UTR-F	atctagaatccaagattccaaggcattagac	RT-PCR (tissues of portulaca)
poppo2 R	agtccttgaagtctgttcttgggtcct	RT-PCR (tissues of portulaca)
poppo3 5'UTR-F	tgatcaatgaccaacttctgctatg	RT-PCR (tissues of portulaca)
poppo4 3'UTR-R	tcagcgtaaaatggacgaaacaagtaatc	RT-PCR (tissues of portulaca)
poppo5 S1	acctcaactatgatggctcggatg	RT-PCR (tissues of portulaca)
poppo5 3'UTR-R	caaacacacaaatccatccaacattc	RT-PCR (tissues of portulaca)
PoUBQ Fw	gcagatcttctgtaaaacccaac	RT-PCR (tissues of portulaca)
PoUBQ Rv	gtaaaccttaggtgagtcacactaccac	RT-PCR (tissues of portulaca)
PoPPO2-F1 for RT-PCR	gtcaaggccgtattcaacaag	RT-PCR (BY-2 cells)
PoPPO2-R2 for RT-PCR	taagcaaccatcaaccataccaagg	RT-PCR (BY-2 cells)
PoPPO4-F1 for RT-PCR	gattgccacccttctcc	RT-PCR (BY-2 cells)
PoPPO4-R3 for RT-PCR	atcagcgtaaaatggacgaaacaag	RT-PCR (BY-2 cells)
PoPPO5-F1 for RT-PCR	ccaccctatcctcaaccatc	RT-PCR (BY-2 cells)
PoPPO5-R2 for RT-PCR	aatgacgaccactgaagccaaact	RT-PCR (BY-2 cells)
GAP-C Fw	aagctggtgctgattctgtgtgg	RT-PCR (BY-2 cells)
GAP-C Rv	tgcccttcaacttaccctccgatt	RT-PCR (BY-2 cells)