

Supplementary Table ST5. Splice site locations significantly associated with monophyletic clades (P<0.0001). Locations mapped to consensus sequences of core NR-PKS domains (SAT – starter acyl transferase, KS – ketoacyl synthase, AT – acyl transferase, PT – product template, TE – thioesterase). Inherited splice junctions (i.e. overrepresented at an ancestor node) are given in parentheses.

Clade	Gene tree node	SAT	KS	AT	PT	TE
α (C2-C7a)	<i>g66</i>	403	36, 219, 283	262	-	299
β (C2-C7b: azaphilones, meroterpenoids)	<i>g182</i>	(455)	258	48	-	-
	<i>g341</i>	455	-	-	-	-
γ.C2-C7c monocyclic (orsellinic acid, resorcylic acid lactones)	<i>g404</i>	(174),(404)	(515), 622	-	-	-
	<i>g405</i>	(174),(404)	515	-	-	-
γ.C6-C11 (emodins, atrochyrson, asperthecin)	<i>g454 - alternariol</i>	(174),(404)	(122), 278	-	(67)	-
	<i>g494 – asperthecin/alternariol</i>	(174),(404)	122	-	(67)	-
	<i>g550 -mdp</i>	(174),(404)	254	-	(67)	-
γ.C2-C7d bicyclic (THN, melanins)	<i>g626</i>	(174),(404)	-	-	(67)	597
γ.C2-C7e multicyclic (naphthopyrone, melanins, aurofusarin, bikaverin)	<i>g628 - pksN</i>	(174),(404)	230, (334)	-	(67), (616)	-
	<i>g725 – aur/YWAI</i>	(174),(404)	334	-	(67), (616)	-
γ.C4-C9 (afatoxins, sterigmatocystin, fusarubins)	<i>g809</i>	(174), 203, (404)	-	-	(67), (247), (616)	(592)
	<i>g813</i>	(174),(404)	-	-	(67), (247), (616)	592
	<i>g814</i>	(174),(404)	-	-	(67), 247, (616)	-
γ.C2-C7e+γ.C4-C9	<i>g815</i>	(174),(404)	-	-	(67), 616	-
γ.C2-C7d/e+γ.C4-C9+γ.C6-C11	<i>g820</i>	(174),(404)	-	-	67	-
γ.C2-C7c/d/e+γ.C4-C9+γ.C6-C11	<i>g821</i>	174,404	-	-	-	-