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MycobiomeDB: Body-site-stratified fungal genome database enhancing human mycobiome analysis

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The human microbiome includes fungi, yet this fungal component—the mycobiome—remains poorly characterized because fungal reads are scarce and reference sets incomplete. We developed MycobiomeDB (www.decodebiome.org/mycobiomedb), the first body-site–stratified fungal genome catalogue designed to close this gap. We collated 17,418 pre-existing high-quality fungal genomes (completeness > 90%, contamination < 5%) representing 4,094 fungal species from NCBI and JGI genome portal. Shotgun reads from 24,282 human metagenomes (gut 9,241; oral 2,461; skin 9,187; vagina 3,393) were mapped to species representative genomes. Species that met coverage-and-prevalence thresholds were further curated by nutritional mode and documented host association, yielding tailored panels of 766 gut, 259 oral, 642 skin, and 112 vaginal fungi. When combined with k-mer aligners, MycobiomeDB delivers species-level profiles with a markedly lower false-positive rate than generic databases. Benchmarking demonstrated that profiles generated with MycobiomeDB were largely concordant with those obtained using the exhaustive aligner Bowtie2, yet required 7- to 24-fold less computation time. By providing a rigorously filtered, body-site–aware genome reference, MycobiomeDB is poised to accelerate and standardize mycobiome research and to deepen our understanding of fungal contributions to human health.