Ph D student intake and output over a period of 1999–03, it is found that the intake numbers are consistently higher by a significant margin than the output. This clearly points to a large dropout among Ph D students; in the committee's opinion, poor quality intake and lack of motivation could be the main contributing factors to this disturbing trend. In this context, it is to be pointed out that the number of IIT B Techs opting for Ph D programmes in the IITs is worryingly small. In view of the above facts, it is not surprising that the annual Ph D output per faculty works out to be only around 0.2 and this low number has not changed appreciably since the time of Nayudamma committee review carried out almost two decades ago. The present committee considers the above state of affairs as a serious matter of concern and has recommended several measures to improve the situation. Some of these are: assuring career to highly talented youngsters who choose to pursue Ph D, instituting, for all IITs put together, 100 Golden Jubilee Research Fellowships with a monthly stipend of Rs 20,000 for attracting quality Ph D scholars. In addition, to tap a larger pool of students, it is suggested that the IITs could introduce an integrated Ph D programme, in select disciplines, for B Sc graduates along similar lines as being done successfully at IISc.

Next we turn to the most important issue, namely, faculty matters. As pointed out in the report, it is the faculty members and their academic stature which constitutes the core calibre of the IIT system and it is their intellectual value along with sustained efforts which drives the output. Therefore, attracting and retaining quality faculty is considered to be of prime importance in maintaining and furthering excellence in all the spheres of IIT activities whether it be education, research or industry–institute interaction. To be successful in this endeavour, the committee makes a very important recommendation as follows: a system akin to that prevalent at IISc for faculty induction and faculty assessment and promotion be followed at the IITs. The IISc system is thought to be considerably more flexible than that is in vogue currently at the IITs. The implementation of the new procedure is to be handled by establishing a separate Human Resource Unit headed by a Dean. In addition, it is noted that any mechanisms that can be put in place to zealously guard the faculty time would prove to be highly productive. One example of such a mechanism would be to establish a sizeable internal research grant, which the faculty can tap instead of applying for grants from external funding agencies.

In summary, what the committee has done is to first discover the present scenario of the IITs, then diagnose issues of concern, followed by design of strategies for change with an overall final aim of raising the levels of performance of the IIT system. It is hoped that the recommendations of the committee receive due attention for actual implementation.

Notes and references

1. The composition of the review committee was as follows. Chairman: Dr P. Rama Rao; Members: Dr R. Chidambaram, Prof. Goverdhan Mehta, Dr S. K. Joshi, Shri Anand Mahindra and Shri C. K. Birla; Special Invitee: Shri Subhodh Bhargav; Member Secretary: Joint Secretary (T), MHRD (Ex-Officio).
2. The IITs today consist of seven institutions, five older ones established at Kharagpur (1950), Bombay (1958), Madras (1959), Kanpur (1960) and Delhi (1961) and two newer ones set-up at Guwahati (1995) and Roorkee (2001).
3. The Chapter titles in the report are: 1. Why IITs are important to the Nation?, 2. Scope and objectives of the review, 3. A macroview of the IIT system, 4. Vision for the IIT system, 5. Governance of the IITs, 6. Faculty matters, 7. Research enhancement, 8. IIT educational system, 9. The undergraduate admission process: JEE, 10. Expanding the IIT brand through IPR, 11. IIT–industry linkage, 12. Technology in education and research, 13. Non-faculty employees, 14. Funding policy and the development of the IITs, 15. Expansion within the country and opening campuses abroad, 16. The special case of IIT Guwahati.
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Taxonomy of rhizobia: Current status

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Taxonomy of rhizobia is in a state of flux. This has been driven by technological advances in all three criteria, morphological, physiological and sequence analysis, used in taxonomy.

Rhizobia interact with legumes to produce root nodules, site of biological nitrogen fixation, hence they have been classified and studied extensively. Earliest attempts to name them were made after the host plant[1]. Three decades later, Fred *et al.*[2] coined the modern name *Rhizobium* and proposed a classification based on nodulation range with emphasis on host plant. In sixties, Norris[3] grouped rhizobia according to their biochemical properties. These approaches, however, had their own shortcomings. Development of sequencing protocols in 1970s set the foundation of taxonomy as it is followed today. In 1980s Trüper and Krämer[4] proposed that sequence analysis of conserved genes or parts of genes could serve as a taxonomic chronometer. Thus, the nineties saw the beginning of an era of polyphasic taxonomy[5]. By 1994 it was evident that use of 16S rRNA sequence data would profoundly affect the relationships among bacteria[6]. Group rhizobia, very well exemplified this change. In the first edition of *Bergey's Manual of Systematic Bacteriology*[7] only two rhizobial genera (*Bradyrhizobium*, *Rhizobium*) with four species were described. Since then, extensive phenotypic and genotypic variations have been described in rhizobia. Use of PCR tools and sequencing methods has led to description of new, and re-organization of the existing genera. Till 2003, thirty six-rhizobial species distributed among seven genera were recognized[8]. In the following three years eight new rhizobial species have been described. Currently, there are 44 recognized species of nodule bacteria on legumes within 11 genera, 9 belonging to α-proteobacteria, *Allorhizobium*, *Azorhizobium*, *Bradyrhizobium*, *Devosia*, *Mesorhizobium*, *Methylobacte-*

rium, *Ochrobactrum*, *Rhizobium* and *Sinorhizobium*. Rhizobia have crossed the boundaries where they originally belonged, i.e. α-proteobacteria in the year 2001 when *Burkholderia* spp was described from the nodules of the South African legume *Aspalathus carnosa*[9] and *Ralstonia taiwanensis* in *Mimosa* nodules from Taiwan[10]. Tripathi[11] has reported *Ralstonia* from *Mimosa* nodules from India and how a good science was left behind in the publication race.

Basing bacterial phylogeny on 16S rRNA gene sequence variation presupposes that genes are inherited in hierarchical manner, and each genome harbours a single copy of 16S rRNA gene or that multiple alleles within a single genome have identical sequences. However exceptions to this hypothesis have now been described in various taxa, viz. *Clostridium*[12], *Escherichia coli*[13], *Haloarcula*[14] and *Rhodobacter*[15], all of which contain multiple, and often-divergent 16S rRNA gene. The finding that an actinomycete, *Thermobispora bispora* contains two similar copies of 16S rRNA gene and show a mismatch of 6.4% at the nucleotide level came as a bolt since the practice of 5% mismatch earlier used to place individual strains in separate genera, became questionable! Such discordance in 16S rRNA phylogeny results from lateral gene transfer (LGT) and recombination. However, LGT can be viewed as an agent that promotes and maintains bacterial species. Acquired genes play a major role in bacterial diversification by supplying previously unavailable traits[16]. Young *et al.*[17], on the other hand, have proposed that close relatedness of 16S rRNA sequences of *Agrobacterium* and *Rhizobium* species (<7% mismatch) warrant amalgamation of agrobacteria and rhizobia into *Rhizobium*. Against this background, van Berkum and co-workers[18] have re-examined the evolutionary relationships among the group rhizobia by comparative sequence analysis of 16S rRNA, 23S rRNA and ITS region within the *rrn* operon. Tree topologies generated with 16S rRNA gene sequences were significantly different from those corresponding with 23S rRNA and ITS region sequences. There were few examples of discrepancies in 16S rRNA and 23S rRNA phylogeny. Based on 23S rRNA, *B. elkanii* and *B. japonicum* were placed in a single group whereas, with 16S rRNA they were separated by *B. denitrificans*, *R. palustris* and *A. felis*. Based on 23S rRNA gene sequences, all six species of *Sinorhizobium* nested within *Rhizobium* but with 16S rRNA data they formed a group neighbouring *Rhizobium* and *Agrobacterium*. Also, there were differences between the two data sets relative to the placement of *Rhizobium galegae*, *R. huautlense*, *R. leguminosarum*, *R. gallicum*, *Agrobacterium vitis*, *A. rubi* and *A. tumefaciens*.

According to the recommendations of the adhoc committee on reevaluation of species definition of bacteria[19], DNA–DNA reassociation is considered most important and confirmatory. The committee further adds that sequence analysis of five carefully selected housekeeping genes of diverse chromosomal loci could supplement DNA–DNA reassociation data. However, Zeigler[20] has shown that carefully selected three gene sequences, *rpo*A, *thd*F, *rec*N, can indeed equal or perhaps surpass the precision of DNA–DNA hybridization for quantitation of genome relatedness. In a meeting of the subcommittee for taxonomy of rhizobia and agrobacteria held at Toulose, France in July 2004, there was a consensus that multilocus sequencing was more convenient and reliable for rhizobial taxonomy than DNA–DNA hybridization for proposing new species (Young, pers. commun.). The committee further adds that use of phenotypic traits to distinguish new taxa could be abolished. It suggests that the word 'rhizobium' can be used as a common name for legume nodulating nitrogen-fixing bacteria irrespective of genus. The set of genes available for such analysis in rhizobia is not exactly the same as that used by Zeigler, however, *glu*A (glutamine synthetase 1), *gyr*B, *rec*A and symbiosis genes, like nod (*nod*A or *nod*D) and nif (*nif*H and *nif*K) are considered useful (Bazzicalupo, pers. commun.). With the availability of new set of tools, viz. sequence analysis of housekeeping genes, rhizobial systematics may have to look back at some of the species that were established utilizing 16S sequence as the sole criterion!

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ACKNOWLEDGEMENTS. We thank Dr Peter Young of University of York and Dr Marco Bazzicalupo of Italy for valuable information about multilocus gene sequencing.

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