



**Figure 2.** Flower morphology in dicots and monocots. **a**, *Agrostemma githago* – An insect-pollinated flower, dicot family Caryophyllaceae. The perianth is two-whorled and clearly differentiated into an outer calyx composed of five free sepals (green and leaf-like, hairy) and an inner corolla composed of five petals (pink). **b**, *Crocus scepusiensis* – An insect-pollinated flower, monocot family Iridaceae. Each flower has six tepals, all of them identical. The perianth is two-whorled, but it is not differentiated into calyx and corolla. Such a perianth is called a perigon and its members are termed tepals. In ornamental monocots, tepals are coloured and thus petal-like. The *Crocus* has a petaloid perigon composed of identical tepals. **c**, *Iris germanica*, group *barbata elatior* – An insect-pollinated flower, monocot family Iridaceae. The petaloid perigon is composed of two whorls of three tepals each, but the inner and outer tepals differ in shape and colour. Therefore, some botanists name them sepals and petals. **d**, *Luzula* sp. flower, monocot family Juncaceae. In this wind-pollinated species, the perigon is composed of two whorls of identical sepal-like tepals. Therefore this perigon is sepaloid.

## Conclusion

Our aim is not to claim that *Iris* flowers have or do not have sepals, although we agree that such a discussion is needed. Quite likely only molecular techniques will enable one to say with certainty whether or not *Iris* flowers do have sepals.

It appears that the dataset itself is not interesting for botanists, and only statistics and some other related disciplines

are familiar with it and show any interest in it. Thus we want to direct attention of statisticians, who usually are so far from botany, to this discussion, still contemporary. From a historical point of view, it is interesting that such a famous dataset, so often used and so well known, is problematic in such a simple aspect. As it seems, this aspect is not so simple, and the history of this dataset is still alive.

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## Initiating exploration of the gut microbiome in Indians

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Human gut harbours approximately  $10^{14}$  bacterial cells which outnumber the total number of human body cells<sup>1</sup>. The gut microbiota plays a vital role in development, nutritional, health and disease status of its host. Assemblage of these microbes is known to be predisposed by genetic make-up of an individual, age, dietary habit, ethnicity and environmental factors. India is distinguished

from the rest of the world with vast diversity in the genetic composition of its human population, coupled with the enormous diversity in dietary habits, cultural affiliations with various religions and geographic scattering. However, there are hardly any studies on gut microbial communities in the Indian population. Five of the recent publications have addressed this issue. The results of these

indicate differences in gut microflora of Indians from the previous studies in other populations<sup>2–6</sup>. Although these are preliminary studies, the observations are significant in terms of the gut microbiota in Indian diaspora. These studies have highlighted the necessity to further explore the gut microbiota of Indian individuals.

Colonization of gut by microbes takes place immediately after birth and is

defined by the type of delivery, i.e. vaginal or cesarean. Many studies have analysed the bacterial diversity in infants in the Western population. Pandey *et al.*<sup>2</sup> on Indian individuals compared the micro-eukaryotic diversity in two breast-fed and two formula-milk-fed infants and their mothers using culture-independent techniques. They reported eight micro-eukaryotic microorganisms, of which *Blastocystis* sp. was observed to be predominant in the gut of healthy mothers<sup>2</sup>. *Blastocystis* has been linked to a number of gut-related diseases and there is likelihood that this is a result of predation of beneficial bacteria by *Blastocystis*. In addition, the second most abundant genus was *Saccharomyces* followed by *Candida*<sup>2</sup>. The gut forms a complex ecosystem and in such an ecosystem the role of micro-eukaryotes in modulating the composition of bacterial communities either by antagonism, and predation or inhibition by eukaryotes cannot be underestimated, as the composition of the bacterial communities has major implications in the health status of the human host. The study of micro-eukaryotes has received less attention worldwide and Pandey *et al.*<sup>2</sup> have made important observations in mothers from the Indian subcontinent. In another study, Pandey *et al.*<sup>3</sup> studied the gut microflora of human infants born through vaginal delivery (VB) and through cesarean section (CB) using culture-independent 16S rDNA cloning and sequencing approach. Difference was observed in gut flora of VB and CB infants. The gut flora of VB infants was dominated by *Acinetobacter* sp., *Bifidobacterium* sp. and *Staphylococcus* sp., whereas faecal microbiota of CB infants was dominated by *Citrobacter* sp., *Escherichia coli* and *Clostridium difficile*<sup>3</sup>. *Bifidobacterium* sp. is a beneficial organism and is reported to be one of the early colonizers of human gut. Interestingly, Pandey *et al.*<sup>3</sup> showed the absence of *Bifidobacterium* sp. in CB infants. This study gives important insights into the effect of mode of delivery in development of human gut flora.

Marathe *et al.*<sup>4</sup> assessed the changes in bacterial composition in human gut with age in an Indian family using both culture-dependent and culture-independent methods. This study included two joint-families with three generations living under the same roof and is a first study of its kind in which change in gut flora of genetically related, co-habiting indi-

viduals with age was studied. The difference in composition of gut flora with age was observed in three generations within a family<sup>4</sup>. *Firmicutes* and *Bacteroidetes* were observed to be the major bacterial phyla present in gut of Indian individuals. A consistent decrease in *Firmicutes* to *Bacteroidetes* ratio with increasing age was observed within the same family. This pattern is different from that reported in other populations around the world, suggesting that composition of gut flora of Indian individuals may be different than the Western population<sup>4</sup>. Further support to this hypothesis was provided by the isolation of a high percentage (27) of potential novel bacterial species from the gut of these individuals<sup>4</sup>. Although this was a preliminary study, the observations are important in the context of gut flora studies in the Indian population. The demonstration that gut flora in Indians may be different compared to the Western population necessitates understanding the microbial community structure in Indians in both healthy and diseased individuals.

One such disease condition is obesity. Obesity is a metabolic disorder caused by uncontrolled food intake accompanied by a sedentary lifestyle. In developing countries like India there is increased prevalence of such lifestyle-associated diseases. Patil *et al.*<sup>5</sup> carried out comparative analysis of dominant gut microbiota of lean, normal, obese and surgically treated obese individuals of Indian origin. Body mass index (BMI) and whole body fat was assessed to confirm leanness of lean individuals. In contrast to previous studies on the Western population, no evident trend was observed in the distribution of phyla *Firmicutes* and *Bacteroidetes* in lean and obese individuals in this study. However, at the genus level *Prevotella* was dominant in all the libraries, whereas *Bacteroides* was observed to be dominant in obese and surgically treated obese individuals in comparison with normal ( $P < 0.05$ )<sup>5</sup>. These genera have been found to be dominant in rumen cattle which are herbivores and diet of many Indians consists of more plant-based food in comparison to their Western counterparts and hence the role of diet in shaping these bacterial communities in Indian gut cannot be overruled. The observations of this study suggest that the gut microbiota differed in the different groups under study and that the gut flora of treated obese is

closer to normal individuals in comparison to obese individuals.

All the above studies were based on clone library analysis. The recent use of metagenomics to study the gut microbiota provides much deeper insights into the community structure of microbial communities in human gut. Gupta *et al.*<sup>6</sup> used the metagenomic approach to assess the microbial communities in a malnourished Indian child and an apparently healthy child. It was observed that the gut flora of the malnourished child has an abundance of enteric pathogens belonging to families Campylobacteraceae and Helicobacteraceae<sup>6</sup>. These pathogens are known to reduce absorption in the intestine and also cause intestinal inflammation. The malnourished gut also had specific virulence-associated sequences which belonged to order Campylobacterales, which suggests a role of these virulence genes in pathogenesis of malnutrition. This study indicated a possible dysbiosis in gut community composition of malnourished children.

The studies discussed here have provided vital insights into the gut microbiota composition in Indian individuals, but a broader effort is needed to study the human population in India. Considering the diversity in the Indian population, defining the core gut microbiome in Indians remains a distant achievement. Unless the scientific community makes efforts to explore and understand the microbial community dynamics in the gut environment, elucidating the role played by these microbes in the health status of Indian individuals will be complicated.

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