



Fig. 1. Generalized scheme of the human gut microbiota composition. The different bacterial groups are divided on the basis of whether they exert properties which are potentially damaging or health-promoting for the host. The central vertical line gives approximate numbers in faeces. Modified from Gibson & Roberfroid (4).

generated the development of products with defined starter cultures that eventually led to the formulation of bioyoghurts fermented with specific intestinal microorganisms designed to give positive health benefits.

The 'health-benefit' image of bifidobacteria stems from the work of Tissier (9) who claimed that the faecal flora of breast-fed babies differed from those that were bottle-fed, in that they contained large numbers of bifidobacteria. Although other studies have cast doubt on this observation (10), the possibility remains that bifidobacteria are important in improving the gastrointestinal resistance of breast-fed infants. Neut et al. (11) found that although *B. bifidum* was predominant in breast-fed babies, *B. longum* was most frequently isolated from infants receiving formula-based milk. Interestingly, preliminary studies have shown that *B. longum* is able to exert stronger antimicrobial activities than *B. bifidum* (12). Improved bifidobacterial counts and species composition, as found in breast-fed infants, may account for their improved gastrointestinal resistance. Numbers of bifidobacteria continue to remain high throughout adult life, but

in old age, when susceptibility to disease again increases, populations show a decrease (13).

EFFECTS ON THE MICROFLORA

Because of their potential health-promoting attributes, probiotic and prebiotic supplements are usually directed towards lactobacilli and/or bifidobacteria. The extent to which this may be achieved can be difficult to assess. Measurements of changes in numbers of viable cells of these two groups present problems if the organism being ingested has no special characteristics which make it distinguishable from indigenous, closely related, strains. Modern genetic techniques will make this easier but so far they have not been used to trace probiotics through the intestinal tract. Future possibilities may include accurate typing procedures that are based on the 16S rRNA molecule, or genetic tagging with oligonucleotides.

The effect that a probiotic organism has on the microecology of the gut is to some extent dependent on its ability to survive and preferably multiply therein. Assuming the