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Letter to the Editor

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Gut Microbiota Composition and Function Hardly Influence the Phenotype of Spinal Muscular Atrophy Patients

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We read with interest the article by Feng *et al.* on a study about gut microbiota changes and lipid metabolism in patients with spinal muscular atrophy (SMA) ^[1]. It was found that SMA patients had abundance of the genera *Ruminiclostridium*, *Gordonibacter*, *Enorma*, *Lawsonella*, *Frisingicoccus*, and *Anaerofilum* and shortage of the genera *Catabacter*, *Howardella*, *Marine_Methylotrophic_group-3*, and *Lachnospiraceae AC2044_group* ^[1]. It was concluded that gut microbiome and lipid metabolites differ between SMA patients and controls and that the altered microbiota may be related with the lipid metabolite levels in SMA ^[1]. The study is compelling, but has limitations that are cause of concerns and should be discussed.

Composition of gut microbiota is dependent on multiple factors. There is evidence that the type of gut microbiota depends on the type of food ingested. Food and its components, nutrients or additives, not only affect the composition of gut microbiota but also their function [2]. Fibers (prebiotics), for example, serve as food for beneficial bacteria that can also produce beneficial short chain fatty acids (SCFAs) [2]. Butyrate is a SCFA that plays a crucial role in maintaining proper intestinal barrier and immune function [2]. Although gut microbiota can synthetise various B vitamins and vitamin K, several other micro-nutritients consumed through diet affect gut microbiota composition [2]. Vitamin-D, for example, increases the amount of Lacnobacterium. Since gut microbiota is involved in the synthesis of beta-carotene, they contribute to the body's antioxidative capacity. Excess of micro-nutritients, such as iron and zinc, can promote the colonisation of Clostriudium difficile, a pathogenic bacterium [2]. Also, polyphenols promote greater abundance of beneficial than harmful gut bacteria. Additionally, some polyphenols exhibit prebiotic activity. Gut bacteria themselves can increase the bioavailability of polyphenols [2]. From essential fatty acids, particular omega-3 poly-unsaturated fats, it is known that they increase the level of beneficial bacteria, exhibit an anti-inflammatory effect, and stimulate the production of butyrate [1]. Omega-9 mono-saturated fatty acids impact on the level of bacteria from the genera Parabacteroides, Prevotella, and Turicibacter. Taken together, eating a diet high in fiber, fruits and vegetables promotes a healthy gut microbiota composition, whereas Western diet, which is high in sugar, fat, salt and food additives, can cause a decrease in beneficial bacteria. Therefore, we should know whether the 15 included SMA patients were eating the same diet or whether they were eating according to their individual desire. Constitution of gut microbiota is also strongly dependent on comorbidities. Since SMA patients may not only suffer from SMA but also from acquired diseases or even a second genetic disorder, it is crucial to know whether any of the 15 included patients only suffered from SMA or had other troubles, such as arterial hypertension, diabetes, hyperlipidemia, thyroid dysfunction, immunological disorders, or other diseases. Gut microbiota levels and function also depend on the medication the included patients were regularly taking. Therefore, it is essential to know which drugs patients and controls were regularly taking to assess if any of these drugs influenced gut microbiota composition.

Gut microbiota composition may also depend on the immune competence of an individual, whether healthy or diseased. Therefore, we should know if any of the included SMA patents or controls subjects had deficiency of immune competence. In summary, the interesting study has limitations that put the results and their interpretation into perspective. The influence of the gut microbiome on the risk of developing of acquired disease or on the phenotype of genetic disease may be overestimated. Particularly, with regard to genetic disease, the underlying genetic defect is the key factor that determines the clinical presentation and gut microbiota only marginally influence the phenotype. In general, however, there is no doubt that the state of the gut microbiome has a significant impact on health.

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Statement of Ethics:

- a. The study was approved by the institutional review board (responsible: Finsterer J.) at the 4th November 2022.
- b. Written informed consent was obtained from the patient for publication of the details of their medical case and any accompanying images.

Data availability statement: Data that support the findings of the study are available from the corresponding author.

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Compliance with Ethics Guidelines: This article is based on previously conducted studies and does not contain any new studies with human participants or animals performed by any of the authors.

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