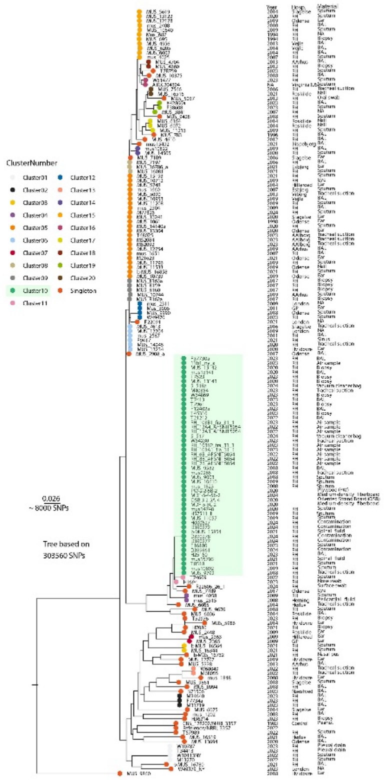
Article DOI: https://doi.org/10.3201/eid3203.251219

Environmental and Phylogenetic Investigations of *Aspergillus flavus* Outbreak Linked to Contaminated Building Materials, Denmark, 2025

Appendix 1



Appendix 1 Figure. Rooted maximum likelihood phylogeny of 167 A. flavus isolates. The tree shows clear distinction of several major clusters, including one monophyletic “Cluster 10” that contained all outbreak isolates. Sampling “Year,” hospital “Hosp,” and “Material” are indicated on the right-hand side of the corresponding isolate names. The tree was reconstructed based on 303,560 core-genome SNPs and rooted with MUS_9860 as outgroup. The scale bar indicates substitutions per site. Clusters were determined using TreeCluster.