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403 - ASSOCIATION BETWEEN GUT MICROBIOME DIVERSITY AND MERCURY EXPOSURE BIOMARKERS IN SPANISH 15 YEAR OLDS

J. Vallejo, R. Soler-Blasco, F. Ballester, R. Beneyto, P. Francino, A. Jimeno, M. Lozano, M.J. López-Espinosa, S. Llop

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Resumen

Background/Objectives: The balance for gut microbiota (GM) is essential for human health, regulating important physiological functions. Exposure to mercury (Hg) may impact neurological development. GM can affect Hg absorption and speciation/metabolism, and Hg may be able to alter GM diversity. There is little epidemiological knowledge of such interactions at the Hg concentrations found in our diet, and even less in adolescence The aim of this study is to examine the association between exposure to Hg in two INMA cohorts (Valencia and Gipuzkoa) and diversity of GM in adolescence.

Methods: Hg was measured in hair (n = 175), blood (n = 200), and feces (n = 97) between 2019 and 2022 (mean age 15.3 years). The ratio of Hg in stool to Hg in blood (SBrat) was calculated. GM diversity was measured from stool samples at genus level, using shotgun metagenomics, as ?-diversity (Chao1, Shannon), ?-diversity (Bray-Curtis, Aitchison), and differential abundance analysis (DAA). Sociodemographic, dietary and lifestyle data were obtained via questionnaires. Multivariate linear models were used to evaluate association of Hg exposure with ?-diversity DAA, and permutational analysis of variance (PERMANOVA) for evaluating association of Hg and ?-diversity. The models were adjusted by fish consumption and other covariables.

Results: The SBrat was positively associated with ?-diversity indices Chao1 (? [CI95%] = 1,3 [0.9-1.7]) and Shannon (0.051 [0.034-0.068]), as well as with ?-diversity by Bray-Curtis (R2 = 3%; p < 0.01) and Aitchison distances (R2 = 3%; p = 0.011). There were differences in dispersion of the distances between the lower and upper SBrat tertiles (p < 0.01 for Bray-Curtis and Aitchison). No other associations were observed between Hg concentrations and GM diversity. In the DAA analysis, only *Streptococcus* was negatively associated (log2FC = -0.05) with the SBrat, while for other 46 genera a positive association was found (q < 0.05). *Akkermansia* had the highest log2 fold-change (log2FC = 0.12); and along with Oxalobacter, Victivallis, and Sanguibacteroides conformed a group with the highest log2FC and prevalence.

Conclusions/Recommendations: While hair, stool and blood Hg concentrations were not significatively associated with GM diversity, the SBrat was positively associated to ?-diversity (Chao1, Shannon) and ?-diversity (Bray-Curtis, Aitchison). *Akkermansia* and *Oxalobacter*, commonly categorized as beneficial bacteria, were two of the genera with the highest association to the SBrat.

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