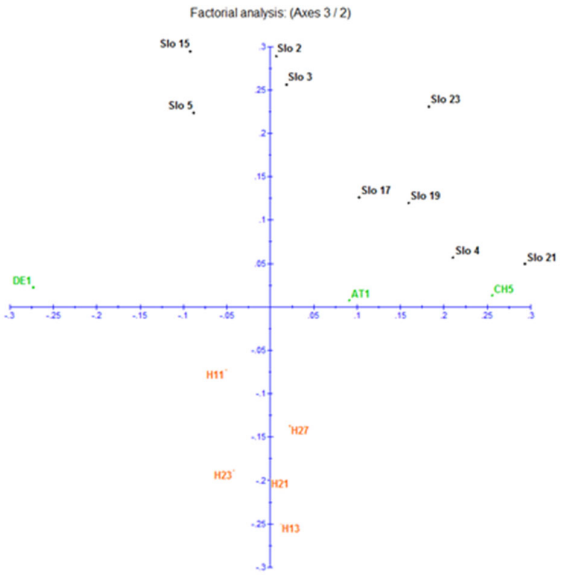

Figure S1. Principal component analysis of 14 MLGs (MultiLocusGenotypes) within the experimental Phylloxera populations employed (SLO = Slovenian genotypes employed in the VEM experiments, H = Hungarian genotypes employed in the GF experiments. AT1, CH5, DE single founder lineages kept as reference biotypes at the Institute of Viticulture and Pomology, Vienna (BOKU) and serve as defined genotype controls. Genotypic Diversity displayed per Axis: x-axis reflects to 44,78% and y-axis 42,05%. In total 35 samples (VEM: 14, GF: 18, BOKU-standard: 3) were individually genotyped and further modified according to Forneck et al. [23] based on seven SSR markers (Phy_III_55, Phy_III_30, Phy_III_36, Dvit6, DV4, DV8 and DVSSR4). In this set of samples three control genotypes were included to keep allele calling.