The impact of age progression in the intestinal microbiome: insights from a European cohort

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INTRODUCTION

Research in the field of microbiome has revealed intriguing associations between age and microbial composition within the human body. While the microbiome undergoes dynamic changes throughout life, influenced by various factors, including diet, environment, and health status, age itself has been recognized as a significant contributor [1,2,3].

AIM

To investigate sequential changes in the intestinal microbiome, the stool microbiome profile of 11,322 research participants was extracted from the proprietary database of Biome Diagnostics GmbH (Vienna, Austria). Questionnaire data containing demographic data, information regarding diseases, usage of drugs, diet, etc. was also retrieved and paired with the corresponding microbiome profile.

MATERIALS AND METHODS

Sample counts, taxonomy mapping file and questionnaire metadata were imported as a TSE file using the mia package v1.3.23 and transformed into a phyloseq (v1.44.0) object. All stool microbiome samples were divided in 9 categories according to age. Participants reporting current or recent antibiotic usage were excluded, leaving a total of 7,942 samples in the analysis.

RESULTS

A total of 1,234 participants were currently taking probiotics, while 1,545 have reported taking probiotics in the last 3 months. No effect of probiotic use was found for any of the diversity metrics ($P < 0.05$) and therefore these samples were not excluded from any subsequent analysis.

Table 1. Descriptive statistics regarding the number of samples in analysis and respective diversity metrics according to the age group initially defined in this explorative study. Given the fact that infants < 1 year of age are mainly breast- or formula-fed, they were not included in this analysis.

Age group	Samples (n)	Observed ASVs Mean	Observed ASVs SD	Shannon Diversity Mean	Shannon Diversity SD	Inverse Simpson Mean	Inverse Simpson SD
(0,10]	97	208.75	57.41	3.84	0.4	25.61	10.94
(10,20]	136	235.04	64.41	4.01	0.39	30.01	12.05
(20,30]	1,280	240.48	65.83	4.02	0.37	29.75	11.51
(30,40]	2,494	251.23	69.28	4.07	0.37	31.2	12.47
(40,50]	1,730	265.72	74.06	4.12	0.38	32.18	13.09
(50,60]	1,388	272.29	73.93	4.16	0.37	33.38	13.08
(60,70]	624	266.07	75.38	4.12	0.41	32.78	13.65
(70,80]	155	275.31	69.74	4.17	0.36	33.69	13.77
(80,90]	38	270.11	70.64	4.15	0.3	31.46	10.27

A significant effect of age group was found for the number of observed ASVs, Shannon diversity and Inverse Simpson ($P < 0.001$). Participants (0,10] years of age had a significantly lower Shannon diversity index than all the other age segments. However, the number of observed ASVs and the Inverse Simpson index did not differ from participants in the (10,20] age group. Further differences between groups were found regarding these metrics, up until categories above the (40,50] segment, showing that overall diversity indices increase until (30,40], but then seem to stabilize.

Table 1. Pairwise differences between age groups according to PERMANOVA. The number of observed ASVs are given in blue, Shannon index is given in orange, Inverse Simpson is given in green. ns, all P >0.05; *, P <=0.05 and > 0.01; ** P <= 0.01 and > 0.001; *** P =< 0.001.

	(0,10]	(10,20]	(20,30]	(30,40]	(40,50]	(50,60]	(60,70]	(70,80]	(80,90]
(0,10]	-	-	-	-	-	-	-	-	-
(10,20]	ns * ns	-	-	-	-	-	-	-	-
(20,30]	*** *** *	ns ns ns	-	-	-	-	-	-	-
(30,40]	*** *** ***	ns ns ns	*** ** ns	-	-	-	-	-	-
(40,50]	*** *** ***	*** * ns	*** *** ***	*** *** ns	-	-	-	-	-
(50,60]	*** *** ***	*** *** ns	*** *** ***	*** *** ***	ns * ns	-	-	-	-
(60,70]	*** *** ***	*** * ns	*** *** ***	*** ** ns	ns ns ns	ns ns ns	-	-	-
(70,80]	*** *** ***	*** * ns	*** *** ns	*** ns ns	ns ns ns	ns ns ns	ns ns ns	-	-
(80,90]	*** ** ns	ns ns ns	ns ns ns	ns ns ns	ns ns ns	ns ns ns	ns ns ns	ns ns ns	-

A significant difference between age groups was found using PERMANOVA ($P < 0.01$). A pairwise PERMANOVA further revealed significant differences between all groups ($P < 0.05$), except between (50,60] vs (70,80], (40,50] vs (80,90], (60,70] vs (80,90], (60,70] vs (70,80] and (80,90] vs (70,80].

CONCLUSION

Our results indicate a continuous aging progression of the intestinal microbiome up until adulthood, followed by a stabilization in richness and diversity at later stages of life. To better depict the differences in microbiome diversity and composition at a very early stage and a later stage in life, recruitment of participants in these age groups is essential.

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