Correction to: Secondary metabolite gene clusters arrangement and conservation within the genome of *Stemphylium lycopersici* codes the pathways for the synthesis of specific and non-specific toxins

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Published online: 6 October 2020

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Correction to: Australasian Plant Pathology.
<https://doi.org/10.1007/s13313-020-00737-1>

The original version of this article unfortunately contained mistakes introduced during the production process. The corrections are given in the following list:

- (1) In Introduction section, second paragraph, the third sentence should be rewritten as:
The etiological agents are three species of the genus *Stemphylium*: *S. solani*, G. F. Weber, *S. lycopersici* (Enjoji) W. Yamamm. (syn *S. floridanum* Hannon and G. F. Weber) and *S. botryosum* Wallr. F. sp. *lycopersici* Rotem, Y. Cohen, and I. Wahl (Jones et al. 2014).

- (2) In Fig. 7 caption, the word “desmethylobassianin” has been spelt incorrectly by the author to “desmethulbassianin”. The caption should be rewritten as:

Fig. 7 Gene cluster within the CIDEFI 212, CIDEFI 213 and CIDEFI 216 genomes at position 32.1, 104.1 and 205.3, respectively and similar gene clusters in other fungi corresponding to desmethylobassianin, tenellin and fumosorinone biosynthesis

- (3) Table 4 should be formatted horizontally. Also, the expression “CIDEFI number” in each row should be in a same line. The correct Table 4 is now given in this article.

The original article has been corrected.

The online version of the original article can be found at <https://doi.org/10.1007/s13313-020-00737-1>

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Table 4 Results of the prediction cluster analysis within the genome sequence of *Stemphylium lycopersici* CIDEFI 212, CIDEFI 213 and CIDEFI 216 performed. Columns 2, 3 and 4 provide the data to position the cluster within the isolates genome. Column 5 describes the homologous clusters found. Column 6 describes the core biosynthetic gene that gives the name to the cluster, and column 7 contains the size in base pairs of the cluster

Terpenes	Position	From	To	Most Similar known cluster	Core biosynthetic genes	Size (bp)
CIDEFI 212	6.1	199,054	220,684	Elsinochrome A (100%)/ Elsinochrome B (100%)/ Elsinochrome C (100%)	Squalene synthase*	21,631
CIDEFI 213	9.1	40,859	62,489		Squalene synthase*	21,631
CIDEFI 216	249.1	344,415	365,945		Squalene synthase*	21,631
CIDEFI 212	44.2	114,854	136,234	Elsinochrome B (100%)/ Elsinochrome C (100%)	Geranylgeranyl pyrophosphate synthetase*	21,381
CIDEFI 213	43.1	74,214	95,594		Geranylgeranyl pyrophosphate synthetase*	21,381
CIDEFI 216	242.1	148,756	170,136		Geranylgeranyl pyrophosphate synthetase*	21,381
CIDEFI 212	194.1	1	17,770	Elsinochrome B (100%)/ Elsinochrome C (100%)	Aristolochene synthase*	17,770
CIDEFI 213	235.1	502	22,564		Aristolochene synthase*	22,063
CIDEFI 216	278.1	3,008	25,070		Aristolochene synthase*	17,198
CIDEFI 212	79.1	6,649	29,885	Elsinochrome B (100%)/ Elsinochrome C (100%)	Terpenoid synthase*	23,237
CIDEFI 213	132.1	55,252	78,488		Terpenoid synthase*	23,237
CIDEFI 216	402.1	188,687	211,923		Phytoene synthase: Lycopene cyclase*	23,237
CIDEFI 212	16.1	245,556	267,948	Elsinochrome B (100%)/ Elsinochrome C (100%)	Terpenoid synthase***	22,393
CIDEFI 212	40.1	85,171	106,529		Terpenoid synthase*	21,359
CIDEFI 213	166.1	41,729	57,915		Terpenoid synthase*	16,187
CIDEFI 212	416.1	1	3,627	Elsinochrome B (100%)/ Elsinochrome C (100%)	Oxidoesqualene: Lanosterol cyclase**	3,627
CIDEFI 213	307.1	1	14,617		Oxidoesqualene: Lanosterol cyclase**	14,617
CIDEFI 216	227.1	1	21,613		Oxidoesqualene: Lanosterol cyclase**	21,613
CIDEFI 216	245.1	1	17,198	Elsinochrome B (100%)/ Elsinochrome C (100%)	Terpene synthase*	17,198
CIDEFI 213	11.2	291,207	315,569		Squalene- hopene cyclase	24,363
PKS						
CIDEFI 212	11.1	232,892	279,581	Most Similar known cluster Melanin (100%)/ Elsinochrome A (100%)/ Elsinochrome B (100%)/ Elsinochrome C (100%)	Core biosynthetic genes Polyketide synthase*	Size (bp) 46,581
CIDEFI 213	24.1	11,720	58,300		Polyketide synthase*	46,581
CIDEFI 216	165.1	301,560	348,140		Polyketide synthase*	46,581

Table 4 (continued)

CIDEFI 212	15.1	352,703	403,321	Fujikurins (50%)	Putative Polyketide synthase	50,619
CIDEFI 213	42.1	84,880	133,641	Fujikurins (50%)	Polyketide synthase	48,762
CIDEFI 216	228.1	1	26,873	Fujikurins (50%)	Polyketide synthase	26,873
CIDEFI 212	125.1	1,273	46,904	Neosartorin (40%)/ Asperthecin (28%)/ Tan-1612 (40%)/ Viridicatutoxin (9%)/ Emericellin (14%)/ Pestheic acid (10%)/ Trypadicin (14%)/ Alternariol (100%)	Polyketide synthase	45,632
CIDEFI 213	158.1	1,273	46,904	Neosartorin (40%)/ Asperthecin (28%)/ Tan-1612 (40%)/ Viridicatutoxin (9%)/ Emericellin (14%)/ Pestheic acid (10%)/ Trypadicin (14%)/ Alternariol (100%)	Polyketide synthase	45,632
CIDEFI 216	205.1	35	25,441	Neosartorin (40%)/ Asperthecin (28%)/ Tan-1612 (40%)/ Viridicatutoxin (9%)/ Emericellin (14%)/ Pestheic acid (10%)/ Trypadicin (14%)/ Alternariol (100%)	Polyketide synthase	25,407
CIDEFI 212	146.1	1	39,028	Pyranonigrin E (100%)/ T-toxin (100%)/ Fusarin (100%)	Lovastatin nonaketide synthase***	39,028
CIDEFI 213	225.1	1	28,976	Pyranonigrin E (100%)/ T-toxin (100%)/ Fusarin (100%)	Lovastatin nonaketide synthase***	28,976
CIDEFI 216	318.2	377,417	424,845	Pyranonigrin E (100%)/ T-toxin (100%)/ Fusarin (100%)	Lovastatin nonaketide synthase***	47,429
CIDEFI 212	196.1	1	17,919	(-) – Mellein (100%)	6-methylsalicylic acid synthase**	17,919
CIDEFI 213	259.1	1	21,316	(-) – Mellein (100%)	6-methylsalicylic acid synthase**	21,316
CIDEFI 213	11.1	106,871	152,238	(-) – Mellein (100%)	6-methylsalicylic acid synthase***	45,368
CIDEFI 216	392.1	1	9,699	(-) – Mellein (100%)	6-methylsalicylic acid synthase**	9,699
PKS	Position	From	To	Most Similar known cluster	Core biosynthetic genes	Size (bp)
CIDEFI 212	73.1	102,021	152,699	Betaenone A/ betaenone B/ betaenone C (50%)	Polyketide synthase*	50,679
CIDEFI 213	125.1	24,981	75,659	Betaenone C/ betaenone A (50%)	Polyketide synthase*	50,679
CIDEFI 216	289.1	25,936	76,224	Betaenone C/ betaenone A (50%)	Polyketide synthase*	50,289
CIDEFI 212	92.1	1	28,019	Monascorubrin (100%)	Polyketide synthase	28,019
CIDEFI 213	66.1	145,997	174,015	Monascorubrin (100%)	Polyketide synthase	28,019
CIDEFI 213	151.1	32,666	65,241	Sirodesmin (8%)	Polyketide synthase***	32,575
CIDEFI 216	170.1	1	37,630	Sirodesmin (8%)	Polyketide synthase***	37,630
CIDEFI 212	25.1	256,323	304,323		Polyketide synthase Pks H*	47,960
CIDEFI 213	8.1	227,551	275,510		Polyketide synthase Pks H*	47,960
CIDEFI 216	381.1	123,385	171,344		Polyketide synthase*	47,960

Table 4 (continued)

CIDEFI 212	58.1	15,549	58,757	Chalcone synthase 4*	43,209
CIDEFI 213	67.1	105,339	149,158	Chalcone synthase 4*	43,820
CIDEFI 216	171.1	157,263	201,082	Chalcone synthase b*	43,820
CIDEFI 212	74.1	92,807	143,033	Polyketide synthase Pks G*	50,227
CIDEFI 213	13.1	106,284	156,510	Polyketide synthase Pks G*	50,227
CIDEFI 216	318.1	242,514	283,320	Polyketide synthase*	40,807
CIDEFI 212	96.1	42,982	90,856	Polyketide synthase Pks J*	47,875
CIDEFI 213	107.1	38,071	85,945	Polyketide synthase Pks J*	47,875
CIDEFI 216	182.1	39,016	86,887	Polyketide synthase *	47,872
CIDEFI 212	115.1	1	43,301	Phenolphiocerol synthesis polyketide synthase ppsa*	43,301
CIDEFI 213	224.1	1	30,476	Phenolphiocerol synthesis polyketide synthase ppsa*	30,476
CIDEFI 216	241.1	79,008	120,787	Phenolphiocerol synthesis polyketide synthase ppsa*	41,780
CIDEFI 212	197.1	1	17,416	Polyketide synthase**	17,416
CIDEFI 216	224.1	210,959	258,797	Polyketide synthase	47,839
NRPS	Position	From	To	Core biosynthetic genes	Size (bp)
CIDEFI 212	33.1	14,891	71,149	Nonribosomal peptide synthetase 2*	56,259
CIDEFI 213	4.1	390,240	446,498	Nonribosomal peptide synthetase 2*	56,259
CIDEFI 216	205.2	984,238	1,031,391	Nonribosomal peptide synthetase 2*	47,154
CIDEFI 212	7.1	436,219	498,006	Nonribosomal peptide synthetase 4*	61,788
CIDEFI 213	20.1	65,214	127,001	Nonribosomal peptide synthetase 4*	61,788
CIDEFI 216	285.1	433,114	494,901	Hypothetical protein*	61,788
CIDEFI 212	10.1	410,818	471,615	Nonribosomal peptide synthetase 6/ Acetyl-CoA synthase like protein*	60,798
CIDEFI 213	93.1	52,841	113,638	Nonribosomal peptide synthetase 6/ Acetyl-CoA synthase like protein*	60,798
CIDEFI 216	200.1	432,405	493,202	Nonribosomal peptide synthetase 6/ Long- chain-fatty- acid- CoA ligase*	60,798
CIDEFI 212	138.1	9,632	49,338	Destruxin synthetase***	39,707
CIDEFI 213	186.1	9,632	44,626	Destruxin synthetase***	34,995
CIDEFI 216	181.1	1	44,001	Destruxin synthetase***	44,001
CIDEFI 212	30.1	323,863	351,313	Nonribosomal peptide synthetase	27,451
CIDEFI 213	393.1	1	7,303	Nonribosomal peptide synthetase 1**	7,303

Table 4 (continued)

NRPS-Like	CIDEFI 212	5.1	564,221	600,607	Most Similar known cluster Phomopsis (100%) Phomopsis (100%)	Size (bp)
	CIDEFI 213	157.1	33,384	60,448		
	CIDEFI 216	178.1	942,572	986,420		
	CIDEFI 212	16.2	323,940	367,528		
	CIDEFI 213	74.1	123,853	159,881		
	CIDEFI 216	196.1	931,701	975,289		
	CIDEFI 212	24.1	320,302	363,212		
	CIDEFI 213	57.1	167,122	197,641		
	CIDEFI 216	188.1	19,732	63,494		
	CIDEFI 212	28.1	150,438	194,072		
	CIDEFI 213	60.1	88,893	132,527		
	CIDEFI 216	212.1	1,022,295	1,065,929		
Others	CIDEFI 212	59.1	188,439	215,725	Desmethylobassianin (40%)/ Tenellin (40%)/ Fumosorinone (33%) Desmethylobassianin (40%)/ Tenellin (40%)/ Fumosorinone (33%) Desmethylobassianin (40%)/ Tenellin (40%)/ Fumosorinone (33%) Phenyloxazoline synthase mbtb/ polyketide synthase* nonribosomal peptide synthetase/ nonribosomal peptide synthetase mbtb* Phenyloxazoline synthase mbtb/ polyketide synthase mbtb/ peptide synthetase*	35,359
	CIDEFI 213	54.1	1	27,289		
	CIDEFI 216	251.1	34,559	61,869		
	CIDEFI 212	46.1	237,449	261,018		
	CIDEFI 216	197.1	75,512	118,709		
	CIDEFI 213	72.1	1	28,517		
	CIDEFI 212	32.1	1	35,359		
	CIDEFI 213	104.1	77,810	114,497		
	CIDEFI 216	205.3	1,508,521	1,546,674		
	CIDEFI 212	44.1	428	52,562		
	CIDEFI 216	242.2	232,307	284,441		
	CIDEFI 213	182.1	428	48,639		

Table 4 (continued)

CIDEFI 212	121.1	1	67,708	Emericellin (21%)/ Pesthetic acid (15%)/ Trypacin (14%)/ Endocrocin (22%)/ Neosartoricin (40%)/ Tan-1612 (40%)/ Asperthecin (28%)/ Emericellin (100%).	Ketoacyl-synt-domain- containing protein/ Aromatic prenyltransferase, DMATS type/ KR domain- containing protein*	67,708
CIDEFI 213	105.1	39,444	112,126	Emericellin (28%)/ Pesthetic acid (20%)/ Trypacin (21%)/ Endocrocin (22%)/ Neosartoricin (40%)/ Tan-1612 (40%)/ Asperthecin (28%)/ Emericellin (100%).	Ketoacyl-synt-domain- containing protein/ Aromatic prenyltransferase, DMATS type/ KR domain- containing protein*	72,683
CIDEFI 216	386.1	110	73,068	Emericellin (28%)/ Pesthetic acid (20%)/ Trypacin (21%)/ Endocrocin (22%)/ Neosartoricin (40%)/ Tan-1612 (40%)/ Asperthecin (28%)/ Emericellin (100%).	Polyketide synthase/ dimethylallyl tryptophan synthase 1/ polyketide synthase	72,959
CIDEFI 213	176.1	1	52,111	Deoxysambucinol/ Sambucinol/ Roridin E (100%)/ Harzianum B (100%)/ Gibberellin A3/ Gibberellin A1/ Gibberellin A7/ Gibberellin A4/ Gibberellin A9 (100%)	Nonribosomal peptide synthase/ trichodiene synthase/ Nonribosomal peptide synthase	52,111
CIDEFI 216	164.1	1,908	62,553	Deoxysambucinol/ Sambucinol/ Roridin E (100%)/ Harzianum B (100%)/ Gibberellin A3/ Gibberellin A1/ Gibberellin A7/ Gibberellin A4/ Gibberellin A9 (100%)	Nonribosomal peptide synthase/ trichodiene synthase/ Nonribosomal peptide synthase	60,646

*Clusters described within members of Pleosporaceae family. **Not described in other fungi genome. ***Similarity lower than 15%

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