Response:

John *et al.*[1] proposed division of bamboos into two groups based on the timing of maturation of male and female organs: *Bambusa* type and *Dendrocalamus* type. Our studies[2] in six bamboo species are also in agreement with this division. Bamboos can also be divided, using the nature of opening of florets as a character, into two major groups: (1) species with floral glumes (lemma and palea) widely separated at an angle more than 40° (we proposed the term 'open florets'[2]) and (2) species with floral glumes separated at an angle less than 10° ('tubular florets'[2]). Using this trait, we further grouped the three species of *Bambusa* into (i) species having open florets (*B. bambos* and *Bambusa* sp.) and (ii) species with tubular florets (*B. vulgaris*). *B. vulgaris*, thus, undoubtedly represents another group under *Bambusa* type. The descriptions and figures provided by John and Nadgauda are also in favour of this grouping. Sterility and adaptations are different aspects which are not relevant, at least here.

The statement that the positioning of stigma and anthers at two different levels acts as a physical barrier to self-pollination in *B. arundinaceae*, has to be reviewed in the light of the works of Kondas *et al.*[3] and Indira[4], who have inferred self-pollination in the species.

The cytological evidences[5] in *B. vulgaris* surely raise questions on the status of the taxa. It could be a sterile hybrid or a sterile mutant, as suggested by John and Nadgauda. However, further studies may be necessary to throw more light on this aspect.

The florets in *Bambusa* sp.[2] are similar to those of other species of *Bambusa* studied, except that floret opening and bee visitation were observed twice daily. We do not have any conclusive evidences to categorize it under 'heterodichogamy'.

With reference to co-evolution and point (v) that 'insects have very short life spans and bamboo flower at very long intervals', we feel that the comparison of life span of bees should be made with that of bamboo flowers, and not with the long interval of bamboo flowering.

Insect-pollination in bamboos was first suspected by Soderstrom and Calderon[6]. Chris Stapleton[7], a field botanist who worked extensively on bamboos in the Siwalik Hills of Nepal and West Bengal writes, 'I was puzzled as to how *Dendrocalamus hamiltonii* sometimes produced large quantities of seed when only one clump was flowering in the local area, and I put this down to pollination by bees rather than the wind'. After explaining the floral biology and the chances of probable insect pollination, we suspected the co-existence of autophily, anemophily and hymenopterophily in *Bambusa*[2]. The works of Kondas *et al.*[3], Indira[4] (autophily), Soderstrom and Calderon[6] and Stapleton[7] (hymenopterophily) also support this view.

It is true that the florets in *B. vulgaris* are homogamous. Though John and Nadgauda (legend to Figure 1 *d*, this issue) recognize the variety of *vittata* of *Bambusa vulgaris*, their assumption of *B. vulgaris* as synonym is taxonomically incorrect. *B. bambos* (L.) Voss is the correct name for *B. arundinacea* (Retz.) Willd (see Dransfield and Widjaja[8]).

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NEWS

Could the Basmati rice on your plate be an imposter? Call in the 'rice detectives'

There is quite a hullabaloo about the good old Basmati rice. A rice, which has traditionally adorned the plates of a repast fit for kings. In this day and age we know not what we eat, as a result of adulteration and spurious food doing the rounds. In the case of Basmati, it is of paramount importance to distinguish the valued 'traditional' variety from others, considering the high cost of the raw material. For this, and of vital significance to trade, comes a solution with the latest in gene technology to decipher the truth about Basmati rice varieties that we may encounter in the market-place. This is where efficient DNA molecular markers can authenticate traditional Basmati (TB) from evolved Basmati (EB) and the semi-dwarf non-Basmati (NB) rice varieties.

TB variety has special characteristics 'culminated by centuries of selection and cultivation by farmers'. The TB variety is characterized by 'extra-long, slender grain, pleasant and distinct aroma, and soft and fluffy texture'. However, TB has also not so good characteristics, for example, 'tall stature, low yield, etc.'. To rectify this, and in order to develop better 'elite' strains, rice breeders have resorted to combinations with high-yielding NB resulting in the EB variety. The EB variety however, does not turn out to be quite the best. This is due to difficulties involved in getting the best match, while crossing the most desirable qualities. A recent publication by J. Nagaraju *et al.*[1], titled 'Genetic analysis of traditional and evolved Basmati and non-Basmati rice varieties by using fluorescence-based

ISSR–PCR and SSR markers' is research findings for identification of the genuine Basmati variety from the other Basmati-like NB varieties. Nagaraju and co-workers have, by making use of effective molecular marker systems as 'rice detectives', helped to establish genetic relationships and origins between the various TB, EB and NB varieties.

DNA fingerprinting can establish relationships and test purity. In the case of Basmati, in trying to sort out the various varieties, informative markers in genetic analysis provide the link for plant breeders and geneticists to information derived from sequencing, genome mapping and phenotype evaluation. Nagaraju *et al* have used two classes of DNA markers, i.e. fluorescence-based inter-SSR (ISSR)–PCR-based markers and simple sequence repeat (SSR) markers for the purpose of carrying out the genetic analysis of Basmati rice varieties. They have found such markers efficient, cost-effective and helpful in detecting a 'higher degree of polymorphism' in rice.

A total of 24 rice varieties of *Oryza sativa* were studied by the research team, accounting for six from TB, eleven from EB and seven types from NB varieties. After a selection of primers and conducting an SSR survey, the evaluation of polymorphisms and an analysis of genetic diversity were carried out. The calculation of genetic diversity was based on the number of alleles/locus in SSR and the number of bands/primer in the case of ISSR. According to the paper, a subset of three rice groups were analysed by using 19 SSR loci and 12 ISSR–PCR primers. A total of 70 SSR alleles and 481 ISSR–PCR markers were shown in 24 varieties from the three groups. From an evaluation of the ISSR–PCR markers, both the extent of polymorphisms exhibited in the three rice groups and the genetic diversity were calculated for each of the selected ISSR primers in all three rice groups.

The study has determined, by evaluating the ISSR–PCR markers, that the degree of polymorphism 'differed substantially' among the three rice groups, namely TB, EB and NB varieties, with TB showing the lowest level of polymorphism. The results show that out of 340 bands studied, only 115 were polymorphic in TB. In the case of EB, it was 360 out of 465 bands and from NB, 166 of 321 bands were polymorphic. The results from the calculation of genetic diversity have shown that by using two or three informative primers, the TB from the EB and NB varieties could be 'unambiguously' distinguished. The researchers also evaluated SSR markers obtaining information on polymorphism, allele distribution and genetic diversity in the three rice groups.

The findings of this paper using the fluorescence-based ISSR and SSR markers indicate that 'TB varieties have the least diversity compared with the EB and NB varieties'. Also, after evaluating both the marker assays, no significant differences among TB varieties were seen. The TB varieties used in the analysis 'could be considered the bulk of the narrow gene pool of the Indian subcontinent'. The results have shown that the TB varieties used in the study lack genetic variability, indicating that 'most of the traditional varieties have probably originated from a single land race', which is also supported by data of the historical relationship existing among the Basmati varieties.

According to J. Nagaraju, this research work 'gives a powerful detection method for identification of traditional and evolved Basmati varieties'. Pure (traditional) Basmati 'commands considerable premium price' over evolved Basmati varieties (which are essentially derived from the hybrids of TB variety and semi-dwarf rice variety). Another current area of interest to the researchers is 'the detection of adulteration of TB with evolved varieties', which constitutes a major problem. Also, Basmati breeders who would produce elite evolved Basmati varieties could then compare these, using the DNA markers, with the ruling evolved varieties and traditional varieties. This exercise would help to ascertain their genetic proximity to the traditional ones before finally authorizing them for commercial cultivation. He added that the DNA profiles used in their research paper could help to register the Basmati varieties to protect breeder's rights (in case of evolved varieties) and the country's interests (in case of traditional varieties).

Finally, Basmati breeders could test the set of DNA markers unique to Basmati varieties for their association with Basmati specific traits. Similarly, the set of DNA markers, unique to semi-dwarf varieties could be used to test for their association with the semi-dwarf specific varieties. Such markers, if found associated with the specific trait, could find potential use in the hands of Basmati rice breeders to practice DNA marker-assisted selection (MAS), Nagaraju added.

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