Chinese doctors, over 1000 years ago (Zhang et al., 2012) because of its smart reproduction in any medium, provided the original work is properly cited.

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Another current issue is the relationship between gut microbiota and human ageing that Harald Brüssow has recently reviewed in *Microbial Biotechnology*, in view of the classic book ‘The Prolongation of Life’ by Metchnikoff (1907), and the ELDERMET project that pursues health improvement of elderly people via modification of their gut flora (Brüssow, 2013a). All the reviewed studies show constraints that prevent from drawing a clear conclusion: small samples, high inter-individual variability, changing nutritional habits among populations and/or along life or detecting the presence of bacteria but not their viability. Nevertheless, the decay of gut microbiota in elderly people seems to be more related with poor diet habits and lack of exercise, than with ageing itself. All of that work will facilitate targeted modifications on the microbiome structure – maybe via specific food intake – that will help to improve gut communities in the elderly as suggested by (http://eldermet.ucc.ie/). Complementary to this report and also in *Microbial Biotechnology*, Prof. Brüssow presents an inquisitive review of the different health concepts (Brüssow, 2013b), and discusses whether it can be measured with the appropriate tools. The author also examines the concept of ageing – not only in humans – and how our current knowledge may be biased by short-lived animal studies. Although so far our life expectancy keeps growing, biological systems are not perfect, and so they will probably come to a point where accumulated errors will no longer allow life, particularly on complex organisms. If the focus is not set on increasing our life expectancy, but rather on improving the quality of our ageing, it would be a better choice, and the study of the gut microbiota will undoubtedly contribute to that improvement.

Faecal communities are crucial for health not only in adults or seniors, but also in children, because besides their common functions, they play an important role in the development of their immune system (Jost et al., 2012). Neonates’ initial colonization depends both on transference from their mothers and on their environment, either during birth or through close contact. Benefits from breastfeeding include the acquisition of probiotic bacteria, but also of other anaerobic microbes that have not been extensively investigated yet. Jost and co-workers have published a very revealing paper in *Environmental Microbiology* (Jost et al., 2013), establishing the correlation between micro-organisms found in maternal faeces, breast milk and the gut of their corresponding neonates. The novelty of this report is that the authors not only address the presence of the micro-organisms but also their viability, dealing with one of the deficiencies commonly found in gut communities studies. Their results clearly show divergences between both approaches. Pyrosequencing assigns similar numbers to both mothers’ milk and faeces bacteria, but when determining ribosomal ribonucleic acid or colony-forming unit counts, milk samples contain more than a million-fold less microbes than faecal ones. This report certainly supports the transference of living gut microbes from mothers to infants through breastfeeding, although the route between the mother’s intestines and the breasts still remains unknown.

Where does all this research lead to? Maybe the clue is to be found in a recently published *Microbial Biotechnology* review by Willem de Vos where he highlights the need to understand how intestinal microbial communities work to develop effective biotechnological tools for targeted modification of gut flora (de Vos, 2013). He establishes the concept of minimal microbiome that can be defined as the smallest set of microbes and/or microbial functions necessary to develop a stable community. Systemic analysis of the interaction between intestinal microbes and the host are under way and will allow the prediction of the minimal synthetic microbiomes for the treatment of different diseases. Next-generation therapies against obesity, ageing and metabolic disorders could be based on the targeted implementation of these microbial communities.

**References**


