Botrytis cinerea TE description

Citation : Adeline Simon, Alex Mercier, Pierre Gladieux, Benoît Poinssot, Anne-Sophie Walker and Muriel Viaud (2022).
Botrytis cinerea strains infecting grapevine and tomato display contrasted repertoires of accessory chromosomes, transposons and small RNAs.
Peer Community Journal, 2: e83. https://doi.org/10.24072/pcjournal.211

- **Sequences** of panTE consensus are available at :

https://bioinfo.bioger.inrae.fr/portal/data-browser/public/botrytis/genomes/cinerea/Vv3/PanTE_Botrytis-cinerea.fasta

									Total coverage			# fullLgthCopies (FLC)			coverage by FLC		
Class	Order	Superfamily	W_CODE	*Subfamily name / consensus name*		*Len (Kb)*	*Consensus name in B05.10 (Porquier et al., 2016)*	*Subfamily name in B05.10 (Porquier et al., 2021)*	*B0510*	*Sl3*	*Vv3*	*B0510*	*Sl3*	*Vv3*	*B0510*	*Sl3*	*Vv3*
I	LTR	Copia	RLC	Copia_1		6.4	RLX_P27.0	BcCopia1	0.25%	0.39%	0.54%	12	22	29	0.18%	0.33%	0.41%
				Copia_2		8.2	RLX_G54	BcCopia2	0.14%	0.12%	0.16%	6	4	5	0.12%	0.08%	0.09%
				Copia_3		5.4					0.18%			14			0.17%
				Copia_4		5.4					0.14%			10			0.12%
				Copia_5		6					0.63%			37			0.50%
				Copia_6		5.5				0.14%			8			0.10%	
		Gypsy	RLG	Boty/Gypsy_1	Boty-var1	6.6	RLX_P26.1	BcGypsy1	0.27%	0.30%	0.77%	13	15	25	0.20%	0.23%	0.38%
					Boty-var2	6.5	RLX_P21.1		0.43%	0.17%	0.15%	21	7	9	0.33%	0.11%	0.12%
					Boty-var3	6.4	RLX_P6.1		0.14%	0.18%	0.18%	7	10	8	0.11%	0.15%	0.11%
					Boty-var4	6.5	RLX_P13.1		0.12%	0.12%	0.07%	7	6	3	0.11%	0.09%	0.04%
					Boty-var5	6.1					0.26%			18			0.25%
					Boty-var6	6.3					0.15%			7			0.10%
					Boty-var7	6.2					0.09%			5			0.07%
					Boty-var8	6.2					0.07%			5			0.07%
					Boty-var9	6.6				0.25%			14			0.21%	
					Boty-var10	6.6				0.27%			11			0.17%	
				Gypsy_2		6.4	RLX_ P17.7	BcGypsy2	0.14%	0.12%	0.18%	8	6	9	0.12%	0.09%	0.13%
				Gypsy_3		7.4	RLX_B-R56	BcGypsy3	0.28%	0.35%	0.34%	13	20	11	0.23%	0.34%	0.18%
				Gypsy_4		11	RLX_G57	BcGypsy4	0.57%	0.50%	0.39%	13	14	6	0.33%	0.36%	0.15%
				Gypsy_5		6.5					0.11%			6			0.09%
				Gypsy_6		6.7					0.21%			12			0.18%
				Gypsy_7		6.3					0.34%			23			0.32%
	TRIM	TRIM	RXX-TRIM	Trim_1		0.5					0.01%			7			0.01%
				Trim_2		0.5					0.01%			5			0.01%
II	TIR	Tc1-Mariner	DTT	Flipper		1.8	DTX_P14.9		0.06%	0.14%	0.19%	10	29	41	0.04%	0.12%	0.17%
				Mariner_1		1.9	DTX_G36		0.09%	0.13%	0.13%	16	25	26	0.07%	0.11%	0.11%
				Mariner_2		1.9				0.38%	0.26%		54	29		0.23%	0.12%
				Mariner_3		1.9				0.15%	0.12%		21	16		0.09%	0.07%
				Mariner_4		1.9					0.11%			18			0.08%
				Mariner_5		1.9					0.08%			27			0.11%
			DTX	TIRnoCat		0.7					0.15%			51			0.08%
	Helitron	Helitron	DHH	Helitron		15.5					1.37%			8			0.28%
			DXX-MITE	MITE_1		0.5	DXX-MITE_G19		0.04%		0.02%	6		15	0.01%		0.02%
				MITE_2		0.5	DXX-MITE_P15.8		0.47%			92			0.10%		
				MITE_3		0.4					0.23%			98			0.10%
				MITE_4		0.5					0.03%			15			0.02%
				MITE_5		0.5				0.02%			3			0.00%	
noCat				noCat_1		0.6	noCat_G9		0.45%			38			0.05%		
				noCat_2		13.9	noCat_R20		0.27%			1			0.03%		
				noCat_3		0.5					0.02%			8			
				noCat_4		19.7				0.40%			6			0.27%	
				noCat_5		6.8				0.40%			22			0.35%	
Coverage by shared subfamilies (B05.10, Sl3, Vv3)									**2.49%**	**3.04%**	**3.65%**				**1.84%**	**2.38%**	**2.38%**
Coverage by specific subfamilies (only one genome)									**1.19%**	**0.96%**	**3.62%**				**0.18%**	**0.73%**	**2.04%**
Coverage by subfamilies shared by 2 genomes									**0.04%**	**0.53%**	**0.41%**				**0.01%**	**0.33%**	**0.21%**
Nb consensus				42 consensus (33 subfamilies)					15	19	33						
Genome coverage									**3.72%**	**4.53%**	**7.70%**				**2.02%**	**3.44%**	**4.53%**