THE JOHN INNES PEA PROGRAMME FOR THE '90s

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The primary objectives of the programmes of the Department of Applied Genetics at the John Innes Institute are to further our understanding of the molecular and cell biology of peas. In the past much of its research efforts were devoted to detailed studies of the genetics, breeding and physiology of leafless and semi-leafless peas, and the analysis of the genetics of resistance to some of the main pathogens of this crop; these were among the topics that were considered of most relevance to those breeding new varieties of peas. Today we are equally concerned to apply our efforts to help those who will be concerned with producing new varieties over the next decade, but while this broad objective remains the same as before, the problems being tackled are very different.

One of our main projects is an analysis of the extent to which it is possible to change the composition of the seed to make it more suited for food, for feed or for industrial uses. The project includes biochemical analysis of critical steps in starch biosynthesis, cloning and characterising the genes for the enzymes involved, inducing and isolating mutations affecting the composition of the seed, characterising the storage proteins and the DNA sequences coding for them and establishing the sequences regulating their expression. These studies have already led to some remarkable achievements. The *r* locus has been shown to code for a starch branching enzyme, the DNA sequence isolated and characterised and the difference between the *R* and *r* alleles shown to be due to the insertion of a sequence in the latter. In addition, the *rb* locus has been shown to code for ADPG pyrophosphorylase and evidence has been obtained for a third rugosus locus which also affects storage product composition. The effect of the *r* locus on the ratio of legumin to vicilin in the seed has been demonstrated and a basis for the effect suggested; again the *r* and *rb* loci have been shown to influence the lipid content of the seed. These are merely the initial phases of a project which has as its objective the controlled manipulation of the composition of the seed of the pea.

While it is a general assumption that pea seeds contain low levels of anti-nutritional factors, we wish to establish the extent of trypsin inhibitors present in different genotypes and to study the molecular genetics of these proteins.

Among the other seed constituents being studied in detail are the lipoxygenases; the enzymes and the loci coding for them are being characterised in detail, and attempts are being made to express them in other systems. The lipoxygenases are important in the baking industry and also have a role in lipid degradation and storage.

Detailed analyses of seed development are being undertaken to establish the timing and sites of deposition of particular products in the seed, to characterise the population structure and dynamics of its constituent cells, and to gain a greater understanding of the development and differentiation of the seed. To this end genetic, cytochemical, immunological, tissue culture and molecular techniques are being exploited.

Mapping the pea genome by the use of RFLPs is making good progress; it involves the use of sequences of known and unknown function, classical markers, recombinant inbred lines and trisomics. The need for a well defined linkage map for the pea genome is unquestioned, and it is our intention to provide a focal point for integrating information from other workers in this field. Another need in peas is for a transformation system; as with all the seed legumes this is proving a difficult challenge which we are trying to overcome.

Yet another of our longer term objectives is to use the pea as a test system for establishing the role of glutathione reductase in the response of plants to stress. We are isolating different isoforms of this protein and cloning their cDNA sequences.

This can be but the briefest overview of our projects but will hopefully give an indication to readers of some of our objectives.

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