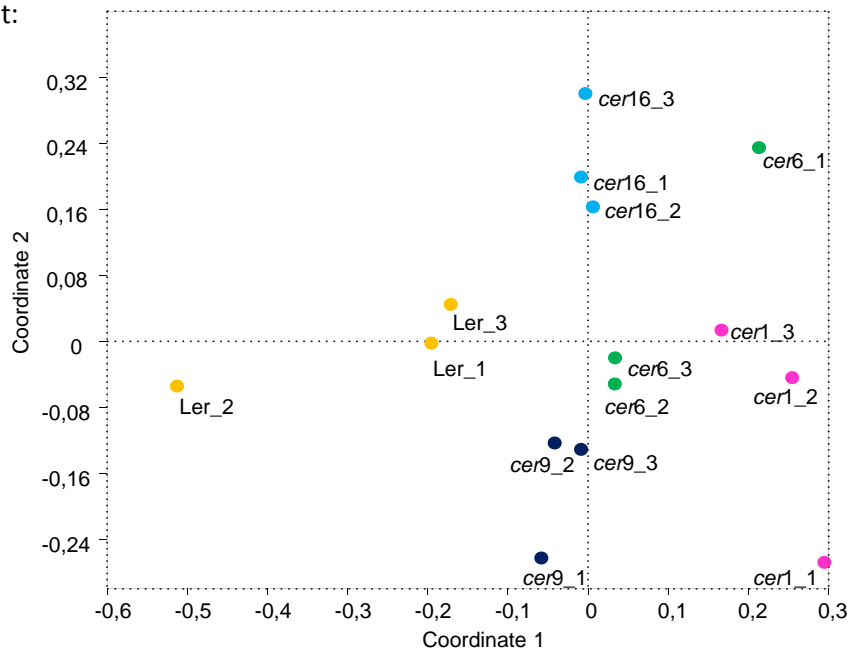


We restricted a rarified amplicon dataset (rarefied to approx. 2300 sequences) to those OTUs which were present in more than one replicate of at least one plant line. This reduced the dataset to 175 OTUs, but still 98% of all sequences were recovered – all removed OTUs were present on only one replicate of one or more plant lines, and thus considered as atypical community members. Thus these OTUs were lost during rarification (44 OTUs) or due to their only sporadic appearance in the dataset (288 OTUs). We analysed this dataset based on relative abundance values of sequences. An NMDS analysis (stress: 0.2763) showed distinct clusters of the communities of the different plant lines. An ANOSIM analysis showed the bacterial communities of the five plant lines to be statistically significantly different. Due to the limited sample size, pairwise comparisons could only be made on a significance level of 0.1%. Under these circumstances the communities of *Ler-cer6*, *Ler-cer9*, *Ler-cer16*, *cer1-cer9* and *cer9-cer16* were found to be significantly different. The analyses were conducted using the Kulczynski similarity index.

NMDS plot:



ANOSIM:

R = 0.7681		p = 0.0001			
R	Ler	cer1	cer6	cer9	
Ler					
cer1	0.8519				
cer6	0.6667*	0.8519			
cer9	0.5926*	0.9259*	0.5926		
cer16	0.7593*	0.8519	0.8148	1*	

In line 1 the overall test statistic is given for the comparison of all five groups. Underneath R-values for pairwise comparisons are shown. Asterisks at pairwise comparisons show the significance at the 0.1% level (lower significance levels could not be tested due to the small sample size (n=3 for each group)).