

Table S4. Single Nucleotide Polymorphisms in dothistromin genes, grouped by dothistromin gene loci

New gene name	Dotse1 Protein ID ^a	Amino acids	Unique missense SNPs ^b	Unique synonymous SNPs ^b	Selection dN/dS mean ^c	% ID ^d Ap	% ID An	Predicted or known function
<i>Ver1</i>	75411	264	1	28	0.0199	79.1	79.2	NAD(P) reductase
<i>DotB</i>	75412	415	16	38	0.2035	-	24.0	peroxidase
<i>DotC</i>	75413	581	13	59	0.0779	31.2	-	MFS transporter
<i>PksA</i>	48345	2400	37	113	0.1653	55.1	58.2	polyketide synthase
<i>CypX</i>	139960	512	6	28	0.0886	58.9	61.6	P450 monooxygenase
<i>AvfA</i>	75546	285	9	18	0.1651	49.3	44.9	NAD(P) reductase
<i>EpoA</i>	57187	421	15	33	0.1513	-	-	Epoxide hydrolase
<i>MoxY</i>	75547	627	9	39	0.1034	55.4	50.6	flavin-binding monooxygenase
<i>AflR</i>	75566	480	6	22	0.1087	27.5	30.4	Regulatory protein
<i>AflJ</i>	57214	457	18	29	0.2424	37.1	40.8	Methyltransferase
<i>Est1</i>	75609	329	9	37	0.0899	29.6	27.8	Esterase (alpha/beta hydrolase)
<i>OrdB</i>	75648	268	5	14	0.1012	54.1	45.3	NAD(P) reductase
<i>AvnA</i>	57312	526	16	79	0.0845	57.5	58.3	P450 monooxygenase
<i>HexB</i>	181128	1905	35	131	0.1380	52.2	46.0	Fatty acid synthase
<i>HexA</i>	75653	1693	34	93	0.1845	55.4	45.5	Fatty acid synthase
<i>HypC</i>	66978	186	12	15	0.2864	35.2	47.9	Anthrone oxidase
<i>VbsA</i>	75656	648	5	48	0.0548	72.3	73.1	VerB synthase (cyclase)
<i>Nor1</i>	75691	269	7	28	0.0662	59.7	58.5	NAD(P) reductase
<i>AdhA</i>	48495	307	5	41	0.0239	58.1	60.6	Alcohol dehydrogenase
<i>VerB</i>	75692	521	5	57	0.1765	67.1	67.6	Desaturase (P450 monooxygenase)

Row shading indicates groupings of genes (top to bottom) in loci 1-6 (Chettri et al 2013, Fungal Genetics and Biology, 51, 12-20).

^aProtein identification (accession; PID) numbers refer to those at (<http://genome.jgi.doe.gov/Dotse1/Dotse1.home.html>). The PID numbers shown are the searchable JGI gene models; updated Dotse1 PID numbers for improved gene models are *HexA* 66976, *PksA* 192192, *Ver1* 192193, *HypC* 75655.

^bNumber of unique SNPs (exon sequence only) compared to NZE10.

^cMean of all pairwise comparisons between each genome and the NZE genome, calculated using CodeML.

^dPercentage amino acid identities (% ID) to *A. parasiticus* (Ap) and *A. nidulans* (An) AF/ST genes determined by CLUSTALW whole sequence alignment.