COMMENTARY

Some experiments with a pre-Ph D course at IISER Mohali

Anand K. Bachhawat

Pre-Ph D courses are conducted in almost every research institute and university in the country, and have been mandated by the University Grants Commission (UGC) to be an essential part of the Ph D programme. These courses, which run from 6 months to a year are focused on strengthening the base of the students, but perhaps the focus should also be on challenging them to think or, still better, to fire their imagination. However, by and large, these courses fail on most of these counts as they often end up to be a little better than repeats of what the students have been taught in the Master's course, and a patchwork of lectures strung together by different investigators. Ph D students from different institutions have often remarked that they found most of the coursework drudgery, as it was either boring or repetitive, and the style didactic. Recognition of the fact that one needs to be more imaginative and creative while designing and handling these courses itself seems to be lacking, or even if it is recognized, there is no effort to correct the shortcomings. It is with the hope to stimulate some thinking in these directions that I share some of my experiences with a pre-Ph D course that I experimented a little with at the Indian Institute of Science Education and Research (IISER), Mohali.

In the even semesters at IISER Mohali, for the last two years (January–April 2012 and this year January–April 2013), I opted to teach a pre-Ph D course entitled, 'Advanced topics in molecular genetics' (BIO610). The course outline was developed keeping a practical approach to the subject in mind, since the theory itself might have been tackled to some extent in many universities. The Ph D students who took the course came from a variety of backgrounds. In 2013, 20 students took this course, 19 of them Ph D students, while one was a fifth year student doing the integrated Master's programme.

The broad contents were available to the students before registering for the course. In the first class I gave a more detailed outline of the course and further reiterated that it would largely be a paper-reading and participatory discussion course and would entail reading at least 2–3 papers per week. This gave the opportunity for any students intimidated by the number of papers they might have to read, an opportunity to drop out. No one actually dropped out, although midway through the course I could see that some of the students were exhausted with the continuous onslaught of papers. The students were also told that the participation in class, presentations and boardwork would be the sole basis of evaluating their performance. There would be no examinations, neither mid-semester nor end-semester. I also thereby underlined the importance in attendance.

The topics included aspects of bacterial genetics, yeast genetics, phage genetics, recombineering, next-generation sequencing technologies, applications of next-generation sequencing to bacterial and human genetics, directed evolution, multiplex methods for genome engineering, aptamers, variants of yeast two-hybrid methods and phage display. (The detailed course outline and list of papers is available on request.) There were 3 h class per week – a 1 h class on Tuesday and a 2 h class on Friday. The scheduling on these days was done based on a specific request made to the timetable coordinator. The 2 h classes were needed for discussing some of the papers. The three-day gap between the two classes also ensured that there was adequate time for the students to read the papers between the two classes. Each of the subjects was covered in a week to a week-and-a-half. There were a total of about 18 weeks in the semester.

I elaborate the approach taken using a paper in bacterial genetics that was discussed in the course. Although microbial genetics is tackled by students in their Master's or undergraduate courses, I included bacterial genetics as I felt it was necessary to confront the students with a more practical approach to the subject. Thus, the first paper in this course was from Jon Beckwith's group entitled 'Mutations that allow disulfide bond formation in the cytoplasm of *Escherichia coli*'[1]. Although this is a two-decade old paper, it is an elegant example of how a genetic strategy can be designed to yield insights to a specific question. It is also, in my opinion, a classic for anyone wishing to teach some of the practical aspects of microbial genetics. The choice of mutagen in the isolation of mutants (why spontaneous mutagenesis and not induced mutagenesis); the related question of when one should use induced mutagenesis; the need to differentiate between multiple mutations causing multiple phenotypes versus a single mutation causing pleiotropic phenotypes during genetic analysis; the design element in a genetic selection strategy to ensure that one not only gets mutants, but mutants that one wants (the selection versus screening option); the number of mutants picked up (the importance of saturation of a mutagenesis hunt); the basis behind naming of the mutants and why the mutants had different numbers, although they were mutations in the same gene (importance of alleles and allele-specific phenotypes); mapping of the mutant (course and fine mapping); loss of function and gain of function mutants (an opportunity to take a different approach to discussing dominance and recessiveness); identification of the WT gene of the mutant (the possibility of suppressors and the need to evaluate and eliminate these possibilities) are some of the possibilities that geneticists encounter that could be flagged to the students as we discussed this short but elegant paper. I included in the back-up reading for the students a biographical article by Beckwith entitled 'What lies beyond uranus? Preconceptions, ignorance, serendipity and suppressors in the search for biology's secrets'[2].

I attempted to discuss – through student participation – many other papers in a similar way. Some papers obviously offered more general insights than others – and therefore the choice of papers was required to be done with care and attention towards the overall goal of the course. (A complete list of papers that were discussed can be provided to anyone on request.) Emphasis was placed on the need to go through and understand the methods of the papers in detail. As the course was essentially designed to take a practical approach to the subject, focusing on the methodologies often was a key aspect of the discussions. This also ensured that the students read the paper

more thoroughly and could not get away by merely reading the abstract and a few of the introductory or end discussion passages.

The paper discussion was often preceded with an introductory lecture-discussion in the preceding class to provide some background (for example, before the bacterial genetics paper I went through the bacterial mapping strategies, and prior to discussing the yeast genetics paper I went over the yeast life cycle. Similarly, the lambda phage life cycle was briefly discussed before tackling the phage-based recombineering papers).

In many cases, I also tried to open up a paper at the end of the discussion with questions whose answers could not be found in the paper. For example, in an experiment if the authors had stopped with three rounds of directed evolution, the question was why did the authors stop with three rounds, bringing one to a more general question of when does one stop in these recursive methods. This invariably yielded lots of ideas and discussions.

The course included presentations by the students. As the batch was somewhat large (20), I put them in groups of two and gave them 15–20 min for their presentations. One of the topics was the next-generation sequencing technologies (where ten different platforms were presented). Each of the two students contributed to the presentation (8–10 min for each student). After each presentation, there was at least 5–10 min of questions. This was helpful in clarifying various points. The second topic on which they gave presentations (also in batches of two) was on papers that applied next-generation sequencing to human genetics. They were asked to choose from a bunch of papers that I picked up that tackled different kinds of problems in human genetics.

The students were also told, somewhere in the middle of the course that in the last week they would each have to individually present for 5–6 min a maximum of four slides where, after a one-slide introduction, they would present to the rest of the class in at least two ways, how methods learnt in the course could be utilized for some aspect of their current Ph D work that was either initiated or being initiated. They were free to talk to their seniors, supervisors or colleagues, but would have to convince the class of the uniqueness and originality in their approach. I was hoping to have some real out-of-the box thinking and some real neat ideas come across, but that was not to be, and it was disappointing that the students were unable to come up with innovative approaches. I definitely felt that this part of the course needed an improved way of tackling that perhaps I could focus on the next time I took the course.

The course was demanding. It was necessary that I myself read the assigned papers thoroughly so I could lead the class through the discussions with ease. It was also imperative to list out for myself beforehand (on a piece of paper) the key points that were needed for discussion, to ensure that all the points I wanted to elaborate were actually touched upon. Reading each paper was therefore very demanding in terms of time and pre-preparation.

A second challenging aspect was to ensure everyone's participation. With a batch of 20 students, it was just about manageable, but smaller numbers are more ideal. There are some students who tend to be reserved or less able to express themselves, and it was essential that they were given ample opportunity to explain different aspects of the paper that were discussed. I thus had to constantly play the moderator often having to silence the more enthusiastic or ebullient, so that the more reticent got a chance to speak. It was also important to expose students who were silent because they had not read the paper thoroughly, and by this indirect embarrassment and exposure I could ensure that no one could take the course lightly.

A third challenging aspect was evaluation. As the course did not include any mid-semester or exams and end-semester examination, I needed a proper evaluation method to eliminate as far as possible the subjective element. Thirty per cent of the evaluation was based on the presentations, while the remaining 70% was based on class participation. Participation by some of the students was easy to see, but in a few cases, for those more reticent it was not easy to assess. The scores given were also normalized by their percentage attendance. Primarily as an aid to assessing their class participation, in the last class, I gave each student a sheet with all the students names on it and asked them to grade their own performance as well as that of their colleagues. The sheets were not to be signed (anonymous). I also added that I wanted each one to give a total of about 8 ± 2 A grades and the rest could be B or C grades, since no one was expected to fall below that level. When I collated the grades, I found that the consensus grade of the class almost completely matched my own!

It was possible to conduct the course in this manner because the flexibility of IISER Mohali allowed it, and this is an important aspect that needs to be borne in mind when administrators lay down guidelines for faculty on how they should conduct their courses. For the courses at the undergraduate level and with larger numbers in the class, this would of course be more challenging, but here again we need to recognize the need for creativity, for innovation and improvising. Likewise administrators need to be tuned to the fact that it is possible to be flexible without compromising on quality or rigour.

At the end of the day, it was important to know how the students reacted to the course. A questionnaire was prepared and anonymous feedback was sought (in the last class) on the format, the usefulness, interest and difficulty level. The course format appeared to have appealed to everyone. The course also scored well in both the usefulness and interest it generated. One question that was posed in the feedback form was whether the students felt they required more background lectures before discussing papers. Lesser background material makes reading of the paper more challenging for the students, and this challenging aspect, once successfully tackled, is likely to significantly increase the interest level in the subject. For example, in the paper on phage display[3], the authors explored how expanding the genetic code could be successfully used in making novel single-chain antibodies in a phage display experiment. For the uninitiated, the paper, which has three stories in one, the level of difficulty is high. For some students this can be very demanding. Not surprisingly, in the feedback the response was mixed with almost half the class suggesting more background lecturing, whereas the other half felt that more background was not required. Eventually balancing this adequately with the choice of papers would be critical.

In conclusion, despite some efforts made toward improving the presentation of this course, clearly much more can be

done. Indeed, while globally there is a lot of discussion and debate about how things should be taught, be it technology-dependant aspects or non-technology related, in India we have largely continued operating in the classrooms – both theory and laboratory courses – with little attention to teaching approaches, even as we lament about the quality of our students. Most of the focus has been on the course content or course structure and on 'improving the syllabus'. And even as institutes strive to improve the content of their courses, perhaps even more thought is required in the way in which the courses are taught. It is only when both these aspects go together will they have a greater impact and effectiveness.

1. Derman *et al.*, *Science*, 1993, **262**, 1744–1777.
2. *Genetics*, 2007, **176**, 733–740.
3. Liu *et al.*, *PNAS*, 2008, **105**, 17688.

ACKNOWLEDGEMENTS. I thank the BIO610 students of both the 2012 and 2013 batches of IISER Mohali for their active participation in this course. Without their participation, it is unlikely that I would have had the motivation to describe the experiences with this course.

Anand K. Bachhawat is in the Department of Biological Sciences, Indian Institute of Science Education and Research Mohali, Sector 81, Knowledge City, SAS Nagar, P.O. Manauli 140 306, India.
e-mail: anand@iisermohali.ac.in