2.3 Statistical Analyses

All raw data (completed paper-and-pencil questionnaires, laboratory reports, electronic data) was anonymised and organised and combined into individual participant data files using a general spreadsheet software (Microsoft Excel). Data in both the individual and the combined population files were structured into spreadsheets aligned with the objectives of the research (POMS, DASS-21, Cognitive Function, gut microbiome biomarkers, gut microbiome, bacteriology, parasitology and mycology, Bristol Stool Scale, and MYMOP®). Data for each functional measure were analysed as population means ± SD for each group and measurement point. Results were also analysed according to the diagnostic ranges for each functional measure. The percentage changes between the measurement points within the protocol were calculated for each individual and averaged across the groups. Participants with missing data for any measurement were excluded from the analysis to maintain data integrity.

Data were analysed using IBM SPSS Statistics for Windows, Version 25.0 (Armonk, NY). Unless otherwise stated, data were expressed as mean ± standard deviation (SD). Anthropometric characteristics were compared using One-way ANOVA for numerical values and Fisher's Exact Test for nominal values. Habitual dietary intake of vegetables, fruit and fermented foods was evaluated using the Kruskall-Wallis test. Gut microbiome and metabolite measurements were reported as population medians with interquartile ranges (25th–75th percentile). Within-group comparisons between baseline and post-intervention values for each of the four groups were analysed using the Wilcoxon signed-rank test. CANTAB data for pre-, mid and post-intervention were analysed using the Related Samples Friedman's two-way ANOVA by ranks. Between groups comparisons across pre-, mid and post-intervention time points were assessed using a two-way mixed ANOVA. POMS and DASS-21 were analysed using Friedman's two-way ANOVA by ranks, with a Bonferroni correction applied for multiple comparisons. Correlation heatmaps were generated using Spearman's correlation coefficients based on post-intervention data collected from all study participants. These visualizations were constructed using the OriginPro version 2018b.9 software (OriginLab Corporation, Northampton, MA, USA), using a custom colour gradient to reflect the strength and direction of correlations. A p-value of < 0.05 was considered statistically significant.