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QUANTITATIVE GENETICS

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Quantitative Genetics is the science that deals with quantitative traits (QTs) whose expression in any organism in its growing environment, is controlled by multiple (or single) genes. QTs as products of gene expression have interfaces with other disciplines like Genetics, Pathology, Entomology, Physiology, Agronomy, Biochemistry and Statistics. The efficient description of a genotype will then be a function of several QTs from those disciplines.

A QT is better defined as one having an underlying continuous distribution. Theoretically therefore, genotypes defined on a QT cannot unequivocally be cast into discrete groups (or classes), though it is done at times, as a matter of convenient description. Obviously, one can set limits to a QT to define High (genotypes with the QT surpassing a limit) and Low (genotypes with the QT falling below a limit), (H and L) genotypes. It is feasible to increase the classes H, L to more for instance, H, M (medium) and L. Concepts using extreme genotypes are deducible. Such concepts have been tested and found to work in plant breeding.

Genes controlling QTs like plant height, for example, are known to be concerned with the production of polypeptides which form proteins either alone or together with other polypeptides produced by other genes. The capability of investigating genetical variation in proteins using electrophoretic separation into bands which can vary in number, extent of mobility and intensity helps to study genetic polymorphisms and also define biochemical marker traits.

However, it is argued that only about 10% DNA is coding DNA and hence looking at structural genes limits the variation available for analysis. Further, a great deal of DNA variation in structural genes may be cryptic at higher levels (Kearsey and Pooni, 1996). Advances in molecular biology in 1980s enabled to study genetic variation at DNA level. Essentially the DNA is cleaved into a number of restriction fragments using specific restriction enzymes. The DNA fragments are subjected to electrophoresis and separated into bands which can be studied as mentioned earlier. This technique allows unambiguous recognition of three genotypes resulting from single base change. The situation resembles the case of *single codominant* gene. 'It is not a gene, because a gene codes for something and the restriction fragment site does not. So, it is conventional simply to call it a *locus* in order to distinguish it from a true gene. Genetic variation that can be recognised in this way is referred to as Restriction Fragment Length Polymorphism (RFLP)' (Kearsey and Pooni, 1996).

Techniques which are more refined than RFLP are now available - RAPD, AFLP, microsatellite and the like. As far as identifying genetic variation using them, the principles remain basically the same. Since they mark genetic variation (gene being implied in the sense of an RFLP mentioned above), they form broadly a class of molecular (DNA) markers. Each marker distinguishes three (marker) genotypes and in that sense they are single gene markers. When probe-restriction enzyme combinations are changed, different marker loci can be detected. Such loci that would mark (one or more) QTs are designated as QTLs.

There are subtle differences between 'Mendelian' and 'Marker' genes. The former have associated QT expression (phenotypes) which the latter do not have. Therefore search is made out of a multitude of markers, for those which have a high association with QT expression.

The exposition made so far is thus to highlight the following two facts:

- Mendelian principles on which the subject of Quantitative Genetics has evolved, is based on phenotypic expression of QTs.
- QTLs defined by DNA (molecular) markers do not have an associated expression. At the most, they can be discovered such that marker genotypes or marker classes defined by them have a high similarity with classes defined on QT genes in the sense mentioned earlier. The similarity is, in general, judged by the degree of commonality of genotypes in various classes.

Once the major differences between Mendelian and marker genes are understood in their proper perspective, it would be easy to see that there is no parallel development of concepts exclusively generated by marker genes. But emphasis has increased on methods of detecting linkage, estimation and mapping marker genes. Marker-assisted breeding/selection has the fundamental need to identify *stable* markers that have a high linkage with QT genes. Methods used to estimate such linkages have conceptual bottlenecks that continue to be areas of argument and concern. Thus the need to teach relevant theory of estimation with particular reference to linkage has become urgent. In turn, concepts of probability distributions, estimation of their parameters, sampling, sample statistics vis-a-vis population parameters become important areas to be covered in a course on Quantitative Genetics.

Over the past decades, use of computer in the analysis of quantitative data has been steadily increasing. The advent of molecular biology in plant breeding has raised the level of computer applications demanding a high level of computer literacy and applications. Users of commercial software need to be aware of the logic and limitations of the methods programmed in. A current syllabus of Quantitative Genetics would profitably include at least an appropriate exposure to computer applications though basio and practical knowledge can be dealt by a balanced course on computer applications in genetics.

A major proportion of students offering the course on Quantitative Genetics comes from Agriculture or Botany stream. In general, therefore, they have restricted access, appreciation and enthusiasm to learn elements of statistics quite basic to a proper grasp of Quantitative Genetics. If interest in the subject of Quantitative Genetics is to be catalysed and sustained, it is essential that this fact must be recognised and required basics included in the syllabus, instead of asking the students to credit one or more ancillary courses on statistics and mathematics. Experience in teaching this course over the past 3 decades clearly indicates that students are seldom able to transfer, for example, probability concepts initiated with a throw of a coin or die in statistics course to genetics. It is therefore, imperative that the required basics of statistics are taught through examples from genetics and plant/animal breeding. The emphasis should be more on making the students firmly grasp the fundamentals then on rigorous exposition/proof of the theory.

Such requirements emphasise the need for capable teachers. The need is urgent for a serious thought to provide guidance courses to teachers ! Otherwise the impact would be far from desired.

A comprehensive course on Quantitative Genetics with a clear objective to extend and strengthen knowledge on plant breeding and improvement cannot be effective unless it is backed up by a good course on fundamentals of plant genetics and breeding. Preferably such courses must be made as pre-requisites.

The syllabus of Quantitative Genetics course as envisaged, cannot also be covered in a single course spanning one semester. With supporting practicals, the course can at best be covered in two courses - Elements of Quantitative Genetics and Advanced Quantitative Genetics - with at least 3L + 1P. Ideally, 3L + 2P could give necessary leverage for a better exposition of the contents.