Erratum to: Collado MC, et al. Gut Microbes Volume 3, Issue 4; pp. 352-65

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The authors regret having missed the inclusion of some relevant references in the original manuscript and other sentences were not accurately referenced. In the following text, authors included the modified sentences and also the list of missing references together with the original ones marked with an asterisk (*).

- The human microbiome (HM) is a complex system of many microbial communities inhabiting a diversity of environmental niches throughout the human body. The human gastrointestinal tract (GIT) is inhabited by a complex and dynamic population of around 500–1000 different microbial species.¹ HM exhibits large variation among individuals in relation to internal and external factors such as genetic factors, age, diet, and health, and remains in a complex equilibrium.² Although the exact composition of the microbiota is not known, advances in genomic technologies have recently begun to unravel our microbial partners.³
- Thereafter, colonization is further modulated not only by environmental bacteria but also by early breast milk, colostrum, which contains live microbes, especially bifidobacteria and lactic acid bacteria, and a spectrum of bioactive substances.⁴
- After the first 6 months of life when solid food is introduced to the infant, the gut microbiota becomes more diverse. The succession of *Bacteroides*, *Clostridium*, and anaerobic bacteria increases rapidly while the proportion of bifidobacteria becomes more stable.⁵
- Microbiota development of the infant is rapid and depends on the first inoculum, the mother's microbiota, mode of delivery, type of feeding, and the environment, including weaning food practices and the use of antimicrobials.^{2,6*}
- In recent years, the increase in microbiota-related research has provided important advances toward establishing the identity of specific microbes and microbial groups or microbial molecules contributing to various aspects of host physiology and health.^{7*}
- Studies on human microbiota should include microbial ecology and analysis of the complex metabolism of the microbial community, as well as various host-microbial interactions occurring at the interface between microbes and host intestinal epithelia.⁸

- Altered intestinal colonization by commensal microorganisms and increased occurrence of potential pathogens, as well as high interindividual variability and reduced microbial diversity, have been reported in preterm infants.^{9-11*} Several gastrointestinal pathologies such as IBD, IBS, NEC, obesity, various forms of colitis, and even autism has been linked to disturbances in human-associated microbiota or alterations of the intimate cross-talk between these microbes and human cells.^{12,13*}
- A subsequent metagenomic study^{14*} with 154 individuals showed that obesity was associated with a markedly reduced bacterial diversity, a relative depletion of Bacteroidetes, and a higher proportion of Actinobacteria compared with lean subjects.¹⁵
- In type-1 diabetes, a combination of multiple factors leading to the development of autoimmunity appears to include an aberrant intestinal microbiota, a leaky intestinal mucosal barrier, and an altered intestinal immune responsiveness.^{16,17*}
- The complex interactions between microbes and host combined with recent clinical observations and epidemiologic trends may point to the convergence of two hypotheses: the "hygiene hypothesis" and the "fetal programming hypothesis."^{18*}
- Also, epidemiological studies indicate that maternal farm environment exposure during pregnancy protects against allergic sensitization, asthma, and disease, and have an upregulation of receptors of the innate immune system whereas exposures during infancy alone are under discussion.^{19*,20*,21}
- A more recent review and meta-analysis reported that a protective effect against allergic disease was only observed if probiotic supplementation were initiated in the prenatal period and continued postnatal, but not if probiotic supplementation was commenced postnatal.^{9,22*}
- NEC is the most common gastrointestinal emergency in low birth weight infants. Delayed enteral feeding, frequent use of antibiotic therapy and altered acquisition of normal digestive microbiota are the most likely factors contributing to the development of NEC in preterm infants.⁵
- The development of metabolic complications associated with obesity during childhood tracks into adulthood.²³

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Submitted: 02/10/2014; Accepted: 02/10/2014; Published Online: 05/21/2014

http://dx.doi.org/10.4161/gmic.29308

Correction to: Collado MC, Cernada M, Baüerl C, Vento M, Pérez-Martínez G. Microbial ecology and host-microbiota interactions during early life stages. Gut Microbes 2012; 3:352-65; PMID:22743759; http://dx.doi.org/10.4161/gmic.21215

Disclosure of Potential Conflicts of Interest

No potential conflict of interest was disclosed.

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