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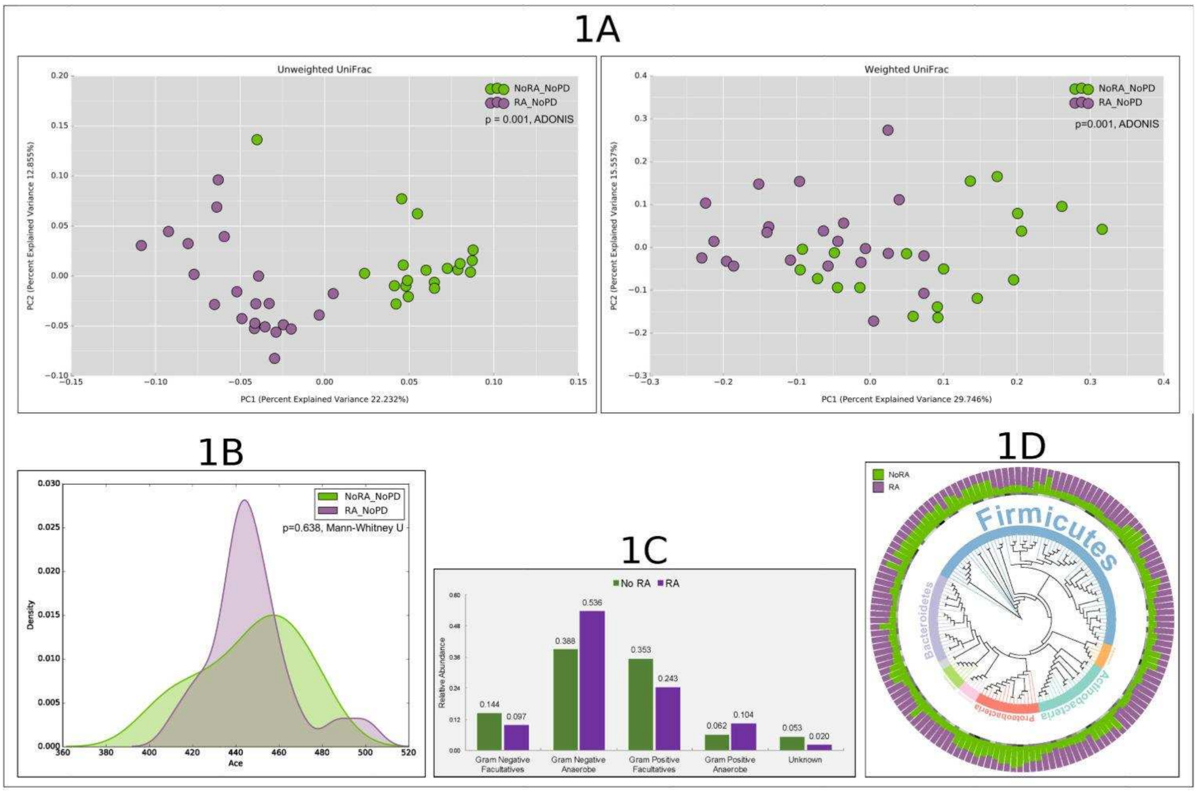

Figure 1. Differences in alpha and beta diversity metrics between periodontally healthy subjects with and without rheumatoid arthritis (RA). (A): Principal Coordinates Analysis (PCoA) plots of unweighted and weighted Unifrac distances (B): Kernel plots of alpha diversity (Abundancebased Coverage Estimator (ACE)). The peak indicates the median values for each group.

The x-axis indicates the data range. (C): Distribution of species by gram staining and oxygen requirement characteristics. Groups that share the same symbol are significantly different from each other ($p < 0.05$, Kruskal Wallis test) (D): Phylogenetic tree representing normalized mean relative abundance (NMRA, stacked bar chart), core species (circles represent species present in ≥80% of samples in a group), significant frequency of detection (stars) and phylum-level taxonomic annotation (colored-strips and text) for significantly different and differentially abundant species-level OTUs (tree leaves). Data for figure 1D is presented in supplemental table 1.

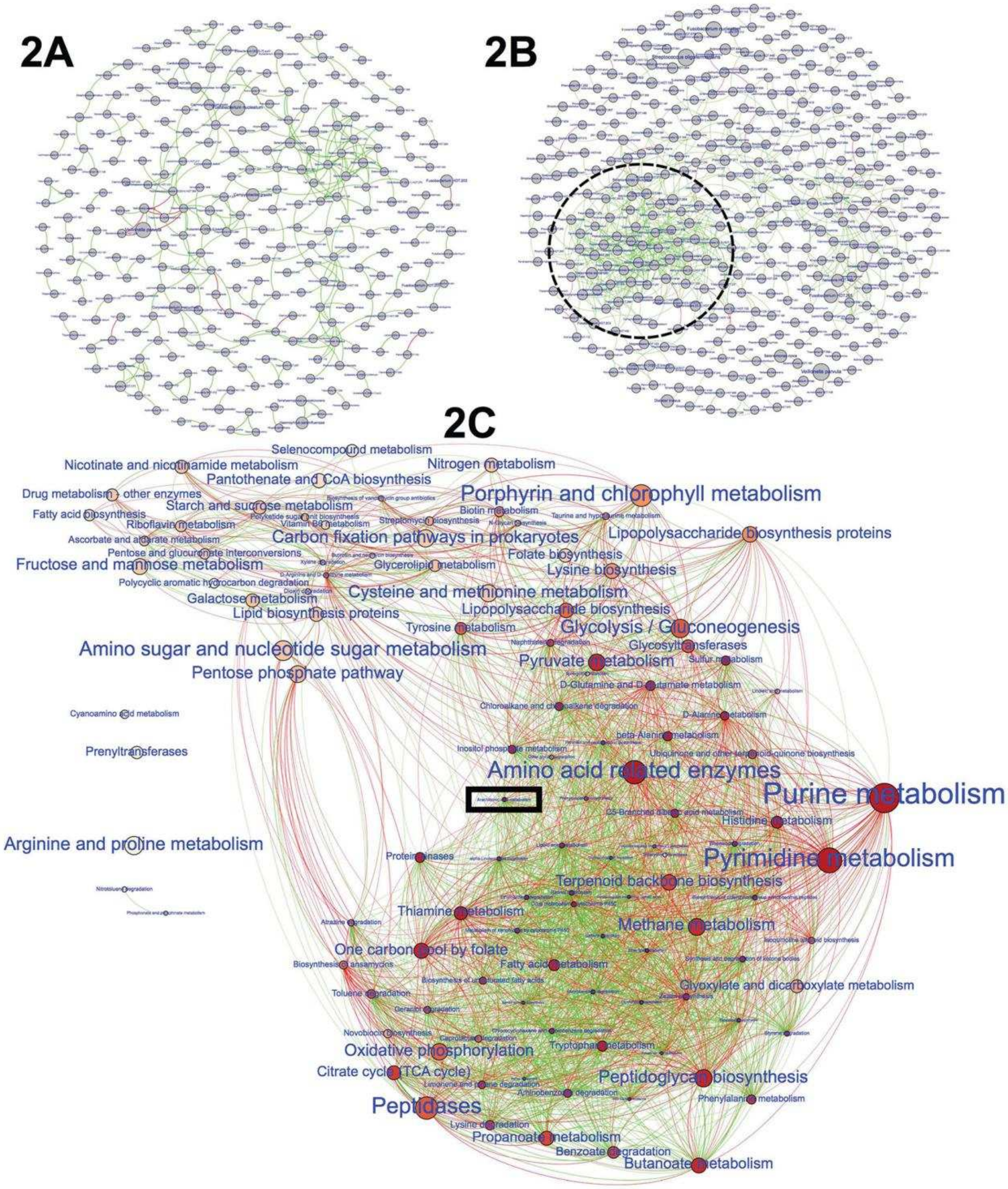

Figure 2. Co-occurrence networks in periodontally healthy subjects with or without rheumatoid arthritis (RA): Each network graph contains nodes (circles) and edges (connections representing Spearman's ρ). Edges are colored green for positive correlation and red for negative correlation. Nodes represent species-level OTUs in 2A and 2B and genes encoding for metabolic functions in 2C; and are sized by relative abundance. Edges represent significant and robust Spearman's correlation ($p<0.05$, $\rho\geq0.75$). Data for figure 2C is presented in supplemental table 2.