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Mono-colonization with *Lactobacillus acidophilus* NCFM affects the intestinal metabolome as compared to germfree mice

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Every single species of the gut microbiota produce low-molecular-weight compounds that are absorbed constantly from the intestinal lumen and carried to systemic circulation where they play a direct role in health and disease. However, very few studies address the host metabolome as a function of colonizing bacteria. In this study the effect of the *Lactobacillus acidophilus* NCFM strain was investigated by comparing the metabolome of mono-colonized and germ-free mice in several compartments. By liquid-chromatography coupled to mass spectrometry, we were able to show that the metabolome differed between the mono-colonized and germ-free mice, not only in ileum, caecum and colon, but also in plasma and liver. These observations suggest that *L. acidophilus* NCFM highly influence the metabolism in multiple compartments, underlying that the gut microbiota metabolism affects the host systemic metabolism.