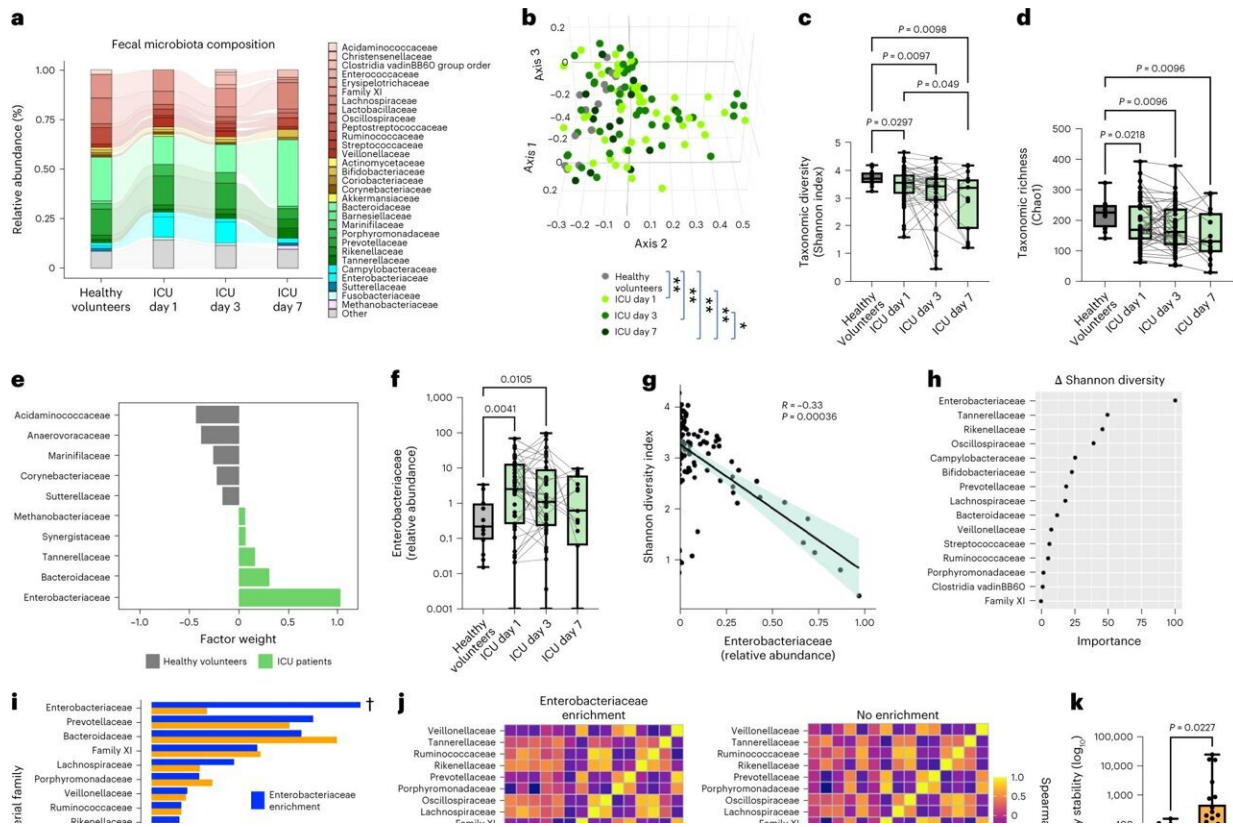


A healthy microbiome may prevent deadly infections in critically ill people

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Intestinal dysbiosis with progressive Enterobacteriaceae enrichment in critical illness is associated with nosocomial infections. **a**, Taxonomic composition by relative abundance of bacterial families. **b**, Three-dimensional principal-coordinates analysis (Bray–Curtis dissimilarity distances, genus level) analyzed by PERMANOVA. **c**, Shannon index. **d**, Chao1 index in rectal swabs from critically ill patients on day 1 ($n = 51$) and again from survivors who remained in ICU on day 3 ($n = 44$) and day 7 ($n = 15$), compared to healthy volunteers ($n = 15$). Dots represent individual patients, central line indicates median, box shows

interquartile range (IQR) and whiskers show range; analyzed by two-sided Kruskal–Wallis test (healthy versus ICU days) with pairwise comparisons of repeated measures across days using a mixed linear regression model with a post hoc Tukey’s test. **e**, MOFA of microbiota composition between healthy volunteers and ICU patients showing top ten taxonomic factors (families) and their relative contributions to explained microbiota variance (factor weight). **f**, Enterobacteriaceae relative abundance on days 1, 3 and 7 of ICU admission compared to healthy controls. Dots represent individual patients, central line shows median, box shows IQR and whiskers show range, analysis as per **c** and **d**. **g**, Correlation between Enterobacteriaceae relative abundance and Shannon index, analyzed using Spearman correlation test. Dots show individual patient samples, regression (line) and 95% confidence intervals (shaded area) are shown. **h**, Penalized ridge regression of the 15 most abundant bacterial families and their importance toward change in Shannon diversity from days 1–3 of ICU admission. **i,j**, Mean relative abundance (\dagger indicates P_{adj}

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