

A

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DNA: ATGGATGAGCGCGGGGAGAAGGAGGAGGAGCACGGAGTAGTGGAGGAGGAGACGGCGGCG 60
+1: M D E R G E K E E E H G V V E E E T A A 20
DNA: GTTGTGCTCAAGGAGGTGGAGGTGGAGATGGAGATGGTCCGGCGCTCTGAAGAAGCCTCG 120
+1: V V L K E V E V E M E M V G G S E E A S 40
DNA: GCGGCGCCGCTCCTCCTCGCGCACCCGTGCTCGCTGCTGCAGCTCCTGCTCCGCGCCTGC 180
+1: A A P L L L A H P C S L L Q L L L R A C 60
DNA: GCCGGCTGCCTGGTGCGCCTGCTGCACGGCCACTGCAGCGACGGCGCCAACGACGACCCA 240
+1: A G C L V R L L H G H C S D G A N D D P 80
DNA: AAAGCTGCTGCCGACGACGACGACGCTGCGCCTGAAGCTGCTGCTGCTGCGGGCGGGGGC 300
+1: K A A A D D D D A A P E A A A A A A A G 100
DNA: GATGGCGGCGACAAGGCAGCCACCGTAAGTGTCTGTTCCGAGACCACCGCTTGATATATTTG 360
+1: D G G D K A A T 108
DNA: TCGGTCGTACACGTAACGTACGTACGGTAACCGGTCGGATCGATCATCGTGTAACATGC 420
DNA: ATGCAAACCTTTGCAGTACTTGTACATGCAGGAGGTGTGGGCACTGAGGAGGAGCCGAC 480
+2: Y L Y M Q E V W A V R R R P T 123
DNA: GACGCCCCGCCGTCCGAGAGAAGGTTCCGGTGGCAATGGAGGGAACCACCACTAG 535
+2: T P G R P R E G S G G N G N H H * 140

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B

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B73: MDERGEKDEE EHGVAEEEMA AVVLKEVEVE MVGGSEEASA APLLLAHPCS 50
GQ: MDERGEK-EE EHGVEEETA AVVLKEVEVE MVGGSEEASA APLLLAHPCS 49

B73: VLQLLLRACA GCLVRLLLHG CSDGDDADPK AAADDDDDAA PEAAAAA-D 99
GQ: LLRLLLRACA GCLVRLLLHY CSDGDDDDPK AAADDDDDAA PEAAAAAAD 99

B73: GGDKAATYLY MQEVWA VRRRPTTPGRPREGSGGNGGNHH* 140
GQ: GGDKAATYLY MQEVWA VRRRPTTPGRPREGSGGNGGNHH* 140

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Supplemental Figure 1. ZmPROPEP1 A, genomic sequence cloned from Zea mays variety Golden Queen (GQ) aligned with the encoded protein. “EKE” motifs in the precursor are shown in maroon, amphipathic helix in green, alternatively spliced amino acids in gold, and ZmPep1 peptide in blue. The intron is shown in grey; B. alignment of cDNA sequence from var. B73 and var. GQ. Differing residues are highlighted in blue. The active ZmPep1 peptide is underlined.

Supplemental Table 1: Primers used for semi-quantitative RT-PCR analysis

Gene	GenBank #	Forward primer (5' to 3')	Reverse primer (5' to 3')	Cycles	Amplicon Size (bp)	Reference
ACC Oxidase	AY359573	GATCGACTTCTCCAAGCTG	TGTAGAAGATGTCCCTCCAGT	27	281	Doehlemann <i>et al.</i> , 2008
Actin	J01238	TCAGCAGGTCTTCTCTTTCTT	TCCTTCATATTTCCCTTCGTTT	33	303	Kirchberger <i>et al.</i> , 2007
Anthranilate Synthase component 2	NM_001159139	ATCATTTGCAGACTGTTCTTGA	ATGAGTCCATCTTCAGTCCAT	25	288	none
Allene oxide cyclase	AY488136	CTTCTACTTCGGAGACTACGG	TCAGTTGGTGTAGTTGTCGAG	27	295	Erb <i>et al.</i> , 2009
Allene oxide synthase	AY488135	ACAAGGTGGAGAAGAAGGAC	GTCGTTGAGCTTGTGAACT	27	257	Erb <i>et al.</i> , 2009
Bx1 Tryptophan Synthase α subunit	NM_001111749	AGTGAAGCCAAGAACAACAA	GGGCTTGTAGTACCTTCT	25	201	Erb <i>et al.</i> , 2009
Endochitinase A	EU963425	GTTCTTCAACGGCATCAAG	CGTAGTTGTAGTCCACGAGA	33	311	Doehlemann <i>et al.</i> , 2008
Peroxidase	AY107804	CATCTACAACGACACCAACAT	TAGTTCACGTGGAGCAGGTA	27	345	Doehlemann <i>et al.</i> , 2008
PR Protein Precursor	BT039519	GAGAACFCGCCTCAAGACTAC	GGCGTATTTGTACCACTGTTT	34	255	Doehlemann <i>et al.</i> , 2008
Endochitinase PR-4	EU968115	CAGATCTCCTGGAACCTCAAC	TGGCAGAAGCTGCTTGTAGTAG	30	263	Doehlemann <i>et al.</i> , 2008
SerPIN (Serine Proteinase INhibitor)	NM_001154840	GGAAGCTAGGAGGAAATCAA	ATGCAGCAAATATAGCCAAC	30	162	Erb <i>et al.</i> , 2009
ZmPROPEP1	DY240150	AGTAGGTGGCTGCCTTGT	GAGTAGTGGAGGAGGAGACG	39	294	none