

**Article title: A Maize *necrotic leaf mutant* Caused by Defective of Coproporphyrinogen III Oxidase in the porphyrin pathway**

**Authors:** Yan Zhao<sup>1,2</sup>, Wei Xu<sup>2</sup>, Li Jing Wang<sup>3</sup>, Shuai Han<sup>2</sup>, Yong Zhong Zhang<sup>2</sup>, Qing Zhi Liu<sup>2</sup>, Bao Shen Liu<sup>2\*</sup>, Xiang Yu Zhao<sup>1\*</sup>

**Supplementary Tables**

**Table S1.** Markers used in this research.

Gene	Primers	Forward primer (5'-3')	Reverse primer (5'-3')
For <i>necrotic4</i> sequencing	<i>Nec4-1</i>	GGAGAGTTAGGGTTGAGTTGTTTATG	CGTGTCAAGTTAGGTTTTTTTGTG
	<i>Nec4-2</i>	GCCGGACTGCAACACACGAC	CCACCAGAGAATGCCCAAGA
	<i>Nec4-3</i>	AGCTAGTCCCTCCTTTCTAATTTA	CACTGGGTCTGTTCTCTTTTTTT
	<i>Nec4-4</i>	GCCCACGCCGCTCATT	CTTCACCCCAAGAACCATT
	<i>Nec4-5</i>	CGGTGGCAGACACATTGAAG	GCCGGGCTATCGGAAGAA
For <i>Zm00001d002359</i> sequencing	YS-1	TCACTACTGCCTCAGCCATT	GTCCAGCGTCCATATTCTCA
For <i>Zm00001d002360</i> sequencing	<i>EP-P</i>	TGGTATTAACCGAGGAGCTG	AAGACACGTTGCGGTACAAG
	<i>EP-1</i>	AGCTTGTACCGCAACGTGTC	TGCATCTGCGATCAGGAGAG
For <i>Zm00001d002361</i> sequencing	<i>MA-P1</i>	TGCTCTCCGCTATAATGCAC	CCATTGACATCTCTACTCGG
	<i>MA-P2</i>	CCGAGTAGAGATGTCAATGG	GGACGAACAAGCAAGAGGA
	<i>MA-1</i>	TTAGTCCTTACCTACAGCGG	CATAGTCAAGAACACGAGCC
	<i>MA-2</i>	GCTCGTGTTCTTGACTATGC	GATCTTGCTGGTTCTTGTTGG
	<i>MA-3</i>	CCACAAGAACCAGCAAGATC	AGAGAGTCATTGAACACCGC
	<i>MA-4</i>	CGGTGTTCAATGACTCTCTC	GCAAGCACTCTTCAGTAACC
	<i>MA-5</i>	GGTACTGAAGAGTGCTTGC	AGGAGAACGTCACGAGACAT
For <i>Zm00001d002362</i> sequencing	<i>H15-1</i>	AAAACATCTCCTAAACTCTCCC	CTTCCCACCTGATCATTAACTAC
	<i>H15-2</i>	GAGGATGATGAAGAGGAGGAG	TGGAACCAATGGAAGATGTAA
	<i>H15-3</i>	TATGTTTTGGTTGTCCTTTGGG	AACTATGGTGATTACCTGTTGCA
	<i>H15-4</i>	CATTATTTATTATTTGGGAGGA	GAGATGTATGAACGATTTTGAG
	<i>H15-5</i>	CTTATTTTATGCTGGCTTTTCTT	TGTCTTTATACCCGTATCTGTGC

	<i>H15-6</i>	AGGTTCCCTTTTCCAACGTGTATG	CTCGGTGTTTAGGCTTTTGTCTT
For qRT-PCR	<i>Nect-RT</i>	ATTGCGGAGAGGTCGTTATG	TAAGTGGAAGGGACACAAGTATG
	<i>ACTIN</i>	TCACCCTGTGCTGCTGACCG	GAACCGTGTGGCTCACACCA
	<i>Zm00001d038806</i>	GATGAAGTCGGACATCCTGATC	CTCCTCCATGATCCTCATCTTC
	<i>Zm00001d039566</i>	CTTCGGTTTCGTATGAACCATG	TGTCAGGATAACGTGTGTAGTC
	<i>Zm00001d010411</i>	CTATCCTTACACAGTCCGGTAC	TGTCCATAGACGATGTACCAAG
	<i>Zm00001d022550</i>	GCATTTGATTTCTTTGCAGGTG	AGTGGGACGACATTGTCTGAA
	<i>Zm00001d012731</i>	TTGCTCTAAAAGTACCGGCTAT	GCGATGAACAGAGTATTCACAC
	<i>Zm00001d039624</i>	TTTGTTTGAGAGTTCATGGCTC	AGTGTTACGACGAAACAAACAG
	<i>Zm00001d008841</i>	CTGTGCTTCTGAACTTTGTGT	AGCAAAAACCCCAGTCGATATA
	<i>Zm00001d031064</i>	GTTTTTGTAAGCGCGAAAAGAC	TTCCAAGAGAAGCTGGTTATT
	<i>Zm00001d051556</i>	GGCTTCAACATGATGCACTC	GATGCCGAGGTATCCGTAC
	<i>Zm00001d020717</i>	GGAGCTGAGGAAGAATTACTCC	CTGCATCGCCTTGTAAATGGAG

**Table S2.** The expression value of 10 selected genes in RNA-seq and qRT-PCR.

Genes	RNA-seq		qRT-PCR		Gene name
	WT	<i>nec-t</i>	WT	<i>nec-t</i>	
<i>Zm00001d038806</i>	1	44.592	1	28.9	heat-shock_protein_101
<i>Zm00001d039566</i>	1	99.073	1	120.54	heat_shock_protein18f
<i>Zm00001d010411</i>	1	0.112	1	0.067	Aux/IAA-transcription_factor_38
<i>Zm00001d022550</i>	1	0.097	1	0.022	bZIP-transcription_factor_92
<i>Zm00001d012731</i>	1	0.343	1	0.166	ARF-transcription_factor_26
<i>Zm00001d039624</i>	1	0.291	1	0.207	Aux/IAA-transcription_factor_8
<i>Zm00001d008841</i>	1	222.86	1	117.90	heat_shock_protein18c
<i>Zm00001d031064</i>	1	0.486	1	0.075	ARF-transcription_factor_34
<i>Zm00001d051556</i>	1	0.027	1	0.019	nine-cis-epoxycarotenoid_dioxygenase6
<i>Zm00001d020717</i>	1	0.244	1	0.036	abscisic_acid_8'-hydroxylase4