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# **Exploring plant expression of alkaloid related** genes in Dendromecon rigida and the plant's relationship with the rootzone microbes



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## Introduction

We established the first transcriptome of *Dendromecon rigida*, known as Tree Poppy. It can be distinguished from other *Papaveraceae* by its lanceolate leaves and woody stems, which are uncommon for the family. During the same sampling event, we procured metagenomic data from the rootzone soil bacteria. Alkaloid production and gene expression in this plant have been little studied, although the plant's resilience following a disturbance is most certainly related to its secondary metabolites as well as its fire ecology. The interest in this plant comes from its resistance to pathogens, as well as its potential for synergy in the production of secondary metabolites with rootzone microbes, based on our previous work. The plant is known to have few pest and disease problems due to the high amount of antifungal, antioxidant, anti-herbivory, and insecticidal compounds like berberines within it.



### Methods and Materials

The data we procured consisted of 16S metabarcoding, WGS metagenomics, and plant whole transcriptome data from Tree Poppy leaf, flower, and fruit. The metagenomics analysis employed QIIME2, Nephele, and STAMP. The plant transcriptome was assembled de novo in Trinity, expression was quantified with salmon, and





completeness was assessed using BUSCO. Transcripts were annotated with the best SPROT blastx hits, and of those with a length> 1000 and TPM>10, a subset of secondary metabolite and resistance genes were selected for further analysis.



#### Figure 3 - Description here

#### Results

The assembly had a total of 369,483 transcripts with an average length of 856 and a high degree of completeness >95%. From the transcripts, several candidate genes for alkaloid production were identified including methyltetrahydroprotoberberine, (RS)-norcoclaurine, S-stylopine, and 3-O-actylpapaveroxine. Protoberberines have antifungal properties and contribute to allelopathy. Norcoclaurine is a precursor to benzoisoquinoline alkaloids and is present in other Papaveraceae. S stylopine is bitter and deters insects and animals from eating the plant. Papaverine is an antifungal precursor to hebaine, common in fire-adapted plants in this family.

Compared with other plants from the nearby area on the Green Trail, including Wooly Blue Curls and Yerba Santa, Tree Poppy rootzone soil samples showed a higher proportion of reads from Actinomycetales. When compared with Coast Live Oak rootzone samples from the Gold Creek Preserve, Tree Poppy soil samples reflected elevated copies of mycothiol production genes in the metagenomic data, based on STAMP output. In the next steps, we will map secondary metabolite genes to closely related species from Papaverace are and analyze the potential for the production of related compounds by rootzone bacteria.

8.1

Query_ID	Subject_ID	%_Identity	E-value	Bit_Scor	e Gene_Name			
TRINITY_DN1131_c1_g1 JBGUAT0100000								
_i7	01.1	91.453	117	10	Macleaya cordata isolate BLH2017 scaffold1325			
TRINITY_DN1142_c0_g1 JAOXYG0102245								
_i3	48.1	94.643	56	3	Macleaya cordata isolate BLH2017 scaffold9079			
TRINITY_DN147739_c0_JBCEGI01000000								
g1_i1	2.1	93.506	462	30	Macleaya cordata isolate BLH2017 scaffold209			
TRINITY_DN2929_c0_g1 JBGUAT0100000								
_i17	01.1	91.655	707	56	Macleaya cordata isolate BLH2017 scaffold9101			
TRINITY_DN2929_c0_g1 MVGT01000438.								
_i3	1	90.634	726	58	Macleaya cordata isolate BLH2017 scaffold1837			
TRINITY_DN3028_	c0_g1 MVGT01004035	<b>.</b>						
_i2	1	87.209	86	11	Macleaya cordata isolate BLH2017 scaffold1835			
TRINITY_DN3028_0	c0_g1 MVGT01004035	j.			Eschscholzia californica subsp. californica DNA, contig: Eca_sc002317.1,			
_i20	1	87.209	86	11	cultivar: Hitoezaki			
TRINITY_DN3028_	c0_g3 JBCEGI0100000	D			Eschscholzia californica subsp. californica DNA, contig: Eca_sc001010.1,			
_i1	4.1	92.5	40	3	cultivar: Hitoezaki			
TRINITY_DN3037_	c2_g2 JBLLEJ0100000	)						
_i1	8.1	92.683	41	3	Eschscholzia californica isolate CP2 SCAF_1			
TRINITY_DN310_c	1_g1_ BEHA01000600.							
i2	1	85.635	181	25	Eschscholzia californica isolate CP2 SCAF_4			
TRINITY_DN315_c	0_g1_ JBGUAT0100000	)						
i7	05.1	97.917	48	1	Eschscholzia californica isolate CP2 SCAF_2			
TRINITY_DN351_c	0_g1_ MVGT01004366	j.						
i2	1	96.667	60	2	Eschscholzia californica isolate CP2 SCAF_1			
TRINITY_DN6661_c0_g1 MVGT01002051.								
_i18	1	91.304	46	4	Eomecon chionantha isolate PY-2024a chromosome 5			
TRINITY_DN68158_c0_g MVGT01002328.								
1_i2	1	95.238	84	4	Eomecon chionantha isolate PY-2024a chromosome 1			
TRINITY_DN7528_c1_g1 JBCEGH0100000								
_i1	01.1	100	59	0	Corydalis saxicola isolate ML-2025a linkage group LG08			

Query ID	Subject ID	% Identity	F-value	Bit Score	Gene Name
TRINITY DN1131 c1 $\sigma$ 1	XM 02894807	/o_lucitity	L value		
i7	9 1	94 595	0.012	58.4	Panaver somniferum clone contig2 cytochrome P450 mRNA_complete cds
TRINITY DN11/2 $c0 \sigma1$	XM 02659323	51.555	0.012	50.1	
i3	9 1	78 923	0	1134	Orlava daucoides clone des649477 anonymous marker DC1340 genomic sequence
	5.1	70.525	U	1134	
σ1 i1	IN185328 1	81 963	0	1218	Polygonum minimum voucher Able 5670
	XM 04600415	01.505	U	1210	
i17	A 1	91 228	1 25F-32	156	PREDICTED: Nelumbo nucifera caffeovlshikimate esterase-like
	YM 02004058	51.220	1.252 52	150	
13	7 2	88 462	9 35F-2/	126	PREDICTED: Nelumbo nucifera chorismate synthase, chloroplastic
	VM 05924424	00.402	J.JJL 24	120	
1 i2	0 1	83 516	2 12F-11	86.1	PREDICTED: Panaver somniferum internal alternative NAD
		05.510	2.136 11	00.1	
120	0 1	8/ 615	2 25F-12	01.6	PREDICTED: Panaver somniferum NAD
	VNA 05708020	04.013	J.2JL-1J	91.0	
	XIVI_05798039	83 721	2 44F-10	82.4	PREDICTED: Panaver somniferum caffeovlshikimate esterase-like
	3.2 XM 02650006	03.721	2.44L-10	02.4	
	XIVI_02059000	00 200	2 465 05	264	REPICTED: Ranavor compiferum & formulglutathione hydrolase like
	5.1 VM 01025247	05.200	2.40E-95	504	
IRINITY_DN310_C1_g1_I	XIVI_01025347	06 975	0.049	E 4 7	DREDICTED: Danaver compiferum glutathiana hydrolaca 2 lika
	0.2	90.075	0.046	54.7	PREDICTED. Papaver sommer um giutatmone nyurolase 5-like
I RINITY_DN315_CU_g1_I	XIVI_02657109	06.20	0	024	DREDICTED: Danaver compiferum chaggy related protein kinace eta like
		00.30	0	924	PREDICTED. Papaver sommer um snaggy-related protein kinase eta-like
I KINI Y_DN351_CU_g1_I	XIVI_02655104	00.006	0	011	DREDICTED: Brasanis alba tarnana sunthasa 10 lika
	2.1	69.060	0	911	
IRINITY_DN6661_CU_g1	XIM_02212073	00.476	0.04	<b>F</b> 4 <b>7</b>	DREDICTED, Holionthus annuus heavy motal associated isonronylated plant protain 20
	0.2	90.476	0.04	54.7	PREDICTED: Helianthus annuus neavy metal-associated isoprenyiated plant protein 20
IRINITY_DN68158_C0_g	KDE 27770 1	07 207	0.000074	C2 0	PREDICTED: Xenia sp. Carnegie-2017 succinate dehydrogenase [ubiquinone] iron-sulfur
	KR53///U.1	97.297	1	63.9	subunit, mitochondriai-like
IRINITY_DN/528_c1_g1	XM_02658417	05.00	0	1422	DREDICTED. Salvia biogenica ta utenden envir etranoferane related austein 2 like
	9.1	85.82	0	1432	PREDICIED: Salvia hispanica tryptophan aminotransferase-related protein 3-like
IRINITY_DN8211_c0_g1		00 222	1 6 4 5 1 0	02.4	PREDICTED: Zeugodacus cucurbitae succinate dehydrogenase [ubiquinone] iron-sulfur
	KJ514443.1	90.323	1.64E-10	82.4	subunit, mitochondriai
TRINITY_DN8211_c0_g1			4 005 40		
_13	KJ514443.1	90.323	1.88E-10	82.4	PREDICTED: Magnolia sinica hydroquinone glucosyltransferase-like
IRINITY_DN8875_c0_g1	XM_02655503	04.644	_	700	
	/.1	81.641	0	/63	PREDICTED: Cryptomeria Japonica UDP-glycosyltransferase 72B1
TRINITY_DN9198_c0_g1	XM_01708380	00.077	0.020	F 4 -	
	9.4	96.875	0.039	54.7	Eragrostis tet cultivar Daddi chromosome ZA
[TRINITY_DN920_c0_g1_i	XR_00202295	07.050	2 4 4 5 4 5		
	8.1	87.356	3.14E-15	99	PREDICTED: Drosophila suzukii zeste
TRINITY_DN920_c0_g1_i	V605444	07.007	6	4005	
11	X60544.1	87.097	0	1225	C.sempervirens mRNA for chorismate synthase precursor
[TRINITY_DN920_c0_g1_i	XR 00202295				

87.356 2.67E-15 99 PREDICTED: Nelumbo nucifera chorismate synthase, chloroplastic

Figure 5 (above) - WGS mapping to closely related Papaveraceae Figure 6 (right) - Corent mappings



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