

Why do some people live to be a 100? Intestinal bacteria may hold the answer

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Healthy centenarians display a more diverse and rich virome compared with young and older individuals a, A phylogenomic tree of vOTUs based on 1,415 (out of 2,388) de novo assembled and 29,057 MGV (out of 37,946) vOTUs, created with IQtree and visualized using iToL v5 (https://itol.embl.de/). Predicted host-taxonomic phylum is indicated for each vOTU as either Firmicutes (green), Actinobacteria (orange), Bacteroidetes (yellow), Proteobacteria (blue), Verrucomicrobia (pink) and Desulfobacteriota (purple). Host color indications can be seen in the second ring around the tree. vOTUs not



clustered with an MGV genome at species level are labeled undescribed vOTU (red leaf), otherwise as MGV (black leaf) shown in the third ring. Viral genera of interest (G7, G78 and G2) are indicated in the first ring. The prevalence (0–1) of each vOTU in the microbiome of centenarian, older and young individuals is indicated as orange, blue and gray bars (from the fourth ring outwards). Finally, vOTU enrichment (Wilcoxon rank sum test, one-sided, FDR corrected) on median TPM is indicated as a black rectangle between centenarian vs young, centenarian vs older and older vs young. b, PCoA-based vOTU Bray-Curtis dissimilarity shows separation of centenarian samples from older and young individuals. c,d, Boxplots of viral richness (the number of detected vOTUs in sample) (c) and Shannon diversity (d) show significantly increased richness and diversity in centenarians (t-test, two-sided, *P

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