



Figure 1. Maximum likelihood phylogenetic tree (**a**), Structure Bayesian clustering (**b**), and Principal component analysis (PCA) (**c**) of *Phellinus noxius* populations from 15 locations. (**a**) Different colors represent samples from different locations reflected in PCA legend (c). The branches with $\geq 95\%$ likelihood support are indicated with black squares. The branch support was calculated with 1000 ultrafast bootstrap replicates. (**b**) Structure results K from 2 to 5, each vertical bar corresponds to the sample in the phylogenetic tree above Structure graphs. The height of the bar represents posterior probability of sample assignment to color coded genetic groups. (**c**) PCA represents distinct genetic groups within the studied dataset. Each dot indicates one individual. Percentages between brackets represent variance explained by each principal component (PC). For isolates and locations abbreviations see Table S1.