



**Fig. S1.** The sequences were aligned with Geneious and identified using the RDP2 database online identification. The phylogenetic tree was reconstructed using the neighbor-joining method with the Tamura-Nei model of nucleotide substitution for focal isolates isolated from -7 weeks (pre-liming), 0 weeks (pre-liming) and 8 weeks (post-liming) time points. Numbers on branches represent bootstrapping support for that branch (per cent, 100 bootstraps).