

Figure S1. Preliminary Bayesian ITS tree of all 20 *Fusarium* isolated from *P. unifilis* eggshells, with *Neonectria* as outgroup. Species names are followed by herbarium codes and GenBank accession numbers. Sequences obtained here are in bold. Type strains are marked with a "T". An interrupted branch (//) indicates its length has been reduced. Numbers above and below the branches represent Bayesian posterior probability (PP) and maximum likelihood bootstrap values (BS), respectively (shown only if PP ≥ 0.90 and BS ≥ 50%). Solid dots indicate full support in both analyses. Species complexes are indicated in the right side of the figure (lines are discontinuous if recovered as non-monophyletic). The scale bar represents the average number of substitutions per site.

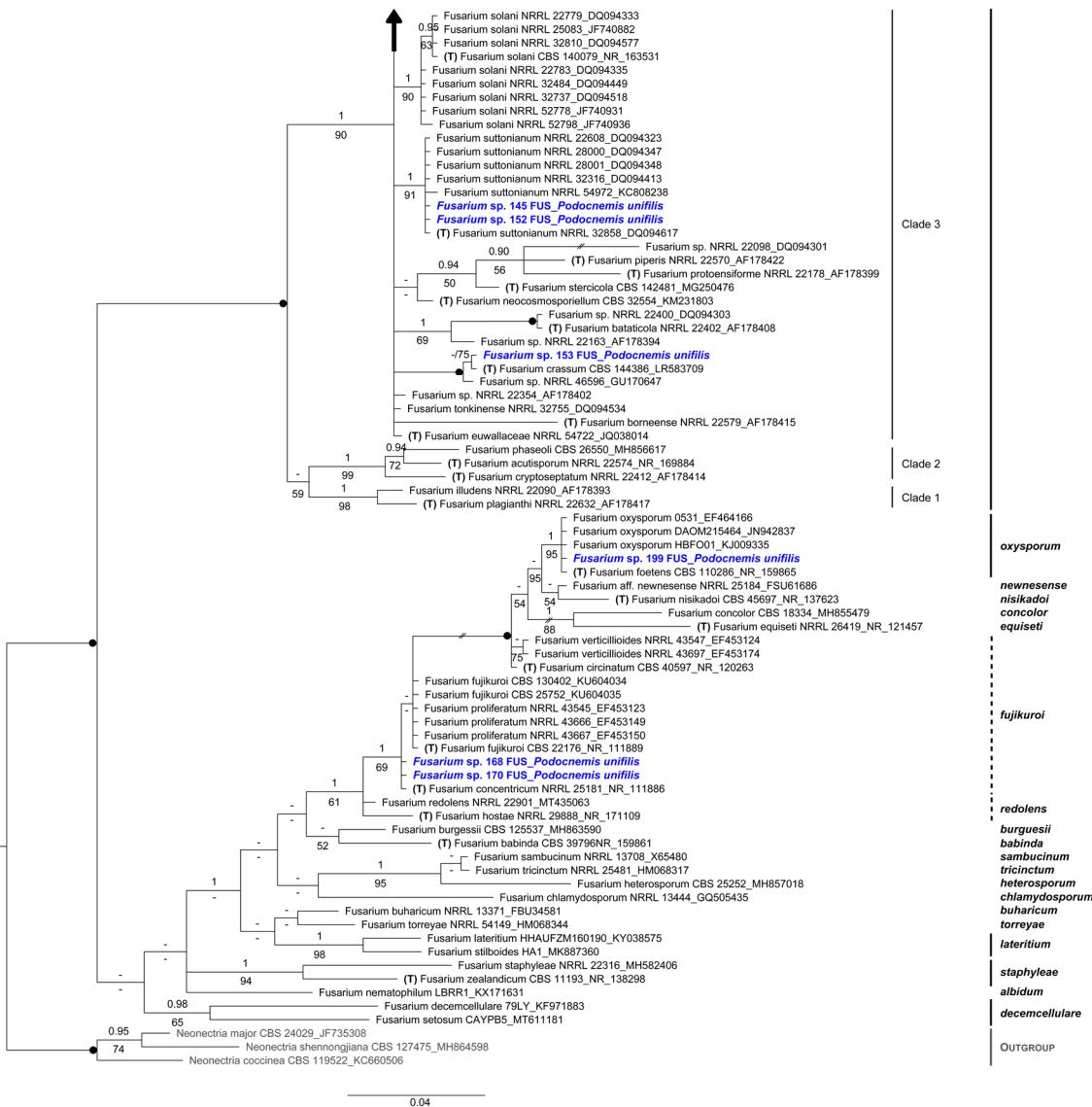


Figure S1. (Continuation).

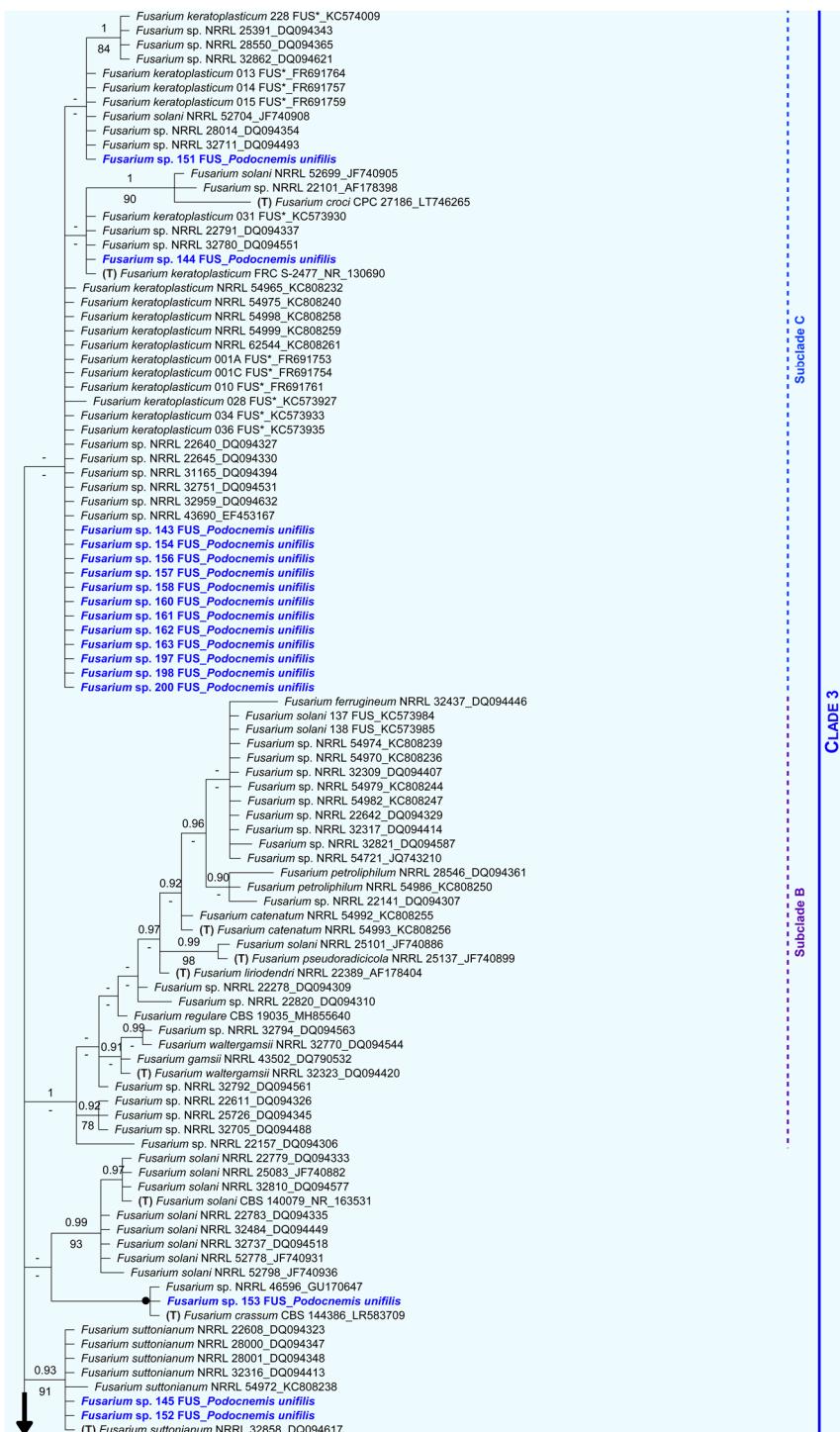


Figure S2. Bayesian ITS tree of FSSC isolates, based on 499 nucleotides, with members of the FSSC Clade 1 as outgroup. Species names are followed by herbarium codes and GenBank accession numbers. Sequences obtained here are in bold. Type strains are marked with a “T”. Specimens corresponding to *F. keratoplasticum*, initially identified as *F. solani*, are marked with an asterisk. Clades 1, 2 and 3 represent designations proposed by O’Donnell et al. [57]. Subclades B and C follow Sarmiento-Ramírez et al. [28]. Numbers above and below the branches represent Bayesian posterior probability (PP) and maximum likelihood bootstrap values (BS), respectively (shown only if PP ≥ 0.90 and BS ≥ 50%). Solid dots indicate full support in both analyses. The scale bar represents the average number of substitutions per site.

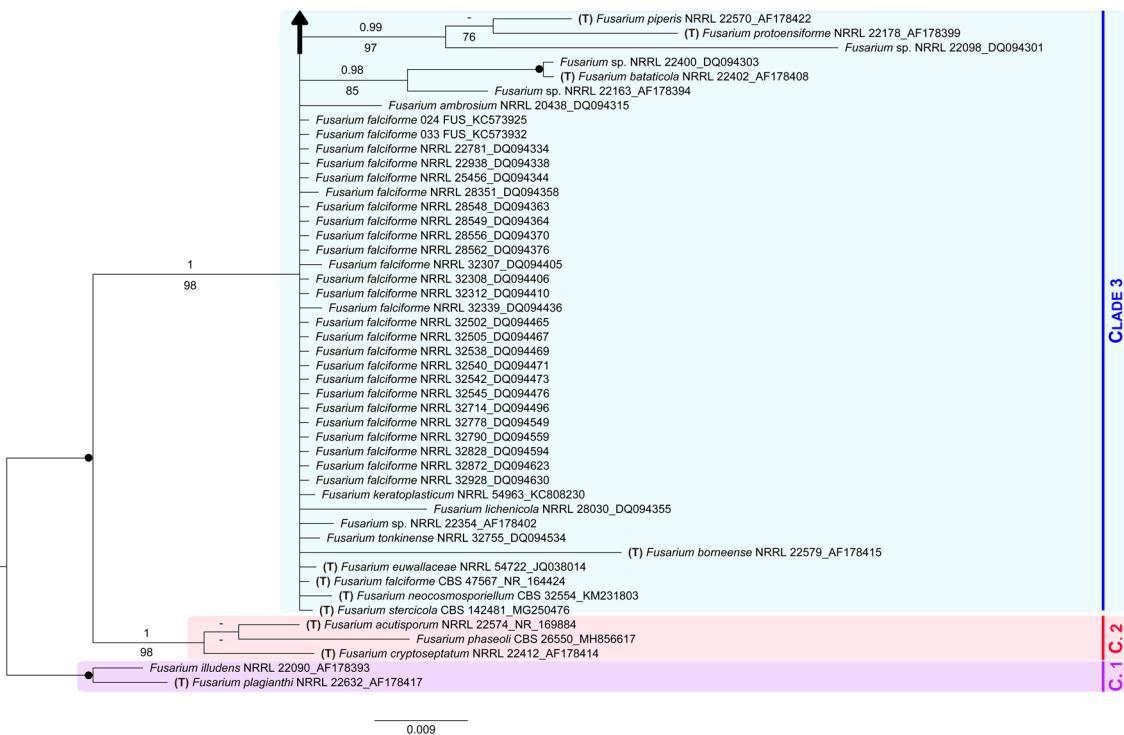


Figure S2. (Continuation).

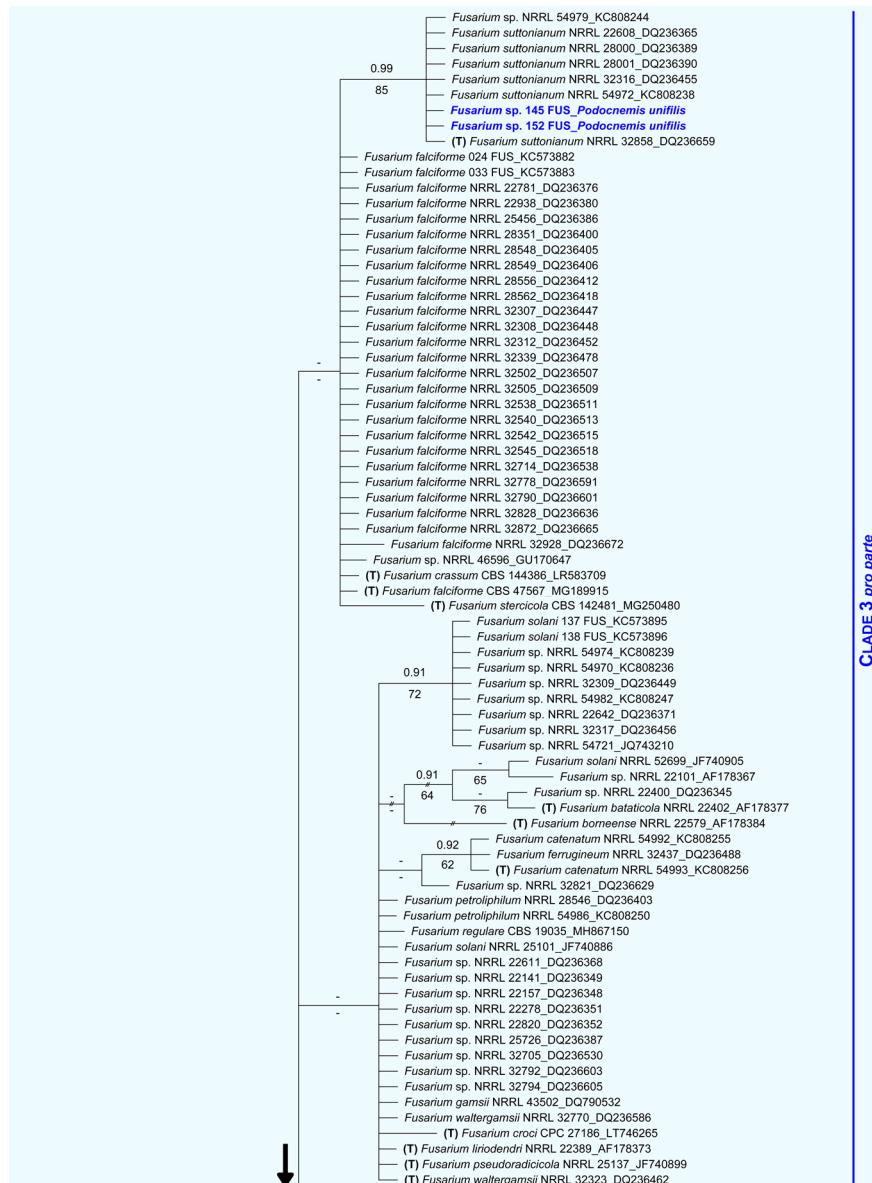


Figure S3. Bayesian LSU tree of FSSC isolates, based on 520 nucleotides, with members of the FSSC Clade 1 as outgroup. Species names are followed by herbarium codes and GenBank accession numbers. Sequences obtained here are in bold. Type strains are marked with a "T". Specimens corresponding to *F. keratoplasticum*, initially identified as *F. solani*, are marked with an asterisk. Clades 1, 2 and 3 represent designations proposed by O'Donnell et al. [57]. Numbers above and below the branches represent Bayesian posterior probability (PP) and maximum likelihood bootstrap values (BS), respectively (shown only if PP ≥ 0.90 and BS ≥ 50%). An interrupted branch (//) indicates its length has been reduced for representation purposes. The scale bar represents the average number of substitutions per site.

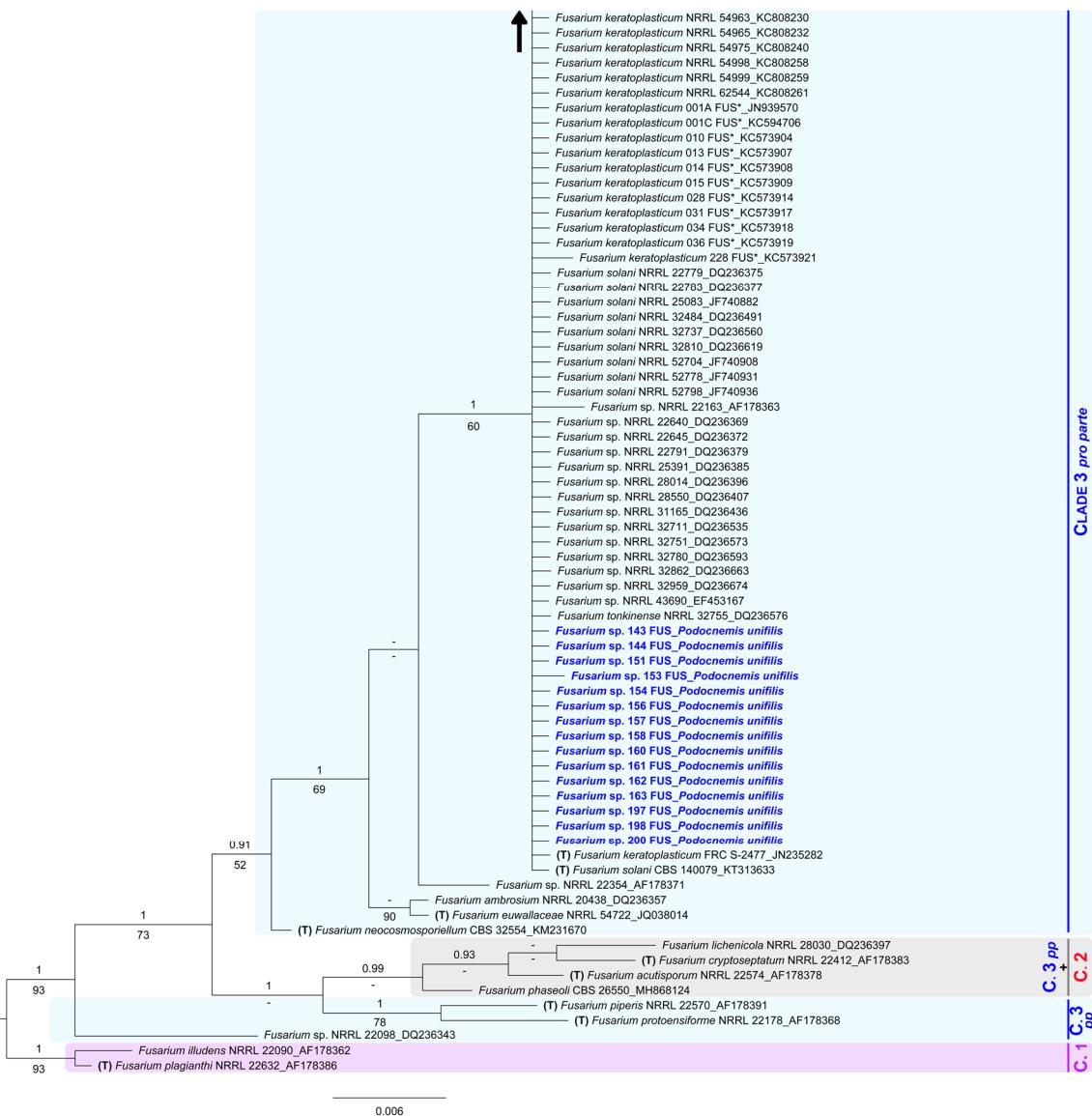


Figure S3. (Continuation).

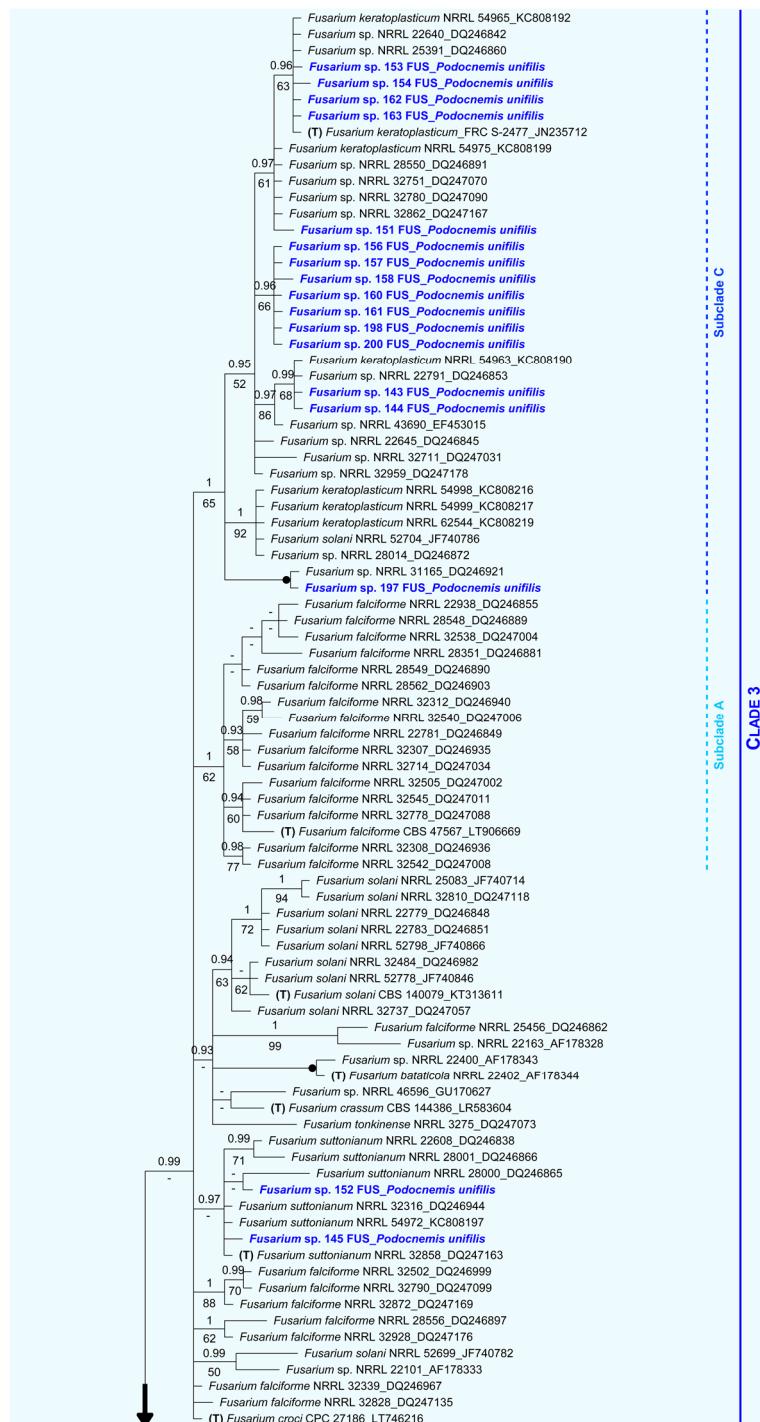


Figure S4. Bayesian EF-1 α tree of FSSC isolates, based on 713 nucleotides, with members of the FSSC Clade 1 as outgroup. Species names are followed by herbarium codes and GenBank accession number. Sequences obtained here are in bold. Type strains are marked with a “T”. Clades 1, 2 and 3 represent designations proposed by O'Donnell et al. [57]. Subclades A, B and C follow Sarmiento-Ramírez et al. [28]. Numbers above and below the branches represent Bayesian posterior probability (PP) and maximum likelihood bootstrap values (BS), respectively (shown only if PP ≥ 0.90 and BS $\geq 50\%$). Solid dots indicate full support in both analyses. The scale bar represents the average number of substitutions per site.

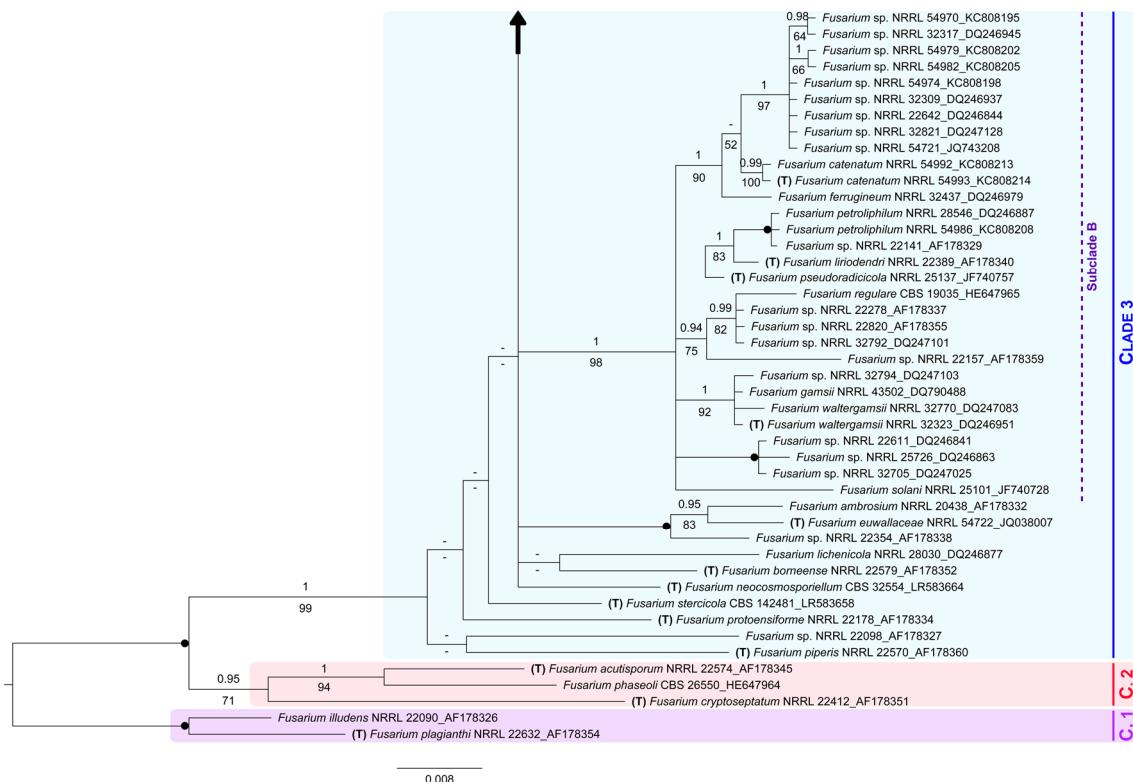


Figure S4. (Continuation).

Table S1. Fungal isolates obtained from *P. unifilis* eggshells, and putative identity based on ITS data.

Isolate	Geographic origin	Putative species name	ITS GenBank Accession No.	Identity	Seq. newly generated
143 FUS ^b	Guayero	<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907495	100%	MW390926
		<i>Trichoderma pubescens</i> [*]	MN644760	100%	
144 FUS ^b	Guayero	Undetermined fungal sp.	KY7760381	100%	
		<i>Fusarium</i> sp.	KU9507271	100%	MW390927
		<i>Fusarium keratoplasticum</i>	KP132216	100%	
		<i>Fusarium falciforme</i>	MT114705	100%	
145 FUS ^b	Guayero	<i>Fusarium solani</i>	MH7290211	100%	MW390928
		Uncultured fungus clone	KF0602101	100%	
146 FUS ^a	Guayero	<i>Rhizopus microsporus</i>	MT279280	100%	MW390929
		Uncultured fungus clone	MF510685	100%	
151 FUS ^b	Guayero	<i>Fusarium</i> sp.	KX953611	100%	MW390930
		<i>Fusarium solani</i>	KY484924	100%	
152 FUS ^b	Nueva Providencia	<i>Fusarium falciforme</i>	MT114705	100%	
		<i>Fusarium solani</i>	MH729021	100%	MW390931
		<i>Fusarium</i> sp.	JQ364977	100%	
153 FUS ^b	Sani Isla	<i>Fusarium solani</i>	KT441029	100%	
		<i>Fusarium</i> sp.	EF687945	100%	MW390932
		<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
154 FUS ^b	Sani Isla	<i>Fusarium</i> sp.	MH681596	100%	MW390933
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i> ^c	KF679815	100%	
		Chaetomiaceae sp.	MT530063	100%	
155 FUS	Sani Isla	<i>Chaetomium homopilatum</i>	MT035919	100%	
		<i>Humicola fuscoatra</i>	MG774450	100%	MW390934
		Uncultured soil fungus	EU826907	100%	
		<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
156 FUS ^b	Sani Isla	<i>Fusarium</i> sp.	MH681596	100%	MW390935
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i> ^c	KF679815	100%	
		<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
157 FUS ^b	Sani Isla	<i>Fusarium</i> sp.	MH681596	100%	MW390936
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i> ^c	KF679815	100%	
		<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
158 FUS ^b	Undetermined	<i>Fusarium</i> sp.	MH681596	100%	MW390937
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i> ^c	KF679815	100%	
		<i>Ectophoma pomi</i>	MT112289	99.80%	
159 FUS	Undetermined	<i>Phoma pereupyrena</i> ^d	KJ767076	99.80%	MW390938
		<i>Paraphoma radicina</i> ^e	MH425313	99.80%	
		<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
160 FUS ^b	Undetermined	<i>Fusarium</i> sp.	MH681596	100%	MW390939
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i>	KF679815	100%	

^aIsolates identified at species level (maximum sequence similarity with GenBank sequences representing a single species). ^bIsolates selected for phylogenetic analyses. ^cTeleomorph of *Fusarium solani*. ^dSynonym of *Ectophoma pomi*. ^ePreviously named as *Phoma radicina*. ^fTeleomorph of *Fusarium verticillioides*. *Wrong identification (based on BLAST searches, all the most similar sequences to this one correspond to *Fusarium* sp.).

Table S1. (Continuation).

		<i>Fusarium solani</i>	MT447548	100%	
161 FUS ^b	Undetermined	<i>Fusarium keratoplasticum</i>	MN907495	100%	
		<i>Fusarium</i> sp.	MH681596	100%	MW390940
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i> ^c	KF679815	100%	
162 FUS ^b	Undetermined	<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907495	100%	
		<i>Fusarium</i> sp.	MH681596	100%	MW390941
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i>	KF679815	100%	
163 FUS ^b	Undetermined	<i>Fusarium solani</i>	MT447548	100%	
		<i>Fusarium keratoplasticum</i>	MN907486	100%	
		<i>Fusarium</i> sp.	MH681596	100%	MW390942
		Uncultured fungus clone	MF510804	100%	
		<i>Nectria haematococca</i>	KF679815	100%	
164 FUS	Undetermined	<i>Penicillium expansum</i>	MT582774	100%	
		<i>Penicillium crustosum</i>	MT582770	100%	
		<i>Penicillium commune</i>	MN371392	100%	MW390943
		<i>Penicillium christenseniae</i>	MK267452	100%	
		<i>Penicillium cyclopium</i>	MH865559	100%	
165 FUS ^a	Undetermined	<i>Rhizopus microsporus</i>	MT279280	100%	MW390944
166 FUS ^a	Undetermined	<i>Rhizopus microsporus</i>	MT279280	100%	MW390945
		<i>Fusarium redolens</i>	MT563395	100%	
		<i>Fusarium proliferatum</i>	MT541890	100%	
		<i>Fusarium concentricum</i>	MN341308	100%	
168 FUS	Undetermined	<i>Fusarium oxysporum</i>	MN856435	100%	MW390946
		<i>Fusarium solani</i>	MN486565	100%	
		<i>Fusarium verticillioides</i>	MH087117	100%	
		<i>Fusarium fujikuroi</i>	KP998524	100%	
		<i>Gibberella moniliformis</i> ^f	IX914478	100%	
		<i>Fusarium redolens</i>	MT563395	99.81%	
		<i>Fusarium proliferatum</i>	MT541890	99.81%	
		<i>Fusarium</i> sp.	MK351450	99.81%	
170 FUS	Undetermined	<i>Fusarium oxysporum</i>	MN856435	99.81%	MW390947
		<i>Fusarium solani</i>	MN486565	99.81%	
		<i>Fusarium concentricum</i>	MH613764	99.81%	
		<i>Fusarium verticillioides</i>	MH087117	99.81%	
		<i>Fusarium fujikuroi</i>	KP998524	99.81%	
178 FUS	Undetermined	<i>Allophoma minor</i>	MH8615011	100%	
		<i>Didymella</i> sp.	KY828938	100%	MW390948
		Fungal species	KY4968361	100%	
		<i>Fusarium solani</i>	MN066126	100%	
		<i>Fusarium</i> sp.	MH681596	100%	
197 FUS ^b	Guiyero	Uncultured fungus clone	MF510804	100%	MW390949
		<i>Fusarium keratoplasticum</i>	KF255446	100%	
		<i>Nectria haematococca</i>	DQ535183	100%	
		<i>Fusarium solani</i>	MN066126	100%	
		<i>Fusarium</i> sp.	MH681596	100%	
198 FUS ^b	Sani Isla	Uncultured fungus clone	MF510804	100%	MW390950
		<i>Fusarium keratoplasticum</i>	KF255446	100%	
		<i>Nectria haematococca</i>	DQ535183	100%	
199 FUS	Nueva Providencia	<i>Fusarium oxysporum</i>	MT530243	100%	
		<i>Fusarium solani</i>	MN452609	100%	MW390951
		<i>Trichoderma</i> sp.*	MK871244	100%	
		<i>Fusarium solani</i>	MN066126	100%	
		<i>Fusarium</i> sp.	MH681596	100%	
200 FUS ^b	Sani Isla	Uncultured fungus clone	MF510804	100%	MW390952
		<i>Fusarium keratoplasticum</i>	KF255446	100%	
		<i>Nectria haematococca</i>	DQ535183	100%	
205 FUS ^a	Guivero	<i>Rhizopus microsporus</i>	KY828894	99.85%	MW390953

Note: based on BLAST searches, the specific identity of most of these isolates could not be determined since their ITS sequences shared high similarity values with several GenBank sequences representing different species. At genus level, 20 isolates belonged to *Fusarium*, four to *Rhizopus*, and one to *Penicillium*. As for the remaining three isolates (155 FUS, 159 FUS and 178 FUS), their generic identity could not be determined as they all showed high sequence similarity with several GenBank sequences corresponding to different genera, i.e., *Chaetomium* or *Humicola*, *Ectophoma* or *Paraphoma*, and *Allophoma* or *Didymella*, respectively. Among the 20 *Fusarium* isolates, 17 (85%) were identified as species of the FSSC Clade 3. Based on BLAST results, the remaining three isolates (168 FUS, 170 FUS and 199 FUS) were tentatively assigned to species belonging to other complexes, i.e., *Fusarium fujikuroi* (FFSC), *Fusarium oxysporum* (FOSC) or *Fusarium redolens* (FRSC). All four isolates representing the genus *Rhizopus* were unequivocally identified as *Rhizopus microsporus*. The specific identity of the isolate 164 FUS remains unknown as its sequence of ITS shared maximum similarity with GenBank sequences obtained from five *Penicillium* species. The isolate 159 FUS was neither unequivocally identified at species level since it matched with several GenBank sequences representing *Ectophoma pomii* (MT112289 and KJ767076) and *Paraphoma radicina* (MH425313).

Table S2. GenBank sequences from 130 fungal specimens used in phylogenetic analyses.

Species ID in GenBank	Isolate ^{a–e}	GenBank Accession No.			Host
		LSU	ITS	EF-1 α	
<i>Fusarium acutisporum</i>	NRRL 22574*	AF178378	NR_169884	AF178345	–
<i>Fusarium ambrosium</i>	NRRL 20438	DQ236357	DQ094315	AF178332	Tea plant
<i>Fusarium bataticola</i>	NRRL 22402*	AF178377	AF178408	AF178344	<i>Ipomoea batatas</i>
<i>Fusarium borneense</i>	NRRL 22579*	AF178384	AF178415	AF178352	Bark
<i>Fusarium catenatum</i>	NRRL 54992	KC808255	KC808255	KC808213	Unknown host
<i>Fusarium catenatum</i>	NRRL 54993*	KC808256	KC808256	KC808214	Unknown host
<i>Fusarium crassum</i>	CBS 144386*	LR583709	LR583709	LR583604	–
<i>Fusarium croci</i>	CPC 27186*	LT746265	LT746265	LT746216	<i>Citrus sinensis</i>
<i>Fusarium cryptoseptatum</i>	NRRL 22412*	AF178383	AF178414	AF178351	–
<i>Fusarium euwallaceae</i>	NRRL 54722*	JQ038014	JQ038014	JQ038007	–
<i>Fusarium falciforme</i>	024 FUS	KC573882	KC573925	–	<i>Eretmochelys</i>
<i>Fusarium falciforme</i>	033 FUS	KC573883	KC573932	–	<i>Chelonia mydas</i>
<i>Fusarium falciforme</i>	NRRL 22781	DQ236376	DQ094334	DQ246849	Human
<i>Fusarium falciforme</i>	NRRL 22938	DQ236380	DQ094338	DQ246855	Human
<i>Fusarium falciforme</i>	NRRL 25456	DQ236386	DQ094344	DQ246862	Human
<i>Fusarium falciforme</i>	NRRL 28351	DQ236400	DQ094358	DQ246881	Human
<i>Fusarium falciforme</i>	NRRL 28548	DQ236405	DQ094363	DQ246889	Human
<i>Fusarium falciforme</i>	NRRL 28549	DQ236406	DQ094364	DQ246890	Human
<i>Fusarium falciforme</i>	NRRL 28556	DQ236412	DQ094370	DQ246897	Human
<i>Fusarium falciforme</i>	NRRL 28562	DQ236418	DQ094376	DQ246903	Human
<i>Fusarium falciforme</i>	NRRL 32307	DQ236447	DQ094405	DQ246935	Human
<i>Fusarium falciforme</i>	NRRL 32308	DQ236448	DQ094406	DQ246936	Human
<i>Fusarium falciforme</i>	NRRL 32312	DQ236452	DQ094410	DQ246940	Human
<i>Fusarium falciforme</i>	NRRL 32339	DQ236478	DQ094436	DQ246967	Human
<i>Fusarium falciforme</i>	NRRL 32502	DQ236507	DQ094465	DQ246999	Human
<i>Fusarium falciforme</i>	NRRL 32505	DQ236509	DQ094467	DQ247002	Human
<i>Fusarium falciforme</i>	NRRL 32538	DQ236511	DQ094469	DQ247004	Human
<i>Fusarium falciforme</i>	NRRL 32540	DQ236513	DQ094471	DQ247006	Human
<i>Fusarium falciforme</i>	NRRL 32542	DQ236515	DQ094473	DQ247008	Human
<i>Fusarium falciforme</i>	NRRL 32545	DQ236518	DQ094476	DQ247011	Human
<i>Fusarium falciforme</i>	NRRL 32714	DQ236538	DQ094496	DQ247034	Human
<i>Fusarium falciforme</i>	NRRL 32778	DQ236591	DQ094549	DQ247088	Horse
<i>Fusarium falciforme</i>	NRRL 32790	DQ236601	DQ094559	DQ247099	Human
<i>Fusarium falciforme</i>	NRRL 32828	DQ236636	DQ094594	DQ247135	Human
<i>Fusarium falciforme</i>	NRRL 32872	DQ236665	DQ094623	DQ247169	Dog
<i>Fusarium falciforme</i>	NRRL 32928	DQ236672	DQ094630	DQ247176	Human
<i>Fusarium falciforme</i>	CBS 47567*	MG189915	NR_164424	LT906669	–
<i>Fusarium ferrugineum</i>	NRRL 32437	DQ236488	DQ094446	DQ246979	Human
<i>Fusarium gamsii</i>	NRRL 43502	DQ790532	DQ790532	DQ790488	Human
<i>Fusarium illudens</i>	NRRL 22090	AF178362	AF178393	AF178326	–
<i>Fusarium keratoplasticum</i>	NRRL 54963	KC808230	KC808230	KC808190	Unknown host
<i>Fusarium keratoplasticum</i>	NRRL 54965	KC808232	KC808232	KC808192	Unknown host
<i>Fusarium keratoplasticum</i>	NRRL 54975	KC808240	KC808240	KC808199	Unknown host
<i>Fusarium keratoplasticum</i>	NRRL 54998	KC808258	KC808258	KC808216	Unknown host
<i>Fusarium keratoplasticum</i>	NRRL 54999	KC808259	KC808259	KC808217	Unknown host
<i>Fusarium keratoplasticum</i>	NRRL 62544	KC808261	KC808261	KC808219	Unknown host
<i>Fusarium keratoplasticum</i>	FRC S-2477*	JN235282	NR_130690	JN235712	Sink drain
<i>Fusarium lichenicola</i>	NRRL 28030	DQ236397	DQ094355	DQ246877	Human
<i>Fusarium lirioidendri</i>	NRRL 22389*	AF178373	AF178404	AF178340	<i>L. tulipifera</i>
<i>Fusarium neocosmosporiellum</i>	CBS 32554*	KM231670	KM231803	LR583664	–

*Type material; ^aCBS = Westerdijk Fungal Biodiversity Institute, Utrecht (The Netherlands); ^bCPC = Culture collection of Pedro Crous, housed at CBS; ^cFRC = *Fusarium* Research Center, Pennsylvania State University (USA); ^dFUS = Real Jardín Botánico CSIC, Madrid (Spain); ^eNRRL = Agricultural Research Service, Peoria (USA). Specimens in square brackets were initially identified as *F. solani* by Sarmiento-Ramírez et al. [61], but actually correspond to *F. keratoplasticum* [57]. Dashes indicate lack of data.

Table S2. (Continuation).

<i>Fusarium petroliphilum</i>	NRRL 28546	DQ236403	DQ094361	DQ246887	Human
<i>Fusarium petroliphilum</i>	NRRL 54986	KC808250	KC808250	KC808208	Unknown host
<i>Fusarium phaseoli</i>	CBS 26550	MH868124	MH856617	HE647964	—
<i>Fusarium piperis</i>	NRRL 22570*	AF178391	AF178422	AF178360	<i>Piper nigrum</i>
<i>Fusarium plagianthi</i>	NRRL 22632*	AF178386	AF178417	AF178354	—
<i>Fusarium protoensiforme</i>	NRRL 22178*	AF178368	AF178399	AF178334	Dicot tree
<i>Fusarium pseudoradicicola</i>	NRRL 25137*	JF740899	JF740899	JF740757	—
<i>Fusarium regulare</i>	CBS 19035	MH867150	MH855640	HE647965	—
[<i>Fusarium solani</i>]	001 AFUS	JN939570	FR691753	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	001 CFUS	KC594706	FR691754	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	010 FUS	KC573904	FR691761	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	013 FUS	KC573907	FR691764	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	014 FUS	KC573908	FR691757	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	015 FUS	KC573909	FR691759	—	<i>Caretta caretta</i>
[<i>Fusarium solani</i>]	028 FUS	KC573914	KC573927	—	<i>Chelonia mydas</i>
[<i>Fusarium solani</i>]	031 FUS	KC573917	KC573930	—	<i>Chelonia mydas</i>
[<i>Fusarium solani</i>]	034 FUS	KC573918	KC573933	—	<i>Chelonia mydas</i>
[<i>Fusarium solani</i>]	036 FUS	KC573919	KC573935	—	<i>Chelonia mydas</i>
<i>Fusarium solani</i>	137 FUS	KC573895	KC573984	—	Aquarium
<i>Fusarium solani</i>	138 FUS	KC573896	KC573985	—	Aquarium
[<i>Fusarium solani</i>]	228 FUS	KC573921	KC574009	—	<i>Chelonia mydas</i>
<i>Fusarium solani</i>	NRRL 22779	DQ236375	DQ094333	DQ246848	Human
<i>Fusarium solani</i>	NRRL 22783	DQ236377	DQ094335	DQ246851	Seal
<i>Fusarium solani</i>	NRRL 25083	JF740882	JF740882	JF740714	<i>Musca domestica</i>
<i>Fusarium solani</i>	NRRL 25101	JF740886	JF740886	JF740728	<i>Boophilus</i> sp.
<i>Fusarium solani</i>	NRRL 32484	DQ236491	DQ094449	DQ246982	Human
<i>Fusarium solani</i>	NRRL 32737	DQ236560	DQ094518	DQ247057	Human
<i>Fusarium solani</i>	NRRL 32810	DQ236619	DQ094577	DQ247118	Human
<i>Fusarium solani</i>	NRRL 52699	JF740905	JF740905	JF740782	<i>Mahanarva andigena</i>
<i>Fusarium solani</i>	NRRL 52704	JF740908	JF740908	JF740786	<i>Tetranychus urticae</i>
<i>Fusarium solani</i>	NRRL 52778	JF740931	JF740931	JF740846	<i>Eurygaster</i> sp.
<i>Fusarium solani</i>	NRRL 52798	JF740936	JF740936	JF740866	<i>T. myopaeformis</i>
<i>Fusarium solani</i>	CBS 140079*	KT313633	NR 163531	KT313611	—
<i>Fusarium</i> sp.	NRRL 54974	KC808239	KC808239	KC808198	Unknown host
<i>Fusarium</i> sp.	NRRL 54970	KC808236	KC808236	KC808195	Unknown host
<i>Fusarium</i> sp.	NRRL 32309	DQ236449	DQ094407	DQ246937	Human
<i>Fusarium</i> sp.	NRRL 54979	KC808244	KC808244	KC808202	Unknown host
<i>Fusarium</i> sp.	NRRL 54982	KC808247	KC808247	KC808205	Unknown host
<i>Fusarium</i> sp.	NRRL 22611	DQ236368	DQ094326	DQ246841	Human
<i>Fusarium</i> sp.	NRRL 22098	DQ236343	DQ094301	AF178327	Cucurbit
<i>Fusarium</i> sp.	NRRL 22141	DQ236349	DQ094307	AF178329	Cucurbit
<i>Fusarium</i> sp.	NRRL 22157	DQ236348	DQ094306	AF178359	<i>Morus alba</i>
<i>Fusarium</i> sp.	NRRL 22163	AF178363	AF178394	AF178328	<i>X. piperitum</i>
<i>Fusarium</i> sp.	NRRL 22278	DQ236351	DQ094309	AF178337	<i>Pisum sativum</i>
<i>Fusarium</i> sp.	NRRL 22354	AF178371	AF178402	AF178338	Bark
<i>Fusarium</i> sp.	NRRL 22400	DQ236345	DQ094303	AF178343	<i>Ipomoea batatas</i>
<i>Fusarium</i> sp.	NRRL 22640	DQ236369	DQ094327	DQ246842	Human
<i>Fusarium</i> sp.	NRRL 22642	DQ236371	DQ094329	DQ246844	Prawn
<i>Fusarium</i> sp.	NRRL 22645	DQ236372	DQ094330	DQ246845	Shrimp
<i>Fusarium</i> sp.	NRRL 22791	DQ236379	DQ094337	DQ246853	<i>Iguana</i> sp.
<i>Fusarium</i> sp.	NRRL 22820	DQ236352	DQ094310	AF178355	<i>Glycine max</i>
<i>Fusarium</i> sp.	NRRL 25391	DQ236385	DQ094343	DQ246860	Shrimp
<i>Fusarium</i> sp.	NRRL 25726	DQ236387	DQ094345	DQ246863	Human
<i>Fusarium</i> sp.	NRRL 28014	DQ236396	DQ094354	DQ246872	Human
<i>Fusarium</i> sp.	NRRL 28550	DQ236407	DQ094365	DQ246891	Human
<i>Fusarium</i> sp.	NRRL 31165	DQ236436	DQ094394	DQ246921	Human
<i>Fusarium</i> sp.	NRRL 32317	DQ236456	DQ094414	DQ246945	Treefish
<i>Fusarium</i> sp.	NRRL 32705	DQ236530	DQ094488	DQ247025	Human

Table S2. (Continuation).

<i>Fusarium</i> sp.	NRRL 32711	DQ236535	DQ094493	DQ247031	Human
<i>Fusarium</i> sp.	NRRL 32751	DQ236573	DQ094531	DQ247070	Human
<i>Fusarium</i> sp.	NRRL 32780	DQ236593	DQ094551	DQ247090	Sea turtle
<i>Fusarium</i> sp.	NRRL 32792	DQ236603	DQ094561	DQ247101	Human
<i>Fusarium</i> sp.	NRRL 32794	DQ236605	DQ094563	DQ247103	Humidifier coolant
<i>Fusarium</i> sp.	NRRL 32821	DQ236629	DQ094587	DQ247128	Turtle egg
<i>Fusarium</i> sp.	NRRL 32862	DQ236663	DQ094621	DQ247167	Unknown host
<i>Fusarium</i> sp.	NRRL 32959	DQ236674	DQ094632	DQ247178	Human
<i>Fusarium</i> sp.	NRRL 43690	EF453167	EF453167	EF453015	Human
<i>Fusarium</i> sp.	NRRL 46596	GU170647	GU170647	GU170627	Human
<i>Fusarium</i> sp.	NRRL 54721	JQ743210	JQ743210	JQ743208	<i>Hippocampus erectus</i>
<i>Fusarium stercicola</i>	CBS 142481*	MG250480	MG250476	LR583658	—
<i>Fusarium striatum</i>	NRRL 22101	AF178367	AF178398	AF178333	Cotton cloth
<i>Fusarium suttonianum</i>	NRRL 22608	DQ236365	DQ094323	DQ246838	Human
<i>Fusarium suttonianum</i>	NRRL 28000	DQ236389	DQ094347	DQ246865	Human
<i>Fusarium suttonianum</i>	NRRL 28001	DQ236390	DQ094348	DQ246866	Human
<i>Fusarium suttonianum</i>	NRRL 32316	DQ236455	DQ094413	DQ246944	Human
<i>Fusarium suttonianum</i>	NRRL 54972	KC808238	KC808238	KC808197	Unknown host
<i>Fusarium suttonianum</i>	NRRL 32858*	DQ236659	DQ094617	DQ247163	Human
<i>Fusarium tonkinense</i>	NRRL 32755	DQ236576	DQ094534	DQ247073	Turtle
<i>Fusarium waltergamsii</i>	NRRL 32770	DQ236586	DQ094544	DQ247083	Human
<i>Fusarium waltergamsii</i>	NRRL 32323*	DQ236462	DQ094420	DQ246951	—

Table S3. Bacteria isolated from *P. unifilis* eggshells and putative identity based on 16S Blast results.

Isolate	Geographic origin	Putative species name ^a	16S GenBank Accession No.	Identity	Phylum
B13	Nueva Providencia	<i>Bacillus thuringiensis</i>	CP050183	99.93%	Firmicutes
		<i>Bacillus proteolyticus</i>	MT184819	99.93%	
		<i>Bacillus wiedmannii</i>	AP022643	99.93%	
		<i>Bacillus cereus</i>	CP028009	99.93%	
		<i>Bacillus albus</i>	CP040344	99.93%	
		<i>Bacillus luti</i>	CP040336	99.93%	
		<i>Bacillus anthracis</i>	KM888109	99.93%	
B14	Nueva Providencia	<i>Bacillus bombysepticus</i>	CP007512	99.93%	Firmicutes
		<i>Bacillus wiedmannii</i>	AP022643	98.31%	
		<i>Bacillus cereus</i>	CP028009	98.31%	
		<i>Bacillus thuringiensis</i>	MT598028	98.23%	
		<i>Bacillus proteolyticus</i>	MT184819	98.23%	
B15	Nueva Providencia	<i>Bacillus paranthracis</i>	MN904873	98.23%	Actinobacteria
		<i>Tsukamurella sp.</i>	MN075319	99.86%	
		<i>Tsukamurella paurometabola</i>	LR131273	99.79%	
		<i>Tsukamurella inchonensis</i>	AB907635	99.79%	
B16	Guayero	<i>Tsukamurella tyrosinosolvens</i>	FJ643549	99.44%	Proteobacteria
		<i>Paracoccus sp.</i>	AM084045	99.86%	
		<i>Paracoccus huijuniae</i>	MN330433	99.85%	
B17	Guayero	<i>Paracoccus aminovorans</i>	HQ005404	99.78%	Actinobacteria
		<i>Pimelobacter sp.</i>	KC252718	99.12%	
		<i>Pimelobacter simplex</i>	NR_119355	99.09%	
B18	Sani Isla	<i>Nocardioides aromaticivorans</i>	GU735484	99.02%	Actinobacteria
		<i>Nocardioides kongjuensis</i>	NR_043651	99.72%	
B19	Sani Isla	<i>Nocardioides panaciterrae</i>	AB257719	99.45%	Actinobacteria
		<i>Gordonia sp.</i>	KC211011	99.93%	
		Uncultured actinobacterium	JQ919182	99.93%	
		<i>Gordonia sihwensis</i>	NR_025505	99.86%	
B20	Sani Isla	<i>Gordonia cholesterolvorans</i>	NR_044445	99.86%	Proteobacteria
		<i>Ralstonia sp.</i>	AY860250	99.86%	
		<i>Cupriavidus sp.</i>	MG725957	99.79%	
		<i>Cupriavidus pauculus</i>	CP044065	99.18%	
		<i>Cupriavidus plantarum</i>	HQ438088	99.18%	
B21	Sani Isla	<i>Ralstonia eutropha</i>	AF027407	99.11%	Actinobacteria
		<i>Pseudoxanthomonas sp.</i>	LC481374	100%	
		Uncultured bacterium clone	HQ218747	100%	
		<i>Pseudoxanthomonas indica</i>	JQ659945	100%	
B22	Sani Isla	<i>Pseudoxanthomonas japonensis</i>	LC015564	100%	Proteobacteria
		<i>Pseudomonas sp.</i>	KP986946	100%	
		<i>Pseudomonas mendocina</i>	EF208965	99.93%	
		<i>Pseudomonas resinovorans</i>	MF943158	99.86%	
B23	Sani Isla	<i>Pseudomonas aeruginosa</i>	KF929419	99.79%	Proteobacteria
		<i>Pseudomonas sp.</i>	CP045118	99.45%	
		<i>Pseudomonas denitrificans</i>	CP043626	99.38%	
		<i>Pseudomonas nitroreducens</i>	MH675504	99.38%	
		<i>Pseudomonas multiresinivorans</i>	CP048833	99.31%	
B24	Sani Isla	<i>Pseudomonas azelaica</i>	AM088475	99.25%	Proteobacteria
		<i>Pseudomonas aeruginosa</i>	MF144534	99.18%	
		<i>Delftia sp.</i>	MT101746	99.93%	
		<i>Delftia tsuruhatensis</i>	MH478206	99.93%	
		<i>Delftia lacustris</i>	MH333093	99.93%	
B25	Undetermined	Uncultured bacterium clone	KX508964	99.93%	Bacteroidetes
		Uncultured Comamonadaceae	JN038272	99.93%	
		<i>Delftia acidovorans</i>	GU459215	99.86%	
		<i>Chryseobacterium gleum</i>	KX579964	99.44%	
		<i>Chryseobacterium aquifrigidense</i>	KP893287	99.42%	
		<i>Chryseobacterium flavum</i>	MK116543	99.37%	Bacteroidetes
		<i>Chryseobacterium indologenes</i>	KX228235	99.37%	
		<i>Chryseobacterium arthrosphaerae</i>	LC040953	99.16%	

^aNone of the isolates could be ascribed to a given species since multiple hits with identical or very similar sequence identity values were found.

Table S3. (Continuation).

B26	Undetermined	<i>Achromobacter</i> sp.	LC093432	99.79%	
		Uncultured bacterium clone	KR233647	99.66%	
		<i>Achromobacter aegefaciens</i>	NR_117707	99.66%	
		<i>Achromobacter xylosoxidans</i>	CP061008	99.59%	
		<i>Achromobacter insolitus</i>	CP038034	99.45%	Proteobacteria
		<i>Achromobacter denitrificans</i>	CP053986	99.45%	
		<i>Achromobacter insuavis</i>	NR_117706	99.38%	
		<i>Achromobacter ruhlandii</i>	CP017433	99.31%	
B27	Undetermined	<i>Elizabethkingia</i> sp.	MN540121	100%	
		<i>Elizabethkingia anophelis</i>	CP034594	100%	
		<i>Elizabethkingia endophytica</i>	CP016372	100%	Bacteroidetes
		<i>Cryseobacterium meningosepticum</i>	AY683476	100%	
B28	Undetermined	<i>Stenotrophomonas maltophilia</i>	LC066105	99.86%	
		<i>Stenotrophomonas</i> sp.	MN714633	99.86%	
		Uncultured bacterium clone	EF509504	99.80%	
		<i>Pseudomonas</i> sp.	LC034239	99.73%	Proteobacteria
		<i>Pseudomonas hibiscicola</i>	KC172017	99.66%	
		<i>Pseudomonas geniculata</i>	KJ147059	99.59%	
B29	Undetermined	Bacterium enrichment culture	HQ440208	99.93%	
		<i>Pseudomonas</i> sp.	KU291441	99.86%	
		<i>Arthrobacter</i> sp.	AY641537	99.79%	Actino- or
		<i>Pseudomonas plecoglossicida</i>	KU597529	99.73%	Proteobacteria
		<i>Pseudomonas putida</i>	CP015202	99.72%	
		<i>Pseudomonas monteili</i>	KF475842	99.66%	
B30	Undetermined	<i>Stenotrophomonas</i> sp.	KY672922	100%	
		Uncultured bacterium clone	KU667239	100%	
		<i>Stenotrophomonas acidaminiphila</i>	KF279369	100%	Proteobacteria
		<i>Stenotrophomonas maltophilia</i>	MK562366	100%	
B31	Undetermined	<i>Delftia tsuruhatensis</i>	DQ864991	99.86%	
		<i>Delftia</i> sp.	MT101746	99.86%	
		<i>Delftia lacustris</i>	MH333093	99.86%	Proteobacteria
		Uncultured bacterium clone	KX508964	99.86%	
		<i>Delftia acidovorans</i>	GU459215	99.79%	
B32	Undetermined	<i>Pseudomonas</i> sp.	MH703466	99.93%	
		<i>Stenotrophomonas</i> sp.	CP029759	99.86%	
		<i>Stenotrophomonas maltophilia</i>	MK841317	99.86%	
		Uncultured marine bacterium	JF925027	99.86%	Proteobacteria
		<i>Stenotrophomonas pavani</i>	MN686363	99.79%	
		[<i>Pseudomonas</i>] <i>geniculata</i>	KT748641	99.73%	
B33	Undetermined	<i>Stenotrophomonas maltophilia</i>	AB683956	99.86%	
		Uncultured <i>Stenotrophomonas</i> sp.	HQ595218	99.86%	
		<i>Pseudomonas</i> sp.	KR911802	99.79%	Proteobacteria
		Uncultured bacterium clone	EU805183	99.65%	
		<i>Vibrio</i> sp.	DQ146981	99.65%	
B34	Undetermined	<i>Pseudomonas putida</i>	AY686638	99.79%	
		<i>Pseudomonas taiwanensis</i>	NR_116172	99.72%	
		<i>Pseudomonas</i> sp.	MT012082	99.72%	Actino- or
		<i>Pseudomonas plecoglossicida</i>	LC507998	99.59%	Proteobacteria
		<i>Pseudomonas monteili</i>	MF045811	99.59%	
		<i>Brevibacterium frigoritolerans</i>	EU073968	99.52%	

Note: the 22 bacterial isolates obtained here represent four different phyla, i.e., Proteobacteria (12 isolates, 54.5%), Actinobacteria (four, 18.2%), Firmicutes (two, 9.1%) and Bacteroidetes (two, 9.1%). Based on the closest matches of BLAST searches, the remaining two isolates (B29 and B34) could belong to either Actinobacteria or Proteobacteria. Among the Proteobacteria, two isolates (16.7%) were assigned to *Pseudomonas*, two others (16.7%) to *Delftia*, and B16, B21, B26 and B30 (33.3%) most probably represented *Paracoccus*, *Pseudoxanthomonas*, *Achromobacter*, and *Stenotrophomonas*, respectively. The genus of the isolates B20, B28, B32 and B33 (33.3%) could not be determined since BLAST revealed significant similarity (> 99%) to several sequences corresponding to different genera, i.e., *Ralstonia* or *Cupriavidus*, *Stenotrophomonas* or *Pseudomonas*, and *Stenotrophomonas*, *Pseudomonas* or *Vibrio*. Among the Actinobacteria, B15 corresponded to *Tsukamurella*, B18 to *Nocardioides*, B19 to *Gordonia*, and B17 could belong either to *Pimelobacter* or *Nocardioides*. Both representatives of Firmicutes (B13 and B14) corresponded to *Bacillus*. The isolates representing the phylum Bacteroidetes corresponded to *Cryseobacterium* (B25) and *Elizabethkingia* or *Cryseobacterium* (B27).

Table S4. GenBank 16S sequences from related bacterial species used in phylogenetic analyses.

Species ID in GenBank	Isolate	16S GenBank Accession No.	Fragment*
<i>Achromobacter aegrifaciens</i>	LMG 26852	CADIJY010000029	2–1435
<i>Achromobacter agilis</i>	LMG 3411	UFQB01000054	247–1773
<i>Achromobacter animicus</i>	R-46662T	HE613448	–
<i>Achromobacter animicus</i>	R-46662	NR_117615	–
<i>Achromobacter animicus</i>	LMG 26690	CADIJM010000037	2–1435
<i>Achromobacter anxifer</i>	LMG 26857	CAHLAR010000027	2–1435
<i>Achromobacter denitrificans</i>	DSM 30026	NR_042021	–
<i>Achromobacter denitrificans</i>	LMG 1231	CADIJN010000119	237–1763
<i>Achromobacter insolitus</i>	LCu2	CP038034	1780713–1782263
<i>Achromobacter insolitus</i>	LMG 6003	CADJK010000027	45–1571
<i>Achromobacter kerstersii</i>	LMG 3441	CADIQ010000032	25–1551
<i>Achromobacter marplatensis</i>	R-46660T	HE613447	–
<i>Achromobacter marplatensis</i>	R-46660	NR_117614	–
<i>Achromobacter marplatensis</i>	LMG 26219	CADIJU010000049	367–1893
<i>Achromobacter marplatensis</i>	B2	NJIG01000044	245–1690
<i>Achromobacter mucicola</i>	R-46658T	HE613446	–
<i>Achromobacter mucicola</i>	R-46658	NR_117613	–
<i>Achromobacter mucicola</i>	LMG 26685	CADIJP010000044	163–1689
<i>Achromobacter panacis</i>	–	KR338991	–
<i>Achromobacter panacis</i>	DCY105	NR_165687	–
<i>Achromobacter pestifer</i>	LMG 3431	CADIJX010000020	263–1789
<i>Achromobacter piechaudii</i>	NBRC102461	NZ_BCTK01000022	–
<i>Achromobacter piechaudii</i>	LMG 1873	CADIJS010000009	10–1536
<i>Achromobacter ruhlandii</i>	SCCH3:ACH 33- 1365	CP017433	688341–689894
<i>Achromobacter</i> sp.	DR405	LC093432	–
<i>Achromobacter</i> sp.	Fo40	MF155647	–
<i>Achromobacter veterisilvae</i>	LMG 30378	UFQC01000090	50–1576
<i>Achromobacter xylosoxidans</i> (T)	0119Ts	MT664080	–
<i>Achromobacter xylosoxidans</i> (T)	GD03	CP061008	1800478–1802131
<i>Arthrobacter</i> sp.	LFTou2	AY641537	–
<i>Bacillus anthracis</i>	IHB-B18033	KM888109	–
<i>Bacillus bombysepticus</i>	Wang	CP007512	89830–91390
<i>Bacillus cereus</i>	SGAir0260	CP028009	1288835–1290389
<i>Bacillus circulans</i>	Sn25-040808	FJ155345	–
<i>Bacillus licheniformis</i>	Sn13-040808	FJ155337	–
<i>Bacillus proteolyticus</i>	NWPZ7	MT184819	–
<i>Bacillus pumilus</i>	Sn6-040808	FJ155331	–
<i>Bacillus</i> sp.	JY14	EU581833	–
<i>Bacillus</i> sp.	0919U	MT664082	–
<i>Bacillus</i> sp.	0519Pg	MT664083	–
<i>Bacillus subtilis</i> (T)	Sn12-040808	FJ155336	–
<i>Bacillus thuringiensis</i>	HER1410	CP050183	9160–10714
<i>Bacillus wiedmannii</i>	PL1	AP022643	2238988–2240538
<i>Bacterium enrichment</i>	CCZU12	HQ440208	–
<i>Brevibacterium frigorifolerans</i>	CMGS4	EU073968	–
<i>Chryseobacterium aquifrigidense</i>	R-21	KP893287	–
<i>Chryseobacterium arthrosphaerae</i>	GS-3	LC040953	–
<i>Chryseobacterium culicis</i>	0819Tu	MT664085	–
<i>Chryseobacterium gleum</i> (T)	EY1	KX579964	–
<i>Chryseobacterium hispanicum</i>	KCTC 22104	QNUG01000096	111–1635
<i>Chryseobacterium indologenes</i>	Amic 5	KX228235	–
<i>Chryseobacterium massiliae</i>	CUVET1223	KJ190179	–
<i>Chryseobacterium</i> sp.	CUVET1222	KJ190178	–
<i>Chryseobacterium</i> sp.	D136	KF322149	–
<i>Cupriavidus necator</i> (T)	JS705	AF027407	–

*16S sequence obtained from a complete genome. The corresponding nucleotide range appears in the last column. T= type of the genus.

Table S4. (Continuation).

<i>Cupriavidus paucus</i>	FDAARGOS	CP044065	3476779–3478401
<i>Cupriavidus plantarum</i>	MA1-4a	HQ438088	–
<i>Delftia acidovorans</i> (T)	QS1	GU459215	–
<i>Delftia tsuruhatensis</i>	–	DQ864991	–
<i>Elizabethkingia anophelis</i>	JM-87 15-247	MAGY01000034	251–1772
<i>Elizabethkingia endophytica</i>	JM87	CP016372	1224828–1226361
<i>Elizabethkingia meningoseptica</i> (T)	YB-29	AY683476	–
<i>Gordonia shandongensis</i>	DSM45094	NZ AUHE01000029	–
<i>Gordonia</i> sp.	LYS13	KC211011	–
<i>Mesobacillus campialis</i>	SA2-6	NZ LAYY01000064	1515–2053
<i>Nocardoides agariphilus</i>	KCTC 19276	NZ JADKPO01000007	351–1891
<i>Nocardoides aromaticivorans</i>	SB10005	GU735484	–
<i>Nocardoides panaciterrae</i>	KCTC 19136	AB257719	–
<i>Nocardoides szechwanensis</i>	CGMCC 1.11147	FNIC01000016	369–1908
<i>Paracoccus aminovorans</i>	CT	HQ005404	–
<i>Paracoccus</i> sp.	C84	KF322148	–
<i>Paracoccus</i> sp.	R24650	AM084045	–
<i>Pimelobacter</i> sp.	N044	KC252718	–
<i>Pseudomonas aeruginosa</i> (T)	VITLWS3	KF929419	–
<i>Pseudomonas denitrificans</i>	BG1	CP043626	676315–677857
<i>Pseudomonas filiscindens</i>	ATCC BAA-697	AY259924	–
<i>Pseudomonas geniculata</i>	OTU-a9	KJ147059	–
<i>Pseudomonas geniculata</i>	C8	KT748641	–
<i>Pseudomonas hibiscicola</i>	SH8	KC172017	–
<i>Pseudomonas mendocina</i>	B6-1	EF208965	–
<i>Pseudomonas monteili</i>	IHB B 2329	KF475842	–
<i>Pseudomonas multiresinivorans</i>	populi	CP048833	817172–818740
<i>Pseudomonas nitroreducens</i>	DSM 9128	AM088475	–
<i>Pseudomonas plecoglossicida</i>	RD_AZPVI_05	KU597529	–
<i>Pseudomonas plecoglossicida</i>	JCM 13970	LC507998	–
<i>Pseudomonas putida</i>	KL33	AY686638	–
<i>Pseudomonas putida</i>	B62	CP015202	374165–375716
<i>Pseudomonas</i> sp.	Fenol2C	KU291441	–
<i>Pseudomonas</i> sp.	LS3K	LC034239	–
<i>Pseudomonas</i> sp.	R5	KR911802	–
<i>Pseudomonas</i> sp.	T2	GU727815	–
<i>Pseudomonas</i> sp.	PVR-YHB-1-2	KP986946	–
<i>Pseudomonas</i> sp.	PT1	MK652307	–
<i>Pseudomonas</i> sp.	PT2	MK652308	–
<i>Pseudomonas</i> sp.	PT4	MK652310	–
<i>Pseudomonas</i> sp.	PT5	MK652311	–
<i>Pseudomonas</i> sp.	PT6	MK652312	–
<i>Pseudomonas</i> sp.	PT7	MK652313	–
<i>Pseudomonas</i> sp.	J1	MN128405	–
<i>Pseudomonas</i> sp.	0619Th	MT664098	–
<i>Pseudoxanthomonas indica</i>	R8-542	JQ659945	–
<i>Pseudoxanthomonas japonensis</i>	AF59	LC015564	–
<i>Pseudoxanthomonas jiangsuensis</i>	DSM 22398	PDWL01000056	388–1932
<i>Pseudoxanthomonas</i> sp.	45-43	LC481374	–
<i>Ralstonia</i> sp.	AU5980	AY860250	–
<i>Stenotrophomonas acidaminiphila</i>	SR50-5	KF279369	–
<i>Stenotrophomonas maltophilia</i> (T)	TI-1	AB683956	–
<i>Stenotrophomonas maltophilia</i> (T)	T6220-6-1b	LC066105	–
<i>Stenotrophomonas rhizophila</i>	0919Es	MT664102	–
<i>Stenotrophomonas</i> sp.	BAB-6435	KY672922	–
<i>Stenotrophomonas</i> sp.	pho	CP029759	351352–352892
<i>Tsukamurella inchonensis</i>	1325	AB907635	–
<i>Tsukamurella pulmonis</i>	Sn10-040808	FJ155334	–

Table S4. (Continuation).

<i>Tsukamurella tyrosinosolvens</i>	Bx-62986	FJ643549	–
Uncultured <i>Achromobacter</i> sp.	ME128	DQ917890	–
Uncultured actinobacterium	GC0AA1ZA07PP1	JQ919182	–
Uncultured bacterium	P7D82-599	EF509504	–
Uncultured bacterium	6C233176	EU805183	–
Uncultured bacterium	CN1-94	HQ218747	–
Uncultured bacterium	15203	KR233647	–
Uncultured bacterium	Ace13(9-10)	KU667239	–
Uncultured bacterium	MTDH201308-62	KX508964	–
Uncultured Comamonadaceae	EK An354	JN038272	–
Uncultured marine bacterium	Tc-42	JF925027	–
Uncultured <i>Stenotrophomonas</i> sp.	IC3081	HQ595218	–
<i>Vibrio atlanticus</i>	Evh13	NZ OSDW01000040	408–1957
<i>Vibrio cincinnatiensis</i>	DSM19608	FUXB01000057	–
<i>Vibrio parahaemolyticus</i>	CFSAN025059	LKQH01000018	–
<i>Vibrio</i> sp.	S1072	FJ457349	–
<i>Vibrio</i> sp.	S1073	FJ457350	–
<i>Vibrio</i> sp.	S1099	FJ457358	–
<i>Vibrio</i> sp.	S1100	FJ457359	–
<i>Vibrio</i> sp.	S1101	FJ457360	–
<i>Vibrio</i> sp.	S1104	FJ457361	–
<i>Vibrio</i> sp.	S1105	FJ457362	–
<i>Vibrio</i> sp.	V205	DQ146981	–
<i>Vibrio viridaestus</i>	LJC006	RJVQ01000027	418–1907