

Table S1 Occurrence of the TTAGGGTTAC / GTAACCCTAA *Knoxdaviesia* telomere repeat in *K. capensis* and *K. proteae*

Scaffold	Repeat	Start	End	Length
<i>K. proteae</i>				
scaffold16 (3')	(TTAGGGTTAC)8-(TTA)	329642	329724	83
scaffold21 (5')	(GTAACCCTAA)8-(GTAACCCTAT)2	1	100	100
scaffold36 (3')	(TTAGGGTTAC)8-(TTAG)	400522	400605	84
scaffold45 (5')	(TAA)-(GTAACCCTAA)8	1	83	83
scaffold50 (5')	(CTAA)-(GTAACCCTAA)8	1	84	84
scaffold51 (5')	(CCTAA)-(GTAACCCTAA)8	1	85	85
scaffold75 (5')	(GTAACCCTAA)7-(GTAA)(CTAA)-CC-(CTAA)(GTAA)(CTAA)-CC-(CTAA)(GTAA)-C-(CTAA)2-C-(CTAA)2-CC-[(CTAA)2-C]3(CTACCCTAA)(GTAACC)	1	164	164
scaffold86 (5')	(ACCCTAA)-(GTAACCCTAA)8	1	87	87
scaffold88 (5')	(AACCTAA)-(GTAACCCTAA)8	1	88	88
scaffold107 (3')	(TTAGGGTTAC)8-(TTAGG)	1987	2071	85
<i>K. capensis</i>				
scaffold3 (in a transposon)	(TTAGGGTTAC)10-T-(TTAGGGTTAC)5-TTAGGGTTNA-(GTAACCCTAA)3-(GAAACCCTAA)-(GTAACCCTAA)7	1165579	1165848	270
scaffold6 (3')	(TTAGGGTTAC)8-(TTAGGGTT)	2648838	2648925	88
scaffold7 (3')	(TTAGGGTTAC)11-(TTAGGGTT)	2670629	2670746	118
scaffold13 (3')	(TTAGGGTTAC)8-T-(TTAGGGTTAC)9-(TTAGGGTT)	212831	213010	180
scaffold17 (5')	(AA)-(GTAACCCTAA)8	1	82	82
scaffold18 (3')	(TTAGGGTTAC)11-(TTAGGGTT)	144117	144234	118
scaffold20 (3 kbp from 5')	(TAGGGTTAC)-(TTAGGGTTAC)13-(TTAGGGTTTC)-(TTAGGGTTAC)27-(TTA)	49916	50334	419
scaffold22 (5')	(CCCTAA)-(GTAACCCTAA)8	1	85	85
scaffold24 (5')	(TAA)-(GTAACCCTAA)8	1	83	83

Table S2 Populous orthogroups identified in the *Knoxdaviesia* genomes.

Orthogroup	<i>K. capensis</i>	<i>K. proteae</i>	Total	Description^a
Knox_OG_0001	5	5	10	ABC transporter, potential drug resistance
Knox_OG_0002	4	4	8	glycosyl hydrolase family 3
Knox_OG_0003	4	4	8	Heat shock protein 70
Knox_OG_0004	4	4	8	DNA/RNA helicase, ATP-dependent, DEAH-box type
Knox_OG_0005	4	4	8	ABC-2 type transporter
Knox_OG_0006	4	3	7	Glucan 1,3-beta-glucosidase (GH55)
Knox_OG_0007	3	3	6	OPT oligopeptide transporter
Knox_OG_0008	3	3	6	sulfate permease
Knox_OG_0009	3	3	6	Phosphate-repressible phosphate permease
Knox_OG_0010	3	3	6	serin endopeptidase
Knox_OG_0011	3	3	6	OPT family small oligopeptide transporter
Knox_OG_0012	3	3	6	MFS general substrate transporter
Knox_OG_0013	3	3	6	Chitin synthase
Knox_OG_0014	3	3	6	potassium/sodium efflux P-type ATPase
Knox_OG_0016	3	2	5	Translation elongation factor 2
Knox_OG_0017	3	2	5	Polyketide synthase
Knox_OG_0015	2	3	5	Phosphotransferase-like protein
Knox_OG_0018	2	3	5	NACHT nucleoside triphosphatase

^a Annotation inferred from the top 20 BLASTp hits and identified InterPro domains for each protein in the orthogroup

Table S3 Outcome of the protein BLAST for the *Knoxdaviesia capensis* and *K. proteae* species-specific proteins

	<u><i>K. capensis</i> proteins</u>	<u><i>K. proteae</i> proteins</u>
NO-BLAST^a	453 (54.9%)	718 (66.8%)
BLASTED	372 (45.1%)	356 (33.1%)
hypothetical/uncharacterised	114 (13.8%)	128 (11.9%)
BLASTED-not hypothetical ^b	258 (31.3%)	228 (21.2%)
TOTAL	825	1075

^a No significant BLAST hits obtained at e-value $\leq 1E-03$

^b Meaningful BLASTp annotation

Table S4 Cysteine-rich secreted proteins and proteins with hits to the Pathogen Host Interaction (PHI) database in *Knoxdaviesia capensis* and *K. proteae*.

	<i>K. capensis</i>			<i>K. proteae</i>		
	Proteins in shared orthogroups (%)	Unique secreted proteins (%)	Species-specific proteins (%)	Proteins in shared orthogroups (%)	Unique secreted proteins (%)	Species-specific proteins (%)
PHI-BLAST mutant phenotypes						
effector (plant avirulence determinant)	3 (1.2%)	1 (1.5%)	1 (3.6%)	3 (1.2%)	0	0
increased virulence	2 (0.8%)	2 (3.1%)	0	3 (1.2%)	0	0
lethal	0	1 (1.5%)	0	0	0	0
loss of pathogenicity	1 (0.4%)	1 (1.5%)	0	1 (0.4%)	2 (4.1%)	0
mixed outcome	1 (0.4%)	0	0	1 (0.4%)	0	0
reduced virulence	40 (16.3%)	9 (13.8%)	2 (7.1%)	36 (14.8%)	6 (12.2%)	0
unaffected pathogenicity	37 (15%)	6 (9.2%)	0	38 (15.6%)	10 (20.4%)	1 (3%)
No hits in PHI database	162 (65.9%)	45 (69.2%)	25 (89.3%)	162 (66.4%)	31 (63.3%)	32 (97%)
Cysteine-rich proteins						
≥ 2 % Cysteine residues	86 (35%)	12 (18.5%)	10 (35.7%)	84 (34.4%)	16 (32.7%)	9 (27.3%)
SSCPs ^a	33 (13.4%)	3 (4.6%)	5 (17.9%)	32 (13.1%)	5 (10.2%)	7 (21.2%)
TOTAL SECRETOME	246	65	28	244	49	33

^a SSCPs = small secreted cysteine-rich proteins; these have a cysteine content of ≥ 2 % and a length of < 200 residues

Table S5 Amplification of the T1PKS-4 cluster deletion in 11 *Knoxdaviesia capensis* and *K. proteae* isolates.

<i>K. proteae</i>				<i>K. capensis</i>			
Isolate	Population ^a	<i>Protea</i> Host	Product size (bp) ^a	Isolate	Population ^a	<i>Protea</i> Host	Product size (bp) ^a
Ceres1	Ceres	<i>P. repens</i>	~300 bp	ATX Y	Ataraxia	<i>P. coronata</i>	~800 bp
F11.2	Franschoek	"	"	DTK F	DuToit'sKloof	"	"
F17.7	"	"	"	GRT3	Greyton	"	"
F27.3	"	"	"	HB9	Helderberg	"	"
G004	Gouritz	"	"	KM6	Kleinmond	"	"
G016	"	"	"	HP10	Betty's Bay 2	<i>P. lepidocarpodendron</i>	"
G046	"	"	"	H4	Hermanus	<i>P. longifolia</i>	"
G105	"	"	"	KL18	Kogelberg 1	"	"
G009	Sir Lowrys Pass	"	"	BB18	Betty's Bay	<i>P. neriifolia</i>	"
SB2.1	Stellenbosch	"	"	KN 3x	Kogelberg 2	"	"
SB2.8	"	"	"	G081	Gouritz	<i>P. repens</i>	"

^a Isolates were previously collected by Aylward et al. 2014a, 2014b, 2015a, 2015b, 2016a, 2017a.

^b A PCR product of ~300 bp in *K. proteae* and ~800 bp in *K. capensis* indicates that a region of the polyketide synthase gene in cluster T1PKS-4 is missing in *K. proteae*