Table S1. Alteration of *clsA* expression affects hyphal growth and branching

		0µg ml^{-1} atc				1.5µg ml^{-1} atc				0µM thiostrepton				100µM thiostrepton			
		A, M145 (n=83)		B, RJ118b (n=60)		C, M145 (n=75)		D, RJ118b (n=88)		E, VJ8600 (n=56)		F, RJ110 (n=74)		G, VJ8600 (n=69)		H, RJ110 (n=108)	
	Parameter	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
1	Substrate hyphal width (µm)	0.54	0.01	0.51	0.01	0.56	0.03	0.67	0.16	0.57	0.06	0.69	0.04	0.54	0.02	1.21	0.26
2	Spore width (µm)	0.96	0.02	ND	ND	0.95	0.02	1.03	0.15	0.97	0.02	1.01	0.06	0.96	0.01	1.89	0.40
3	Tip growth distance (µm)	2.99	0.68	4.90	0.79	3.34	0.47	1.62	0.39	2.49	0.50	2.89	0.13	2.66	0.87	1.98	0.23
4	Inter-branch distance (µm)	6.23	1.63	13.88	4.97	5.18	0.97	2.88	0.64	5.55	1.49	5.28	0.46	6.34	1.22	2.28	0.36
4	Tip growth angle (°)	142.37	2.75	157.38	5.20	141.77	5.46	115.50	15.90	142.19	1.34	138.75	2.49	139.93	4.47	101.70	19.50
6	Branching angle (°)	111.61	5.69	101.08	3.95	114.28	6.81	93.00	16.60	100.82	8.33	97.55	2.96	100.82	8.33	82.46	8.80

M145 (A, C), RJ118b (B, D), VJ8600 (E, G) and RJ110 (F, H) were grown in the absence (A, B, E, F) and presence of 1.5 µg ml^{-1} atc (C, D) or 100 µM thiostrepton (G, H) and a number of parameters that quantitatively described mycelial morphology (see Fig 4a) were measured, means calculated and displayed in the table. 1, hyphal width (µm,); 2, spore width (µm,); 3, tip growth distance (the distance between changes in tip direction) (µm); 4, inter-branch distance (µm); 5, tip growth angle (the angle which a hypha was bent following a change in tip growth direction) (°); 6, branching angle (°). SD, Standard Deviation.

Table S2. Results of tests of significance between treated and untreated strains displaying altered mycelial morphology.

	Parameter	A,B	C,D	A,C	B,D	E,F	G,H	E,G	F,H
1	**Substrate hyphal width (µm)**	S	NS	NS	NS	S	S	NS	S
2	**Spore width (µm)**	ND	NS	NS	ND	NS	S	NS	S
3	**Tip growth distance (µm)**	S	S	NS	S	NS	S	NS	S
4	**Inter-branch distance (µm)**	S	S	NS	S	NS	S	NS	S
5	**Tip growth angle (°)**	S	S	NS	S	S	S	NS	S
6	**Branching angle (°)**	S	S	NS	NS	NS	S	NS	S

S, significantly different ($p<0.05$); NS, not significantly different following a Students t-test between the strains/treatment listed in the column header and referring to the strain/treatment labeled A-H in Table S1A. ND- not determined (RJ118b was unable to produce aerial hyphae or sporulate in the absence of atc).

Table S3. Primers used in this study

CL100	CCCAAGCTTGGATCCAATCGGCTGCGAC
CL101	GGGACTAGTCATATGTCTAGATGTGTATAAGAGACAGTCTGG
CL102	GGGATATCCATATGAGCATCATTGGCTCGTT
CL103	CCCAAGCTTCTAGATCAATCGGCTGCGACGT
CL104	CGAGAGCCAGAGCTTTTTTGCGTTGAGGTAAGGTCAGTGATTCGGGGGATCCGTCGACC
CL105	GGCCATCCGGCCACCGGGACCGCGCAATCGGCGAGTTCATGTAGGCGTGAGCTG
*SCO1389*_F1	GAGCATCATTGGCTCGTTTC
*SCO1389*_R1	GAACACCTGCCCACCAATAC
*hrdB*_F	GAGGCGACCGAGGAGCCGAA
*hrdB*_R	GCGGAGGTTGGCCTCCAGCA

Restriction sites (CL100-CL103) and homologous regions to *am*^{r} (pIJ673; (Gust *et al*., 2003)) are underlined (CL104 & CL105). The sections of CL104 & CL105 not underlined are sequences homologous to regions directly flanking *SCO1389*.

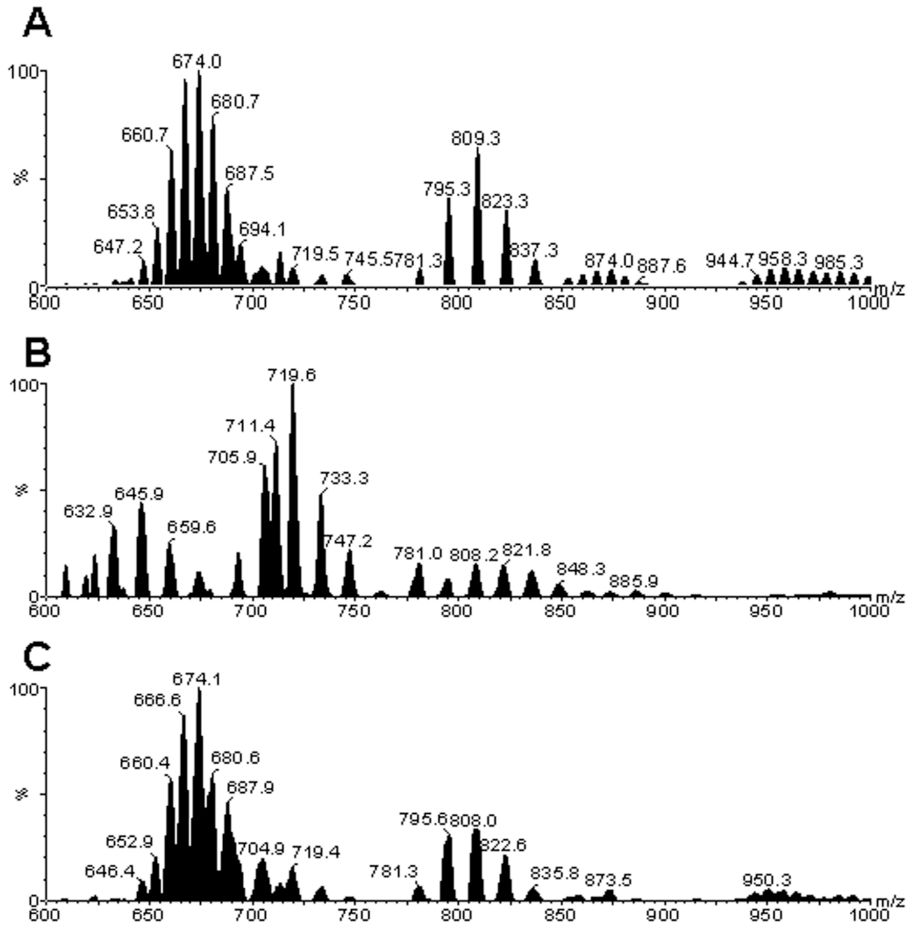

Fig S1. Negative ion ES-MS survey scans (600-1000 m/z) of total lipid extracts from M145 (A) and RJ118b in the absence (B) or presence (C) of 1.5 µg ml^{-1} atc).

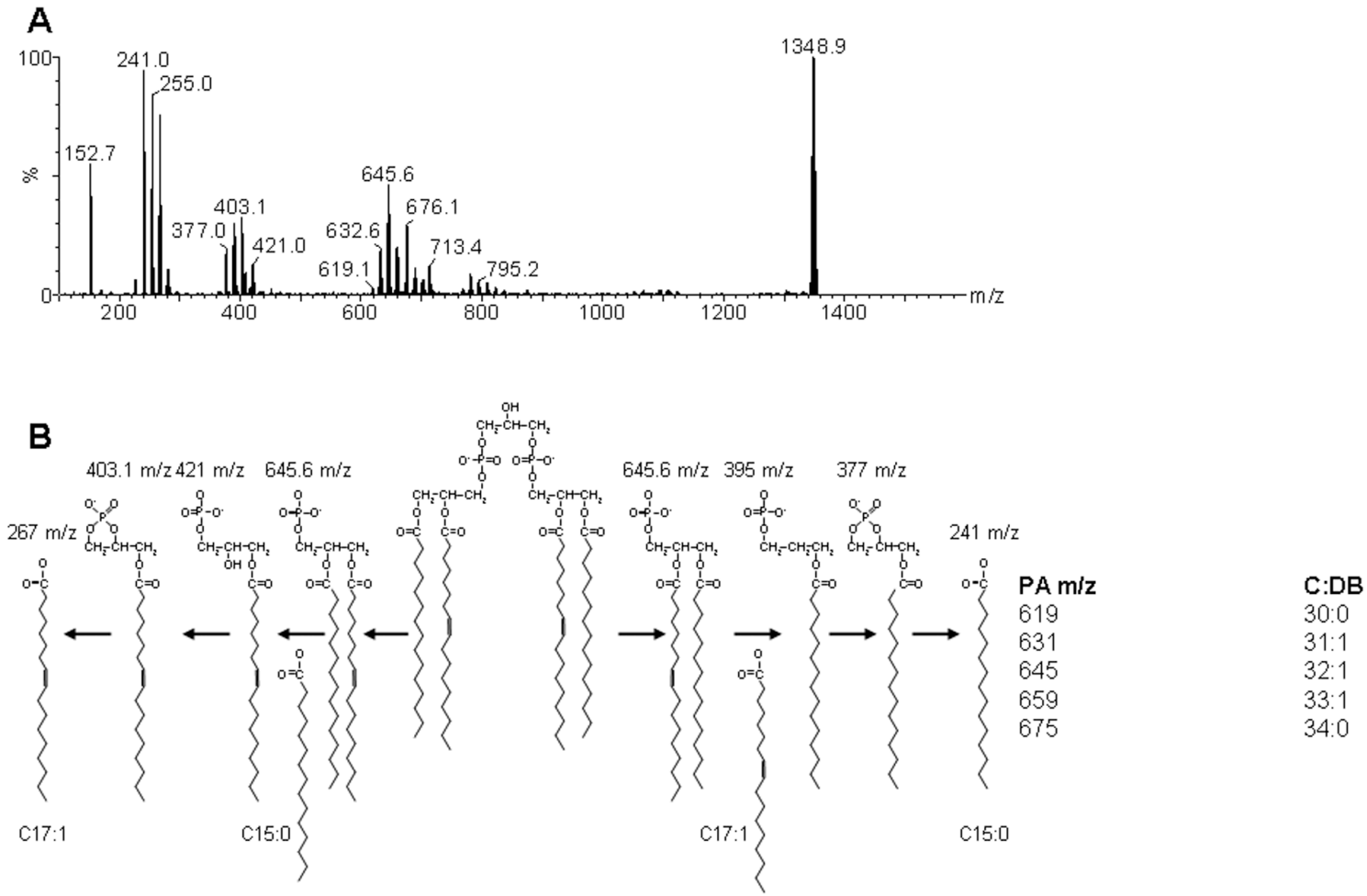

Fig S2. Fragmentation analysis of 1348.9 CL peak. A; ES-MS-MS daughter ion spectrum of the 1348.9 m/z ion. B; Assignment of some of the principal daughter ions from 1348.9 m/z peak according to their daughter ion fragments: [PA-H]-, [lysoPA-H]-, or [lysoPA-H_20-H]- and fatty acids based on their [M-H]- values observed in panel A. m/z of phosphatidic acid (PA) and numbers of carbon:double bond (C:DB) are also displayed.

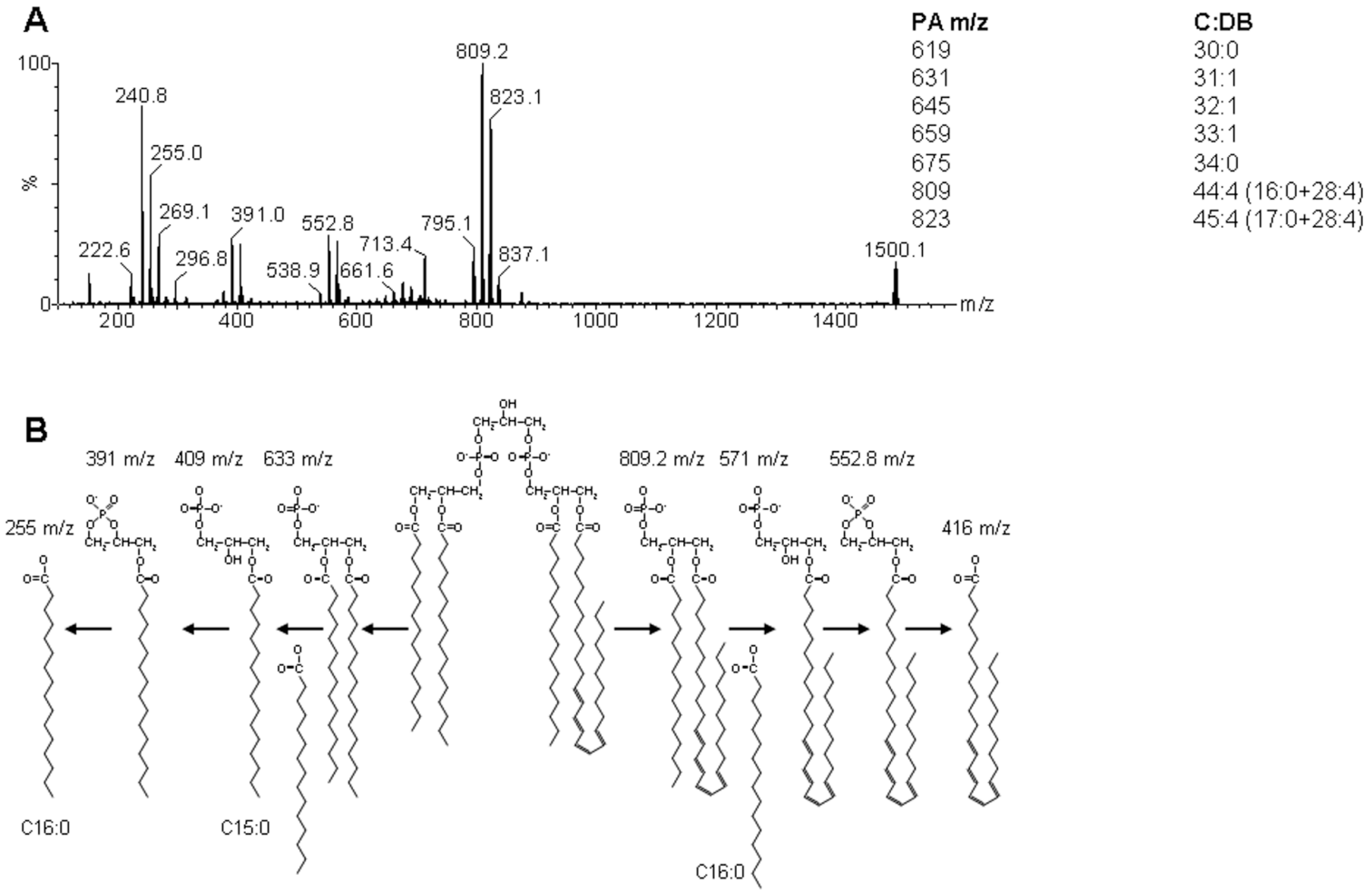

Fig S3. Fragmentation analysis of 1500.1 CL peak. A; ES-MS-MS daughter ion spectrum of the 1500.1 m/z ion. B; Assignment of some of the principal daughter ions from 1500.1 m/z peak according to their daughter ion fragments: [PA-H]-, [lysoPA-H]-, or [lysoPA-$H_2$0-H]- and fatty acids based on their [M-H]- values observed in panel A. m/z of phosphatidic acid (PA) and numbers of carbon:double bond (C:DB) are also displayed.

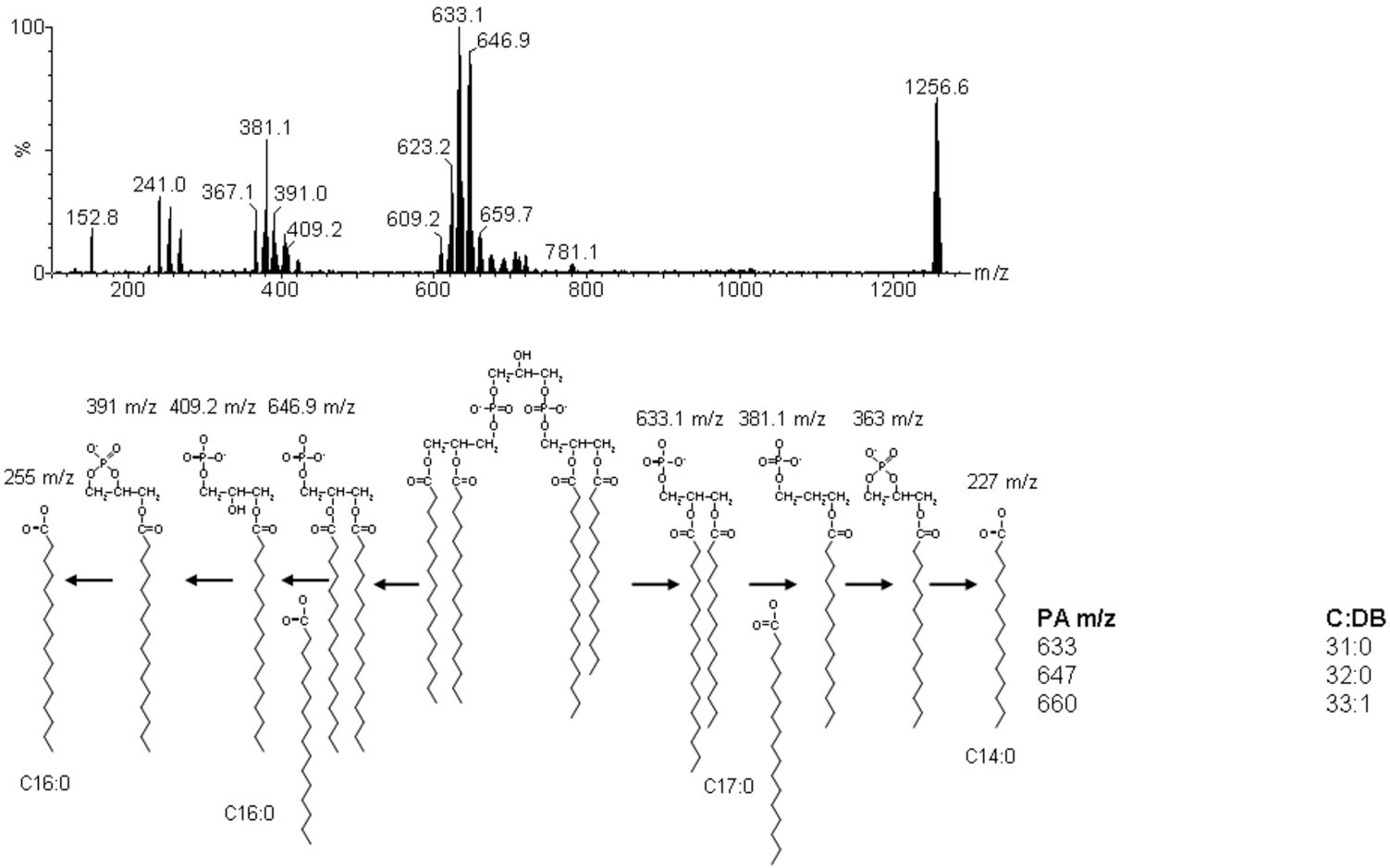

Fig S4. Fragmentation analysis of 1256.6 CL peak. A; ES-MS-MS daughter ion spectrum of the 1256.6 m/z ion. B; Assignment of some of the principal daughter ions from 1256.6 m/z peak according to their daughter ion fragments: [PA-H]-, [lysoPA-H]-, or [lysoPA-$H_2$0-H]- and fatty acids based on their [M-H]- values observed in panel A. m/z of phosphatidic acid (PA) and numbers of carbon:double bond (C:DB) are also displayed