

Figure S1. Mamiellophyceae annotation. The clustering corresponds to the presence/absence of reference sequences in OTUs for different nucleotide identities (Jaccard index; UPGMA). The name of each strain is followed by its accession number.

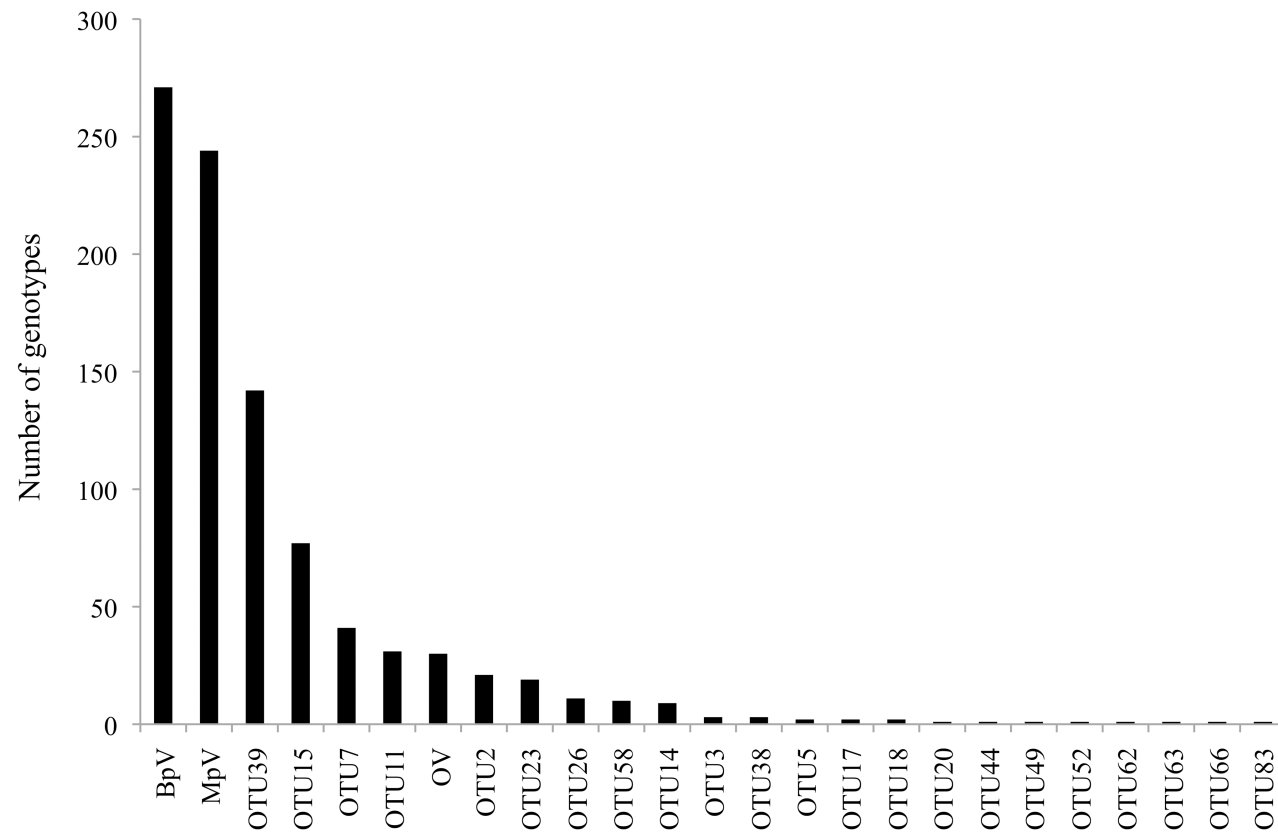


Figure S2. Rank-abundance of the *Prasinovirus* genotypes in the 11 samples. OTUs are defined for a cutoff of 74 %.

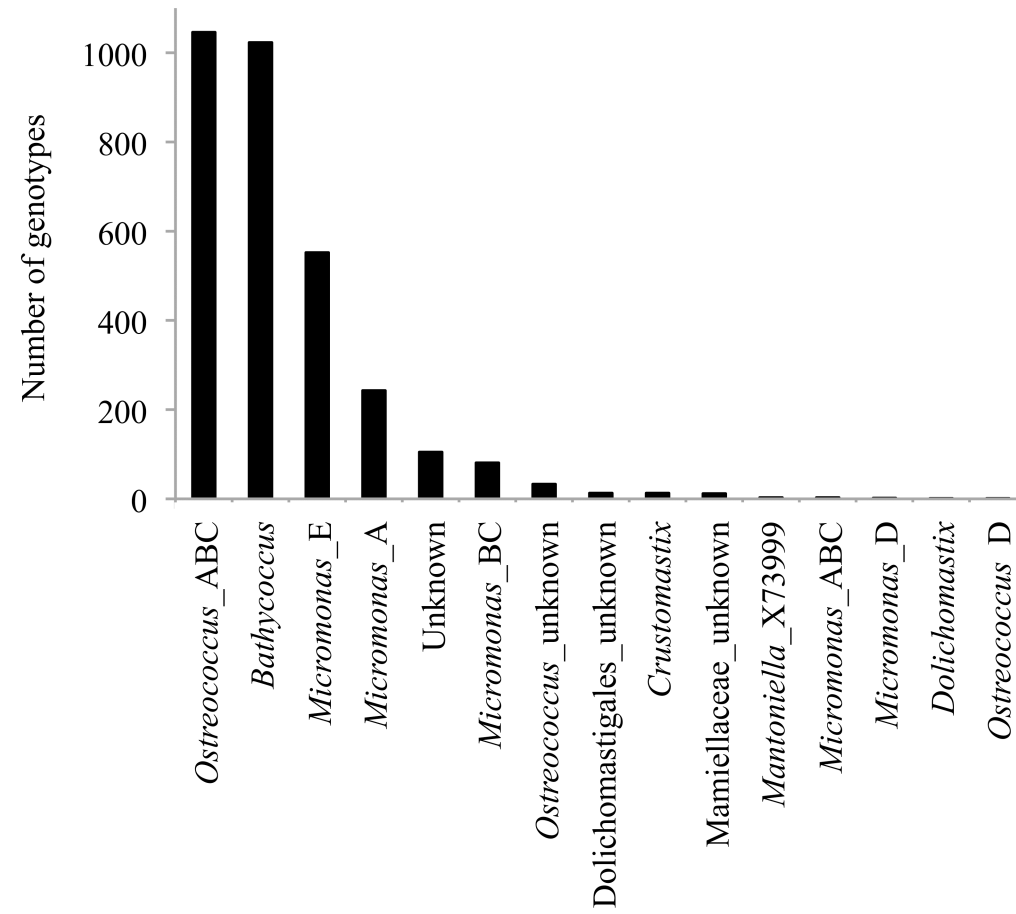


Figure S3. Annotation and rank-abundance of the Mamiellophyceae genotypes in 6 samples. A, B, C, D and E correspond to the clades defined in Marin and Melkonian (2010). Only sequence-containing taxa are shown.

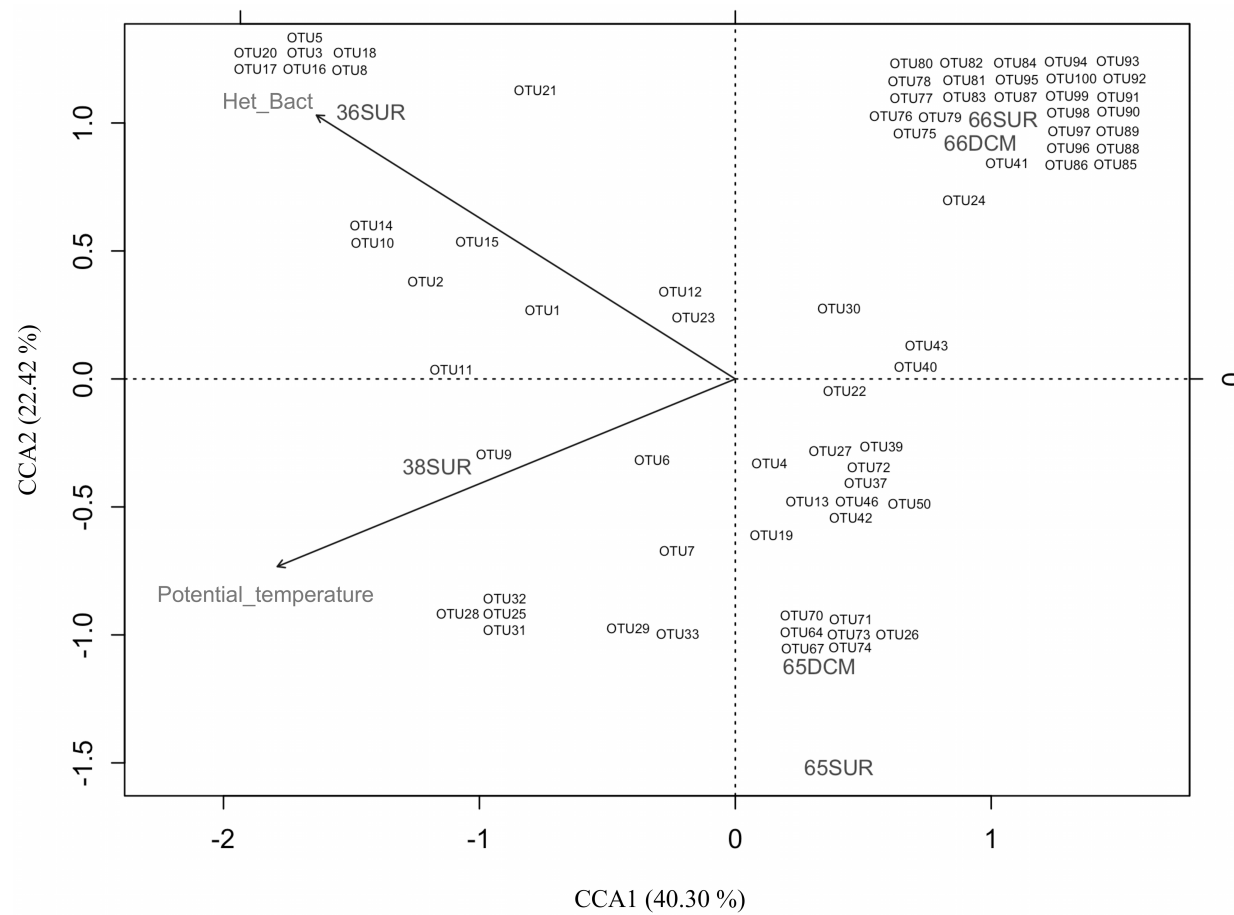


Figure S4. Canonical correspondence analysis of the 6 samples on *Prasinovirus* assemblages constrained by environmental data. Numbers in station names are in chronological order. SUR: Surface; DCM; Deep Chlorophyll Maximum. OTUs are defined for a nucleotide identity of 90 %. Only the significant variables are shown.



