D. Migliorini, F. Pecori, G. Arati, N. Luchi, E. Begliomini, A. Gnesini, L. Ghelardini, A. Santini (2023) Phytophthora spp. diversity in commercial nursery stocks shown through examination of plant health practices for growers and traders of ornamental plants. *Phytopathologia Mediterranea* 62(3): 489–497. doi: 10.36253/phyto-14893

Table S1. Isolates obtained in this study. Details of the isolate nursery of proveniences, types of isolation matrix, taxonomy, and GenBank accession numbers are shown. Totals for each column are in bold font in the last row. Isolates IDs include ID number (1 to 38, M (morphotype), N (Nursery), host plant abbreviation for genus and species name of the host plant (fully reported in the second column), v) FT or PS according to the plant isolation matrix (Flow-through water or Potting soil, respectively).

Isolate ID	Host plant	Nursery		Origin of the isolate					Pathogen taxon	GenBank accession number
				Water				Potting soil		
		1	2	Runoff water	Flow-through	Puddles	Irrigation pond			
M1N2 Runoff (1)			/	/					*Phytophthora acerina*	OR681517
M4N2 Runoff (4)			/	/						OR681534
M10N2 Runoff (14)			/	/						OR681541
M3N2 C. conc. PS (29)	*Ceanothus concha*		/					/	*P. cactorum*	OR681528
M12N2 Runoff (16)			/	/					*P. cambivora*	OR681543
M11N2 Runoff (15)			/	/					*P. chlamydospora*	OR681542
M1N2 Magnolia FT (8)	*Magnolia grandiflora*		/		/				*P. cinnamomi*	OR681516
M1N2 C. conc. PS (27)	*Ceanothus concha*		/					/		OR681512
M1N2 C. conc. FT (30)	*Ceanothus concha*		/		/					OR681511
M2N2 C. conc. FT (31)	*Ceanothus concha*		/		/					OR681521
M4N2 C. conc. FT (33)	*Ceanothus concha*		/		/					OR681533
M1N2 E ang. PS (34)	*Elaeagnus angustifolia*		/					/		OR681515
M2 N2 E ang. PS (35)	*Elaeagnus angustifolia*		/					/		OR681523
M1N2 Puddle (37)			/			/			*P. gonapodyides*	OR681507
M6N2 Runoff (6)			/	/						OR681537
M8N2 Runoff (12)			/	/						OR681539
M2N2 Puddle (38)			/			/				OR681524
M9N2 Runoff (13)			/	/					*P. hydropatica*	OR681540
M2N2 Runoff (2)			/	/					*P. lacustris*	OR681525
M3N2 Runoff (3)			/	/						OR681530
M5N2 (5) Runoff			/	/						OR681536
M2N2 C. conc. PS (28)	*Ceanothus concha*		/					/	*P. multivora*	OR681522
M4N1 C. semp. B PS (17)	*Cupressus sempervirens*	/						/	*P. nicotianae*	OR681531
M1N2 C. azt. PS (19)	*Choisya ternata* 'Aztec Pearl'		/					/		OR681514
M2N2 C. azt. PS (20)	*Choisya ternata* 'Aztec Pearl'		/					/		OR681520
M1N2 C. tern. FT (21)	*Choisya ternata*		/		/					OR681513
M3N2 C. conc. FT (32)	*Ceanothus concha*		/		/					OR681527
M3N2 Magnolia FT (9)	*Magnolia grandiflora*		/		/				*P. plurivora*	OR681529
M7N2 Runoff (11)			/	/						OR681538
M4N2 C. azt. FT (25)	*Choisya ternata* 'Aztec Pearl'		/		/					OR681532
M5N2 C. azt. FT (26)	*Choisya ternata* 'Aztec Pearl'		/		/					OR681535
M1N2 C. azt. FT (22)	*Choisya ternata* 'Aztec Pearl'		/		/				*P. pseudocryptogea*	OR681509
M2N2 C. azt. FT (23)	*Choisya ternata* 'Aztec Pearl'		/		/					OR681519
M3N2 C. azt. FT (24)	*Choisya ternata* 'Aztec Pearl'		/		/					OR681526
M1N1 Lake (7)		/					/		*Pythium kashmirense*	OR681506
M1N1 V tinus PS (36)	*Viburnum tinus*	/						/	*Phytopythium paucipapillatum*	OR681508
M2N1 C semp. A PS (10)	*Cupressus sempervirens*	/						/	*Phytopythium vexans*	OR681518
M1N2 C. conc. FT (18)	*Ceanothus concha*		/		/					OR681510
Total over the 38 isolates		4	34	12	13	2	1	10		

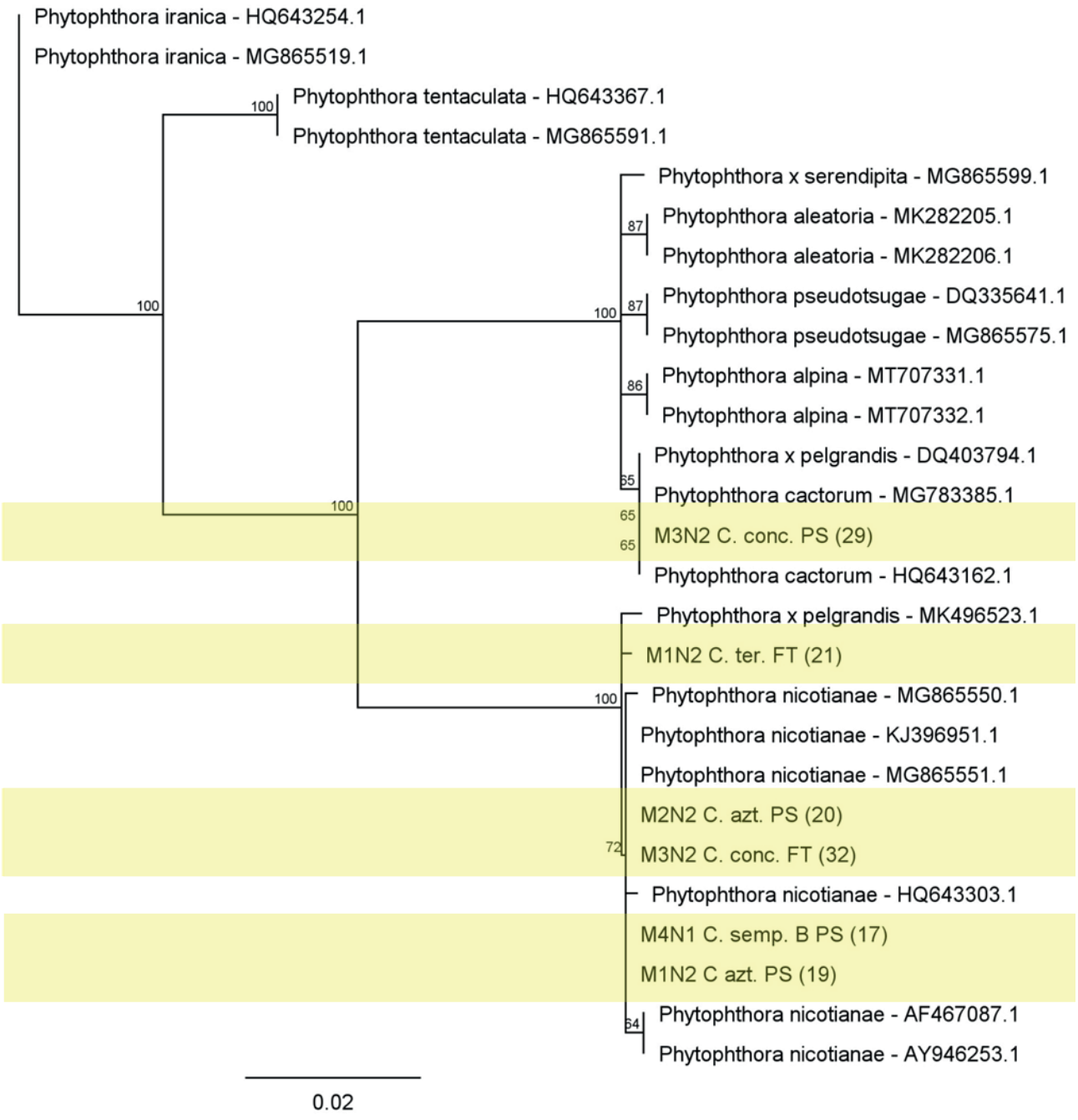

Figure S1. Clade 1.

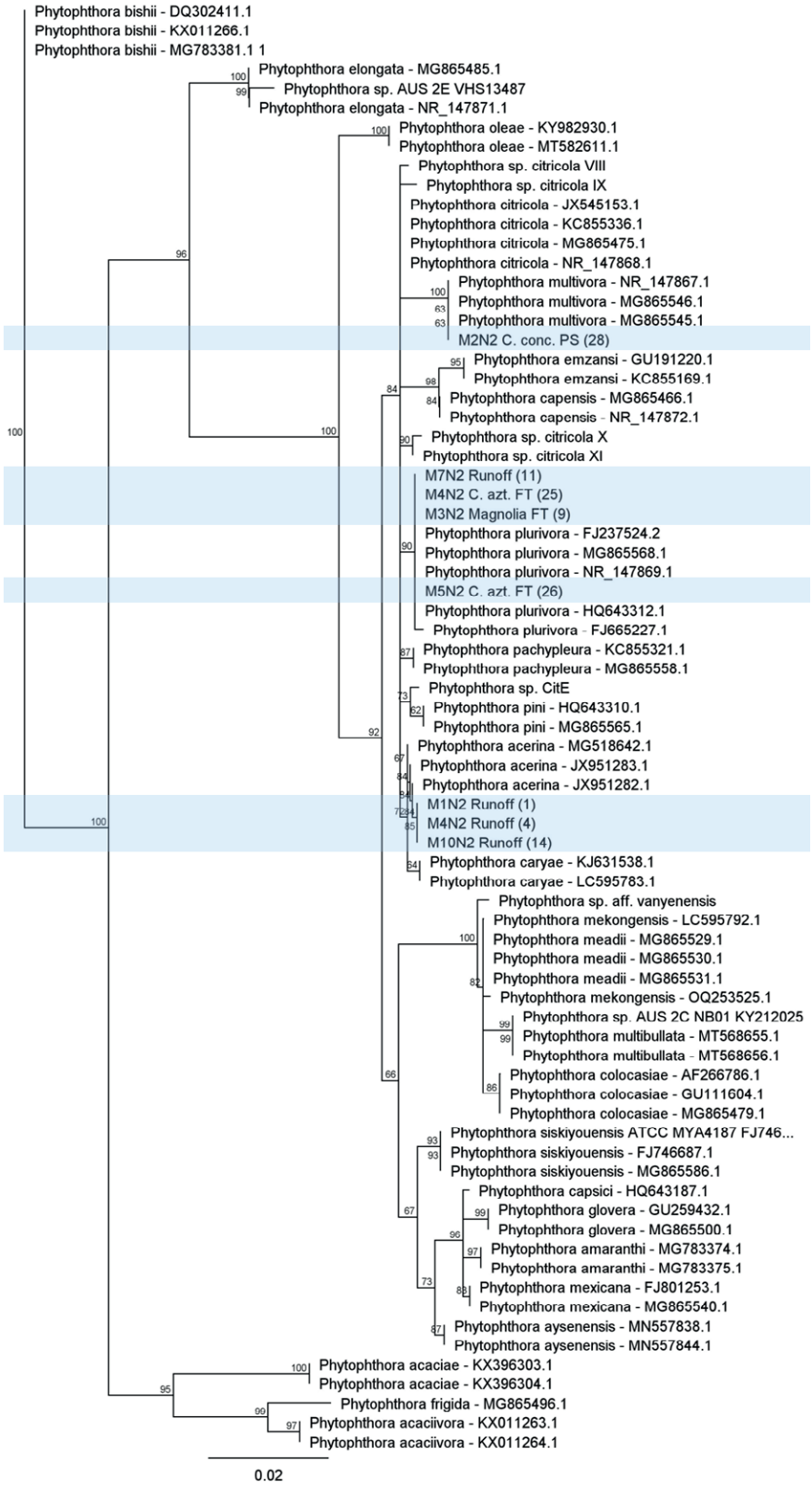

Figure S1. Clade 2.

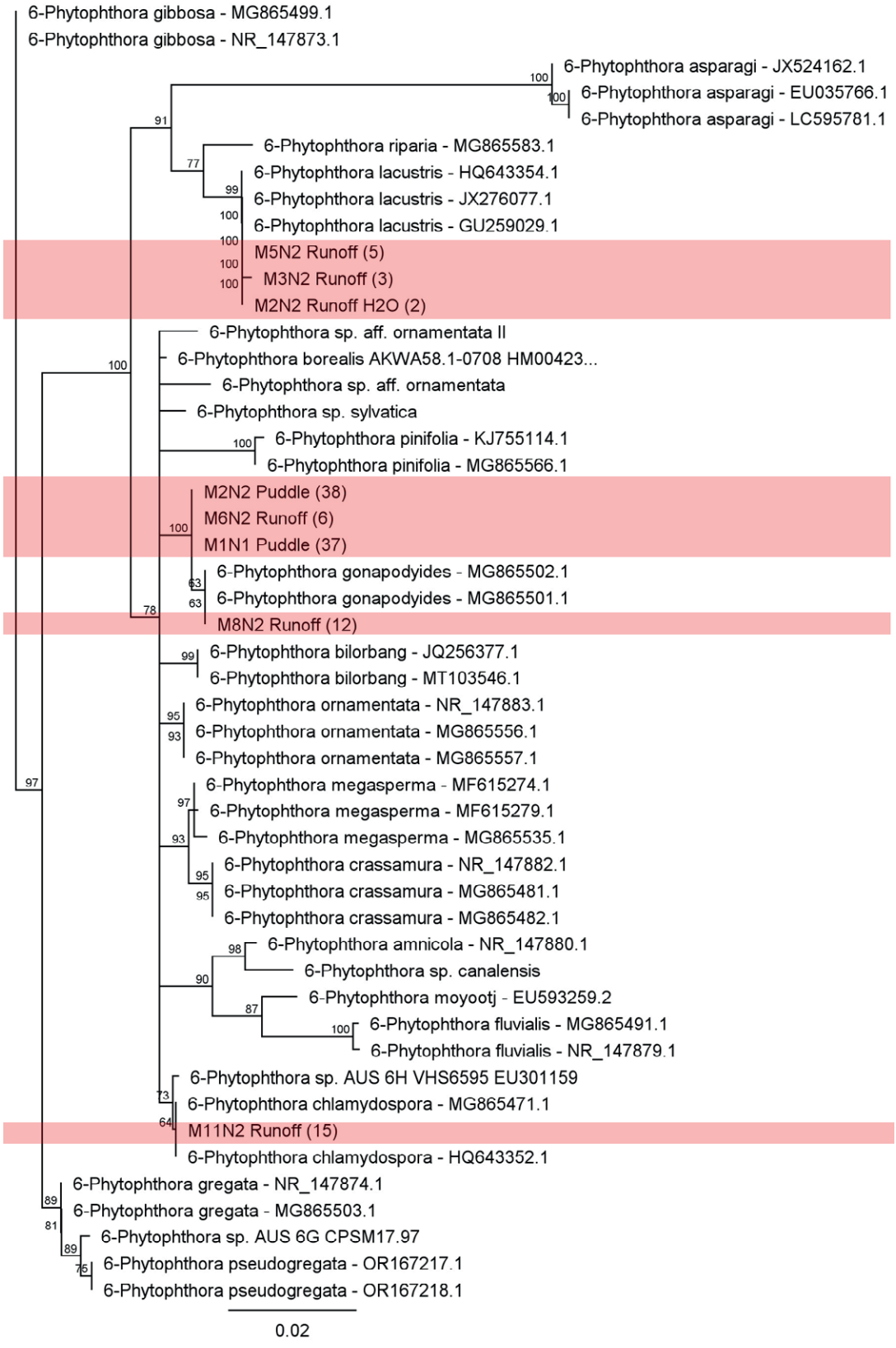

Figure S1. Clade 6.

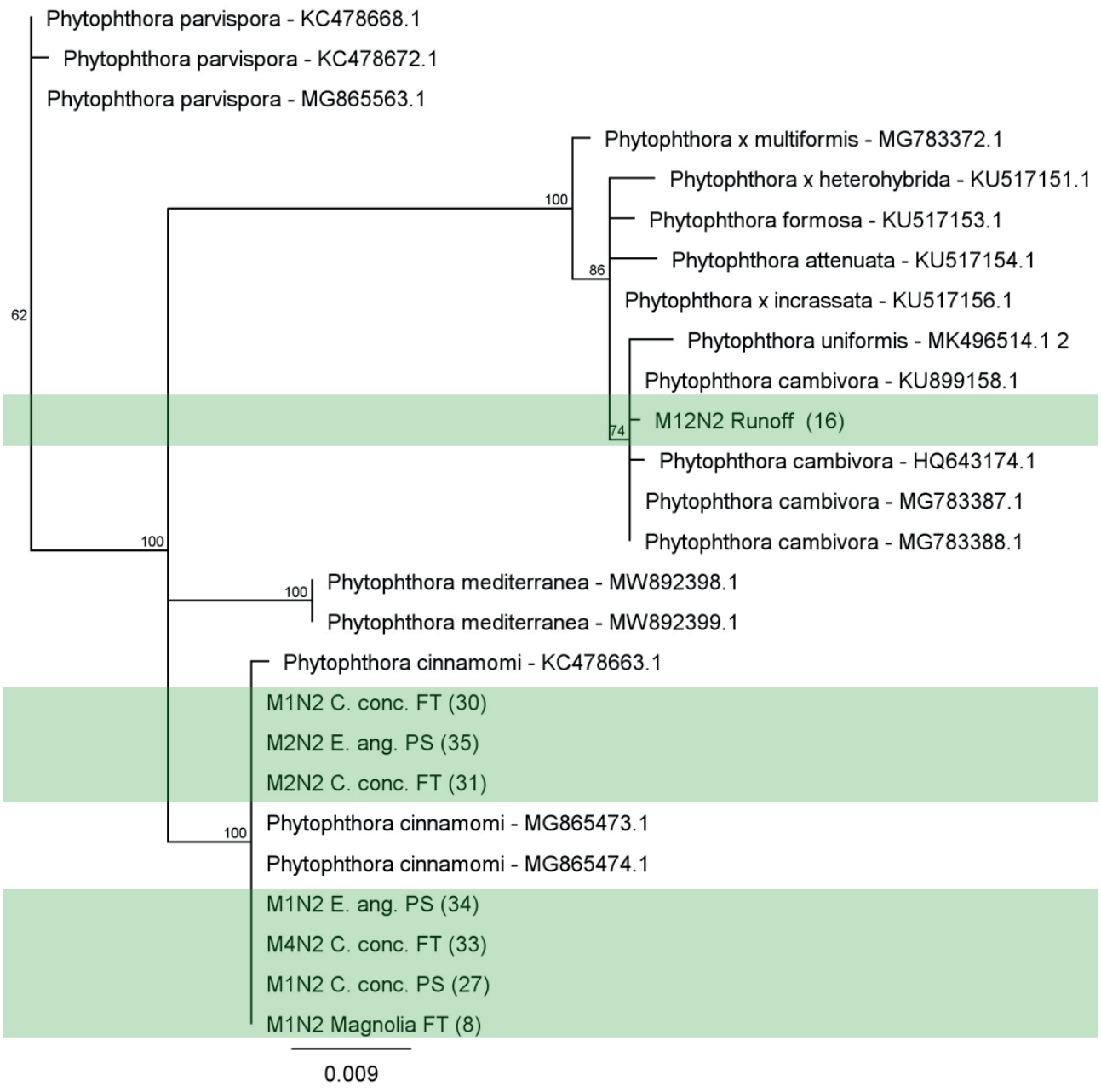

Figure S1. Clade 7.

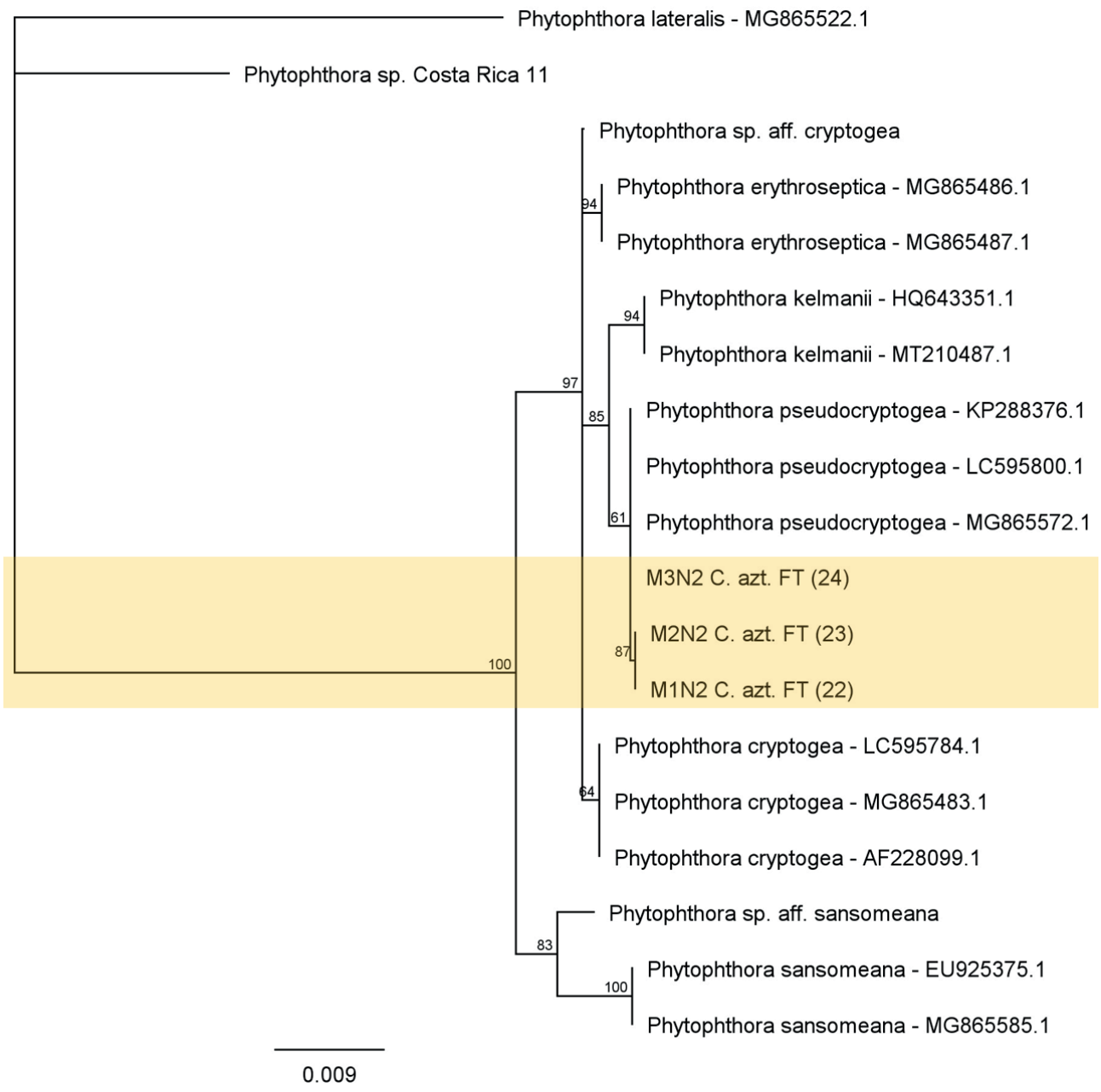

Figure S1. Clade 8.

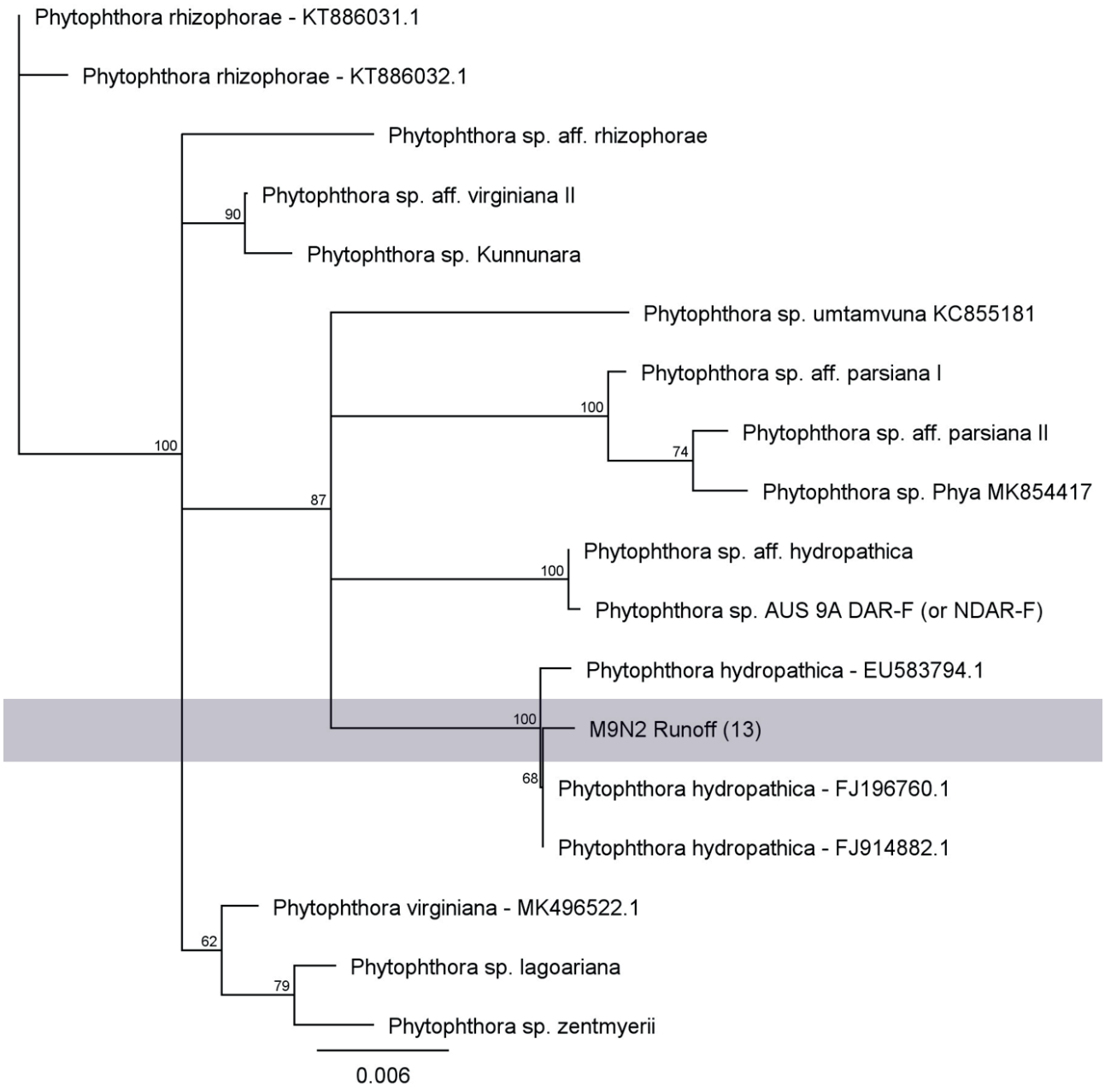

Figure S1. Clade 9.

Figure S1. Phylogenetic trees for *Phytophthora* isolate sequences obtained in this study, and the most closely related species, based on ITS gene regions. Representative sequences for backbone *Phytophthora* species are from the IDPhy database (Abad *et al*., 2023). Species from the same phylogenetic clade are grouped together in separated trees. Isolates are reported with their original GenBank submission names (Table S1), and are marked with different colour shadings.

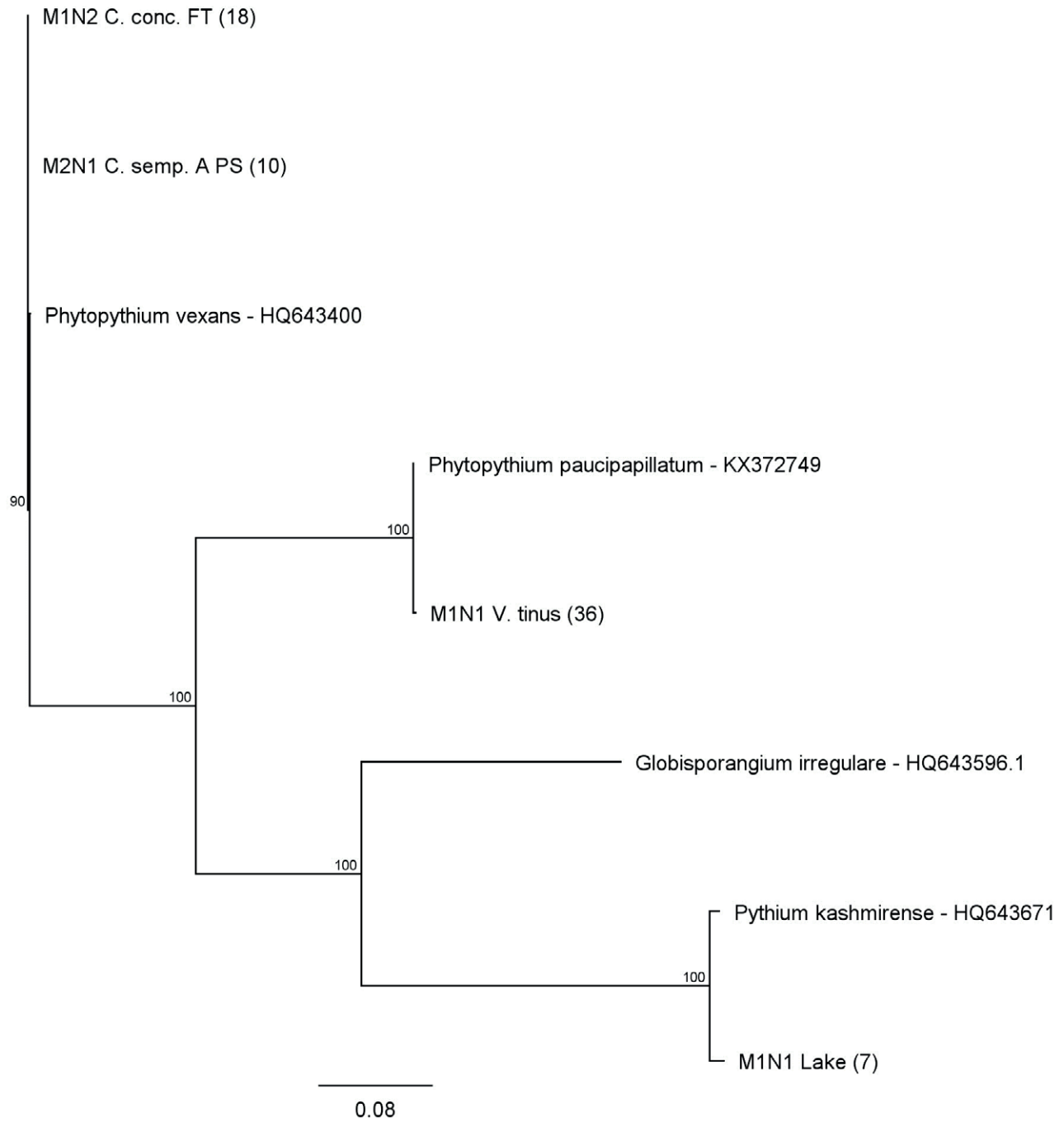

Figure S2. Phylogenetic tree of *Pythiaceae* isolate sequences obtained in this study, and the most closely related species, based on ITS gene regions. Representative sequences for backbone *Pythiaceae* were compared to those of known *Globisporangium* and *Phytopythium* species obtained from GenBank, including *Globisporangium kashmirense* (HQ643671) and *Phytopythium vexans* (HQ643400) (Robideau *et al*., 2011) and *Phytopythium paucipapillatum (*KX372749), Crous *et al.*, 2020). Isolates are reported with their original GenBank submission names (Table S1).