In this issue

How diverse are village agroecosystems?: Investigating tree species diversity in Uttara Kannada

There was a time when villages in the Western Ghats (and perhaps many other regions as well) were surrounded by forests. At least, forests were not too far off from the villages. Many of the needs of the villagers for fuel, fodder, timber for dwellings, etc. were always met from the nearby forests. Unfortunately, this happy (and more importantly, sustainable) state of affairs is no longer true. Because of commercial and unsustainable harvesting of forests to a large extent, as well as because of the increased pressure due to continuously increasing population, forests have shrunk considerably, and are no longer able to meet the village requirements. One of the ways in which the villagers can respond to this situation is by growing trees in and around villages – in home gardens, on bunds of cultivated fields, on boundaries of streams and water bodies, etc. The tree cover so generated would have many other benefits as well; such agro-forestry leads to a more efficient use of sunlight, moisture and nutrients. What are the kinds of tree species that one finds in such a situation? What are the levels of diversity? How much of standing biomass does one find? Answers to these and many such important questions are largely unknown for many climatic regions. In the detailed study described on **page 1080** of this issue, C. M. Shastri *et al.* provide one of the first estimates of the tree species diversity for a village ecosystem in the Uttara Kannada District of Karnataka.

Situated at an altitude of about 500 m asl, having 26 hill peaks in less than four square km area, and receiving about 2500 mm of annual rainfall, Sirsimakki is a typical example of humid tropical village in the Western Ghats. Using an appropriate combination of transect and quadrat-based sampling, the authors have surveyed eight different types of habitats. They have enumerated a total of 2238 stems (each one at least 10 cm in diameter) belonging to 144 species, and have estimated a density of a little over 400 trees and about 30 tons of standing biomass per hectare. For a more detailed account of the diversity as found in different land use categories, as well as for an interesting comparison with other such ecosystems in South America, turn to page 1080 of this issue.

N. V. Joshi

Plant viral *T*-party

'One side will make you grow taller and the other side will make you grow shorter' said the caterpillar to Alice as it got off the mushroom. . . . 'And now which is which?' she said to herself, and nibbled a little of the right-hand bit to try the effect. The next moment she felt a violent blow underneath her chin; it had struck her foot!

Not so dramatic, but quite the same is what Sangita *et al.* report in this issue in their paper (**page 1123**) on the structure of $T = 1$ capsid formed by the recombinant N-terminal 65 residue deletion mutant of the Sesbania mosaic virus (SeMV) coat protein (CP). Sixty units of the truncated CP expressed in *E. coli* assemble into an icosahedral shell of about 19 nm diameter. However, the full-length CP dresses as an icosahedral soccer ball of about 30 nm diameter spruced up with 180 units and with a triangulation number of $T = 3$. Cut off a portion of the N-terminus in the CP and the virus shrinks. Part of life's adventures in the molecular wonderland.

The structure of the 'regular' SeMV capsid, reported first in 1995 through the same collaborative efforts of the laboratories of Murthy and Savithri in the Indian Institute of Science, Bangalore, has a triangulation number of $T = 3$. One hundred and eighty units (60×3) of the capsid protein assemble as a viral ball with icosahedral symmetry. The three units (termed A, B and C) that form the asymmetric units perforce can only have quasi-equivalence, as was enunciated by Caspar and Klug in the 1960s in their ideas on viral architecture. The first atomic structure of a virus – tomato bushy stunt virus (TBSV) – determined to 2.9 Å resolution was published by Stephen Harrison and his colleagues in 1978. Two years later, Michael Rossmann and his group determined the structure of Southern bean mosaic virus (SBMV). Harrison wrote in the *Nature* (1978, **276**, 368–373) paper, 'The most remarkable aspect of the TBSV subunit is the configuration of its N-terminal portion'. And this was later amplified by 'A portion of the polypeptide chain near the N-terminus interdigitates with others in an unusual fashion in one state of the subunit (C) and appears disordered in the other, quasi-equivalent positions (A/B).' Later in his commentary 'Virus crystallography comes of age' to the paper on SBMV (*Nature*, 1980, **286**, 33–39) Harrison comments 'SBMV and TBSV show quite dramatically that the spatial arrangement of modules in a subunit protein is characteristic of the assembly, but not necessarily of the isolated polypeptide; the remarkable interdigitation of N-terminal arms could not have been anticipated (or even seen) in the structure of the subunit alone'. He worries that 'high resolution structures of large assemblies may not be readily constructed from structures of component parts'. In trying to understand the role of the N-terminal arm in viral assembly, Rossmann's group determined the structure of SBMV capsid obtained by the assembly of the proteolytically N-terminal-cleaved CP (*Science*, 1985, **229**, 625–629). However, the result was limited to low resolution. Since then, efforts have been on to investigate at higher resolution the effect of the N-terminal switch. This article presents detailed information on the oligomeric structures of dimeric, trimeric and pentameric units of the $T = 1$ and $T = 3$ particles constituted from the capsid protein of the same virus, in this case SeMV, at a resolution of 3 Å. The question naturally arises: what are the major differences in the quaternary organization between the $T = 1$ and $T = 3$ capsids.

S. Krishnaswamy