**S3 Fig. Population structure analyses.** At K=2 FastStructure results for the RADseq data do not show the resistant populations (first four populations on the left) segregating into a distinct group, suggesting they are not from a single origin. FastStructure analysis suggests either K=6 or K=7 as the best model, both of which leads to some populations being highly admixed (*e.g.* BI) while others are fairly homogenous (*e.g.* SH).

