

<https://doi.org/10.7124/bc.000B7C>

V.A. Kubai^{1, 2}, Kh.V. Malysheva¹

¹ Stepan Gzhytskyi National University of Veterinary Medicine
and Biotechnologies of Lviv
50, Pekarska Str., Lviv, Ukraine, 79010

² LLC "DIAGEN"
34-A, Kyivska Str., Sofiivska Borshchahivka, Ukraine, 08131
vika.kubay4756andr@gmail.com

ASSOCIATIONS BETWEEN THE GA-MAP DYSBIOSIS INDEX AND FAECAL BACTERIAL PROFILE DEVIATIONS

Background/Aim. The human gut bacterial microbiota contributes to metabolic, immune, and intestinal barrier homeostasis. Alterations in its composition are associated with gastrointestinal disorders. This study characterised deviations in predefined bacterial profile blocks and explored their associations with the GA-map Dysbiosis Index (DI) and age. **Methods.** We retrospectively analysed 156 anonymised GA-map Dysbiosis Test reports from stool samples were submitted for routine laboratory testing between 22 November 2024 and 30 March 2026. As the dataset lacked clinical indications, symptoms, diagnoses, dietary data, and information on recent antibiotic or probiotic use, it was treated as a laboratory-based referral sample; findings were descriptive and not population- or disease-specific prevalence estimates. According to the GA-map Dysbiosis Test Lx v2 report form, predefined blocks A1–E5 representing core microbiota and diversity, diet-associated groups, carbohydrate- and probiotic-related bacteria, epithelial integrity and short-chain fatty acid producers, and potentially pathogenic or inflammation-associated bacteria. C1 comprised markers associated with complex-carbohydrate fermentation and cross-feeding, including *Bacteroides* spp., *Parabacteroides* spp., [*Clostridium*] *methylopentosum*, and *Ruminococcus bromii*. C2 included lactic acid bacteria and probiotic-associated markers, including *Bifidobacteriaceae*, *Lactobacillaceae*, *Lactobacillus* spp., *Streptococcus* spp. Descriptive statistics, Pearson's chi-square or Fisher's exact test, and Spearman's correlation were used ($p < 0.05$). The data were anonymized before analysis; consent for personal data processing had been obtained. **Results.** At least one profile-block deviation occurred in 120 participants (76.9%), of these, 72 had DI 1–2 and 48 had DI 3–5. The most frequent deviations were detected in block C2 in 84 (53.9%) and in block C1 in 83 (53.2%), followed by B1 – 54 (34.6%), D2 – 41 (26.3%), and D1 – 32 (20.5%). DI values of 1–2, 3, and 4–5 were observed in 108 (69.2%), 42 (26.9%), and 6 (3.8%), respectively. A1–A2 deviations were descriptively more frequent at higher DI levels, reaching 5/6 (83.3%) in the DI 4–5; however, this subgroup was small. Age was weakly correlated with the number of profile deviations (Spearman's $\rho = 0.211$; $p = 0.008$). Among the participants aged ≥ 60 years ($n = 21$), 16 had at least three deviations. The age association for C2 was nominal ($p = 0.049$). **Conclusions.** Profile-block deviations were frequent in participants with DI 1–2, whereas DI > 2 was observed in 48 (30.8%). Owing to unavailable clinical and microbiota-modifying data, the findings are descriptive and not population- or disease-specific.

Keywords: GA-map, gut microbiota, dysbiosis index.

Received: 06.07.2026; Accepted: 08.09.2026; Published: 29.09.2026

Citation: Kubai V.A., Malysheva Kh.V. (2026) Associations between the GA-map dysbiosis index and faecal bacterial profile deviations. *Biopolymers & Cell*, Special issue(42), 65. <https://doi.org/10.7124/bc.000B7C>

© Publisher PH "Akademperiodyka" of the NAS of Ukraine, 2026. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited