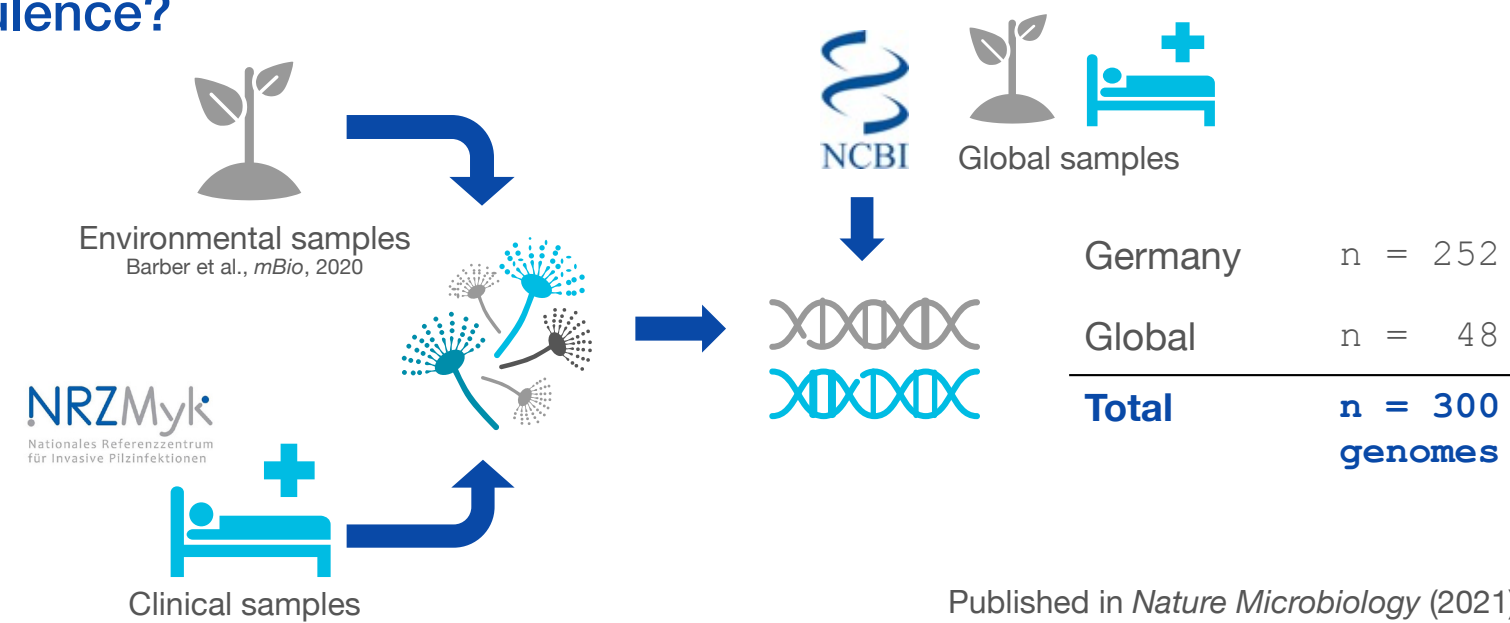


Aspergillus fumigatus pan-genome analysis identifies genetic variants associated with human infection

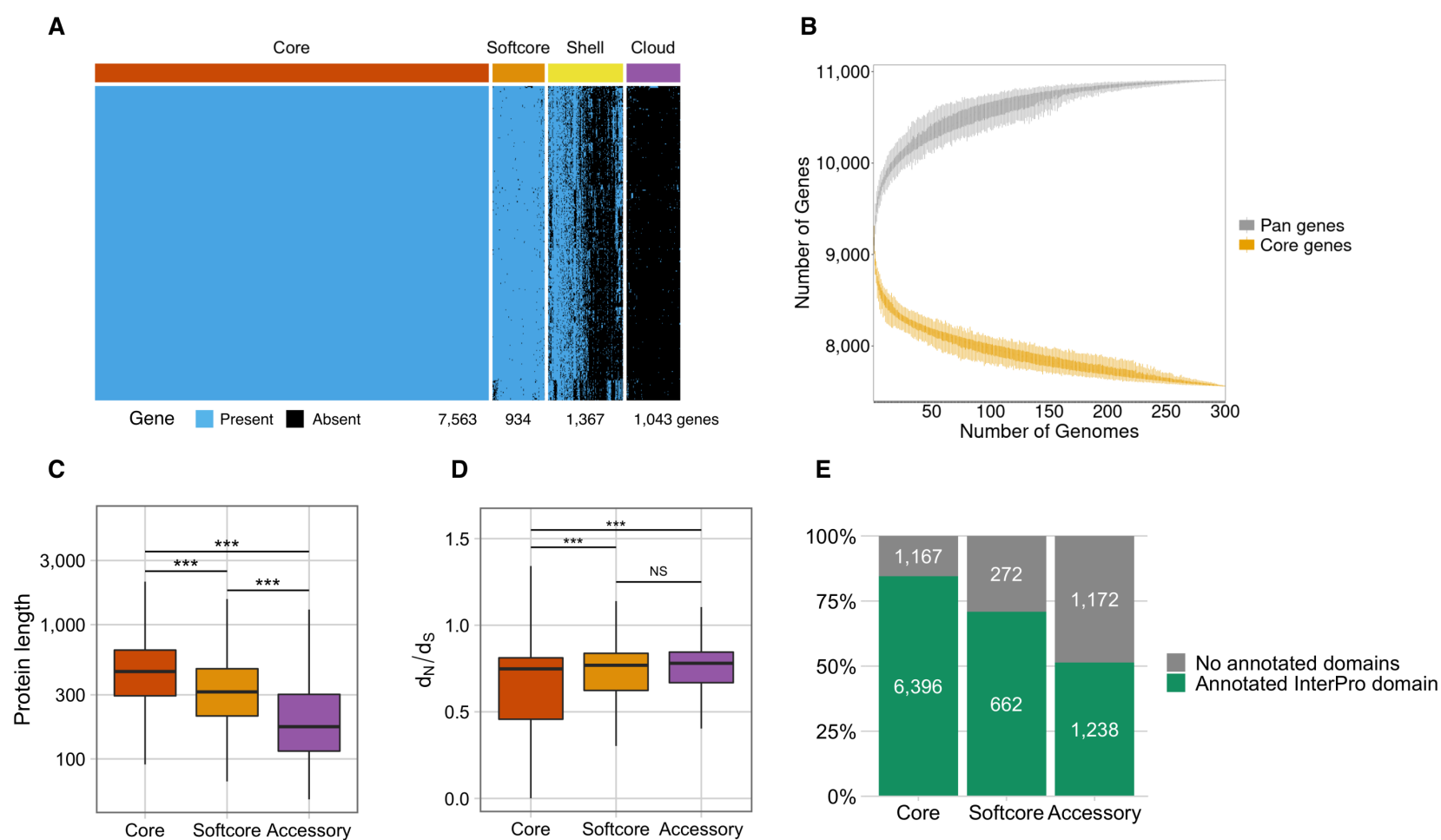
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What is the genomic diversity of *A. fumigatus* and how does it impact virulence?

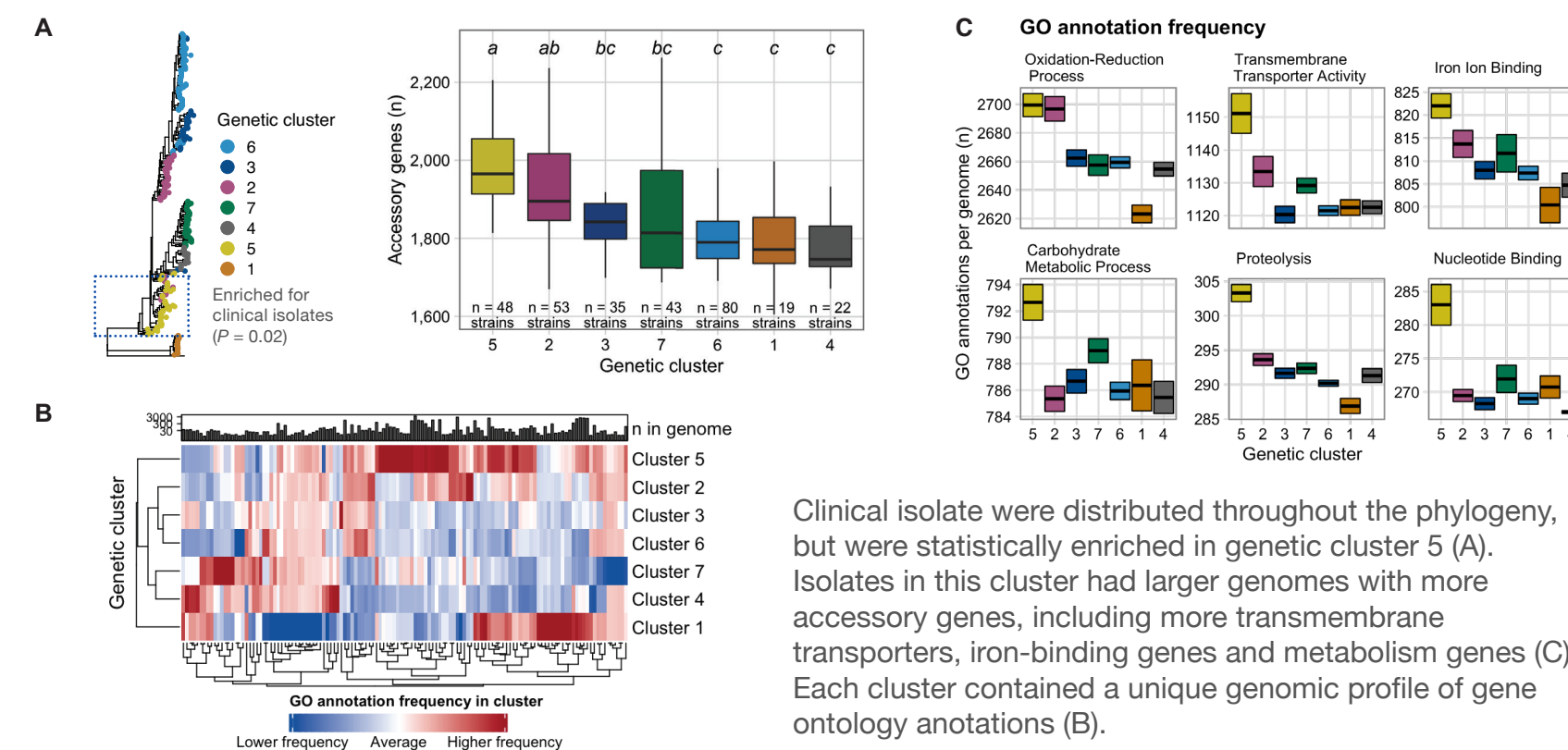


The pan-genome of *A. fumigatus*

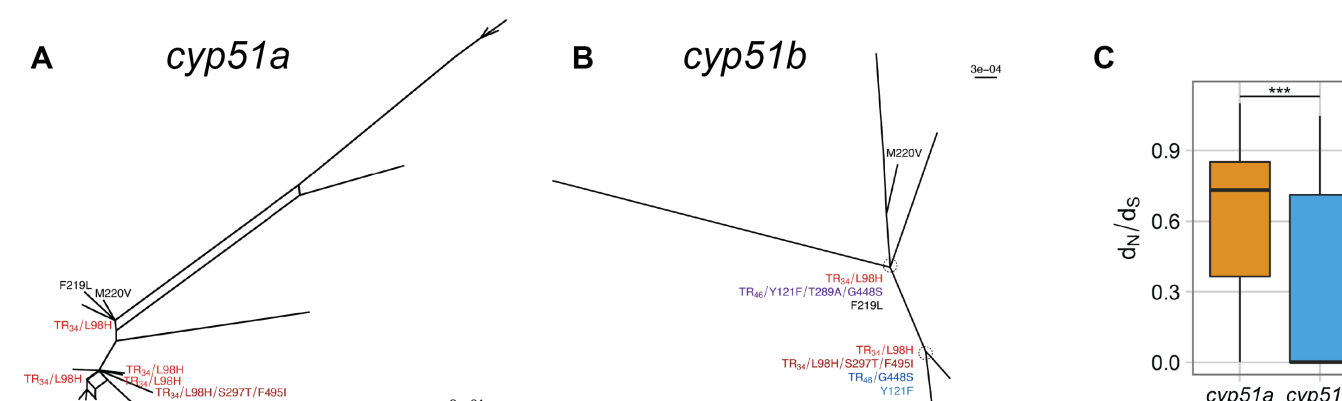


(A) Of the 10,907 non-redundant orthogroups identified, only 7,563 (69%) were found in all genomes. (B) The number of total genes identified did not increase after ~250 genomes. (C-E) Accessory genes are shorter in length (C), under a lesser degree of purifying selection (D) and less frequently possess an annotated function.

Genetic clusters have distinct genomic profiles - and one cluster is enriched for clinical isolates

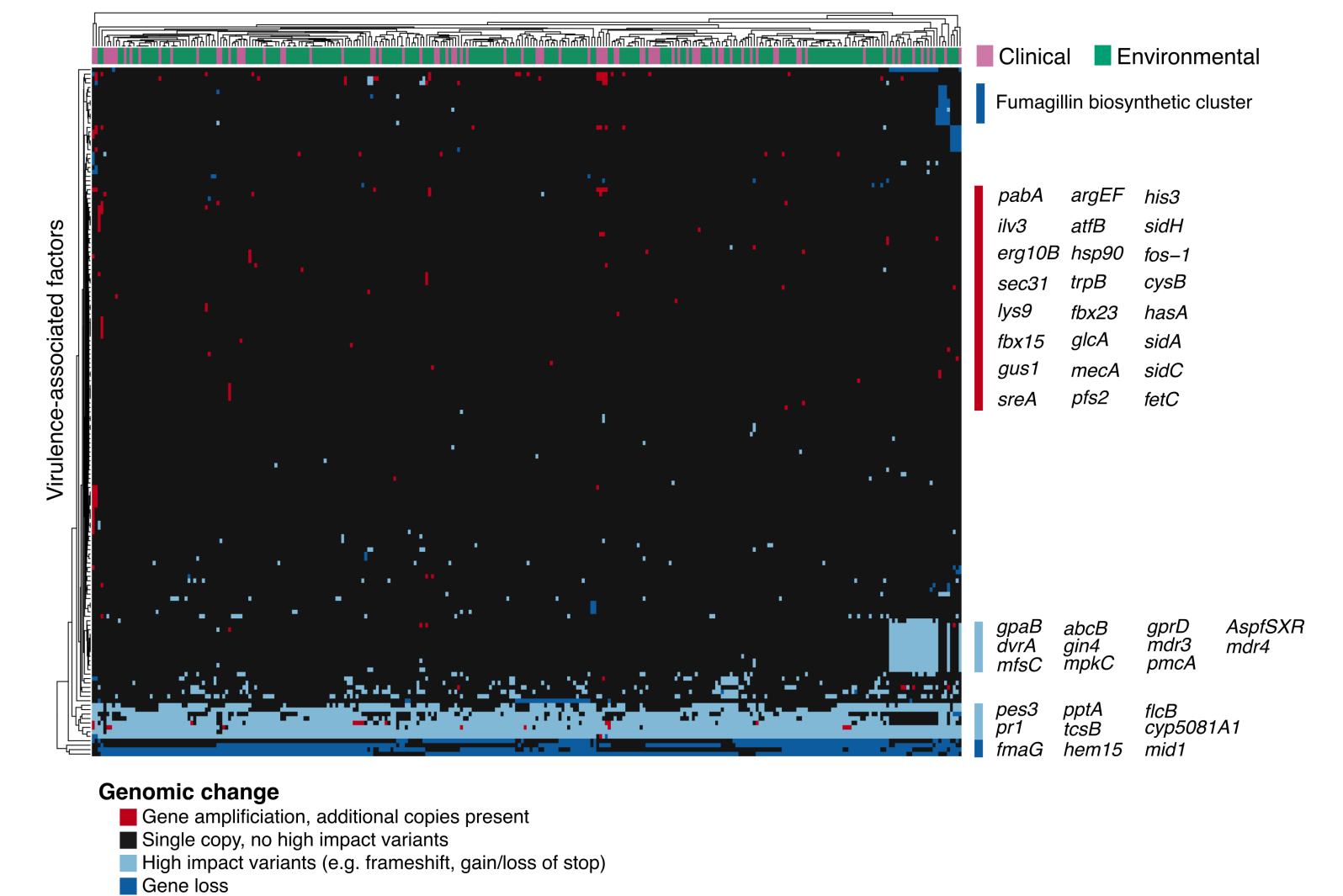


Triazole targets genes display distinct phylogenetic networks and imbalanced levels of stabilizing selection



A. fumigatus contains two paralogous copies of the triazole target gene, *cyp51*. A phylogenetic network of *cyp51a* and flanking sequence (A) contained conflicting genetic information (illustrated by parallel bands), suggestive of genetic recombination at the locus. No splits were observed in *cyp51b* (B). *cyp51b* is also under a stronger degree of stabilizing selection than *cyp51a* (C).

A. fumigatus exhibits genetic variation in virulence-associated genes



43% of virulence-associated genes examined (155/36) exhibited high-impact genetic variation among isolates, such as gene loss or duplication.

Conclusions

16-22% of each isolate's genome was not conserved among the 300 samples, including ~500 non-Af293 genes per isolate.

Notable genetic variation is present between genetic clusters - including variation in virulence-associated genes.

One reference strain and genome are not enough to capture the heterogeneity of *A. fumigatus*!