be some 50,000 genes with many in each band (see Lewin, *Nature*, **251**, 373–375; 1974).

Another approach to defining the genetic unit is to determine the nature of mutations at some locus. The mutations mapping in one complementation group may include *cis*-dominant control elements as well as structural genes; since most loci are identified by the effects whic¹, mutations in them have upon the phenotype, there

is usually no way to tell whether they represent alterations in a control element or structural gene. To determine the class of mutational event therefore demands analysis of loci where a phenotypic effect can be recognised and the protein product is known.

rosy mutants in Drosophila have eyes that are brownish in colour (instead of the wild type red colour). Two sets of observations suggest that this locus is connected with the enzyme xanthine

Strong interactions of the psi

from David J. Miller

SINCE the ψ (or J) particles were first discovered at Brookhaven and the Stanford Linear Accelerator Centre in November 1974 (see Nature, 252, 438; 1974 and Phys. Rev. Lett., 33, 1404, 1406 and 1408; 1974), experimental physicists all over the world have been looking for their effects. Some have scanned the data already collected from previous experiments, others have made proposals for new and more refined experiments, but much of the data now appearing is coming from apparatus which just happens to be set up at the accelerators or storage rings, and which has been rapidly adapted to look for the new particles.

The world of physics has been swept by waves of gossip, often inaccurate, and it has become necessary to separate 'mezzofacts' from real facts which can be reliably traced back to their authors.

The latest pieces of information to leave the mezzo-fact category are data on the photoproduction of the ψ (or J) with a mass of 3.1 GeV/ c^2 . The Brookhaven experiment showed that this ψ is produced with a very low probability in proton-proton collisions. The SLAC, and other subsequent e⁺e⁻ experiments, saw copious production. These two results implied that the ψ takes part in electromagnetic interactions, but might not have strong interactions with nucleons (protons or neutrons). In photoproduction, a particle is produced by bombarding a nuclear target with high-energy γ rays. If the ψ is a 'vector' particle, like the φ meson (as discussed in Nature, 252, 438; 1974), then an interacting photon could sometimes behave as if it were an incoming ψ . The photoproduction of the φ , and the related ρ and ω vector mesons, are very well explained by treating the incoming photon as a vector meson, which then has a strong interaction with the target nucleon. This is called the 'vector meson dominance model'

(VMD) of photon-hadron couplings. If the ψ is a hadron (a strongly interacting particle) then the model would predict the rate of ψ photoproduction, with only two important parameters: the strength of the coupling of γ to ψ , which is measured directly by the e⁺e⁻ $\rightarrow \psi$ experiments, and the cross section (a direct measure of probability) for ψ nucleon scattering.

Three groups have produced results in searches for ψ photoproduction. At the Cornell electron synchrotron (Phys. Rev. Lett., 34, 231; 1975) no sign of ψ production has been seen with 11 GeV photons. An experiment at the SLAC linear accelerator has also seen no ψ production from 18 GeV photons (Phys. Rev. Lett., 34, 288; 1975). But news has come from the Fermi National Laboratory Accelerator near Chicago that a group led by Professor Wonyong Lee of Columbia University has seen ψ photoproduction by photons of about 100 GeV produced from the 400 GeV protonsynchrotron. This result was a mezzo-fact for some months, but has now been reported by Lee himself in an FNAL seminar and can be regarded as authentic.

The tentative rate for ψ photoproduction at FNAL appears consistent with the limits put upon it by the two experiments which saw no effect. Using the VMD model it is clear that Lee's result implies a cross section for ψ -nucleon collisions somewhere in the region of one millibarn (10^{-26} cm^2) . Only the strong interaction could give such a large cross section, but the cross sections of other strongly interacting particles are all in the region of 20 to 40 millibarns. The ψ therefore seems to be a 'semi-strong' particle. It is likely that this inhibted interaction probability is linked to the narrow width of the ψ and slowness of its decays, but there is no agreement on what the link may be.

dehydrogenase. A dosage effect exists in which heterozygotes with only one ry^+ gene possess half of the wild type level of enzyme activity; and abnormal flies with three ry^+ genes have 150% of the wild type level (Grell, Z. Vererb., 93. 371-377; 1962). This could mean that rosy mutations act in a control element to prevent synthesis of XDH or that they represent alterations in the structural gene completely preventing enzyme activity. Isoalleles that affect the electrophoretic mobility of XDH (but which are wild type in eye colour) map close to the rosy mutations, an indication that the structural gene is in or close to the rosy locus (Yen and Glassman, Genetics, 52, 977-981; 1965). By fine mapping of some of these isoalleles. Gelbert, McCarron, Pandey and Chovnick (Genetics, 78, 869-886; 1974) now define their relationship to rosy mutations in a report on the organisation of this locus.

rosy mutants entirely lack XDH activity, since even low levels of this enzyme are sufficient to allow expression of the ry^+ phenotype, so that it is the ry^+ isoalleles alone that can be used to define the structural gene by their effect on the mobility of the enzyme. Since it is not practical to map such sites directly, the first step in this analysis was to derive rosy mutants from each of five of the ry^+ isoalleles. When two such rosy mutants are crossed, ry^+ progeny can be selected by growth on a purine-supplemented medium which kills larvae lacking XDH. In these experiments, 170 ry⁺ survivors were obtained from a total of 7×10^6 zygotes. The markers present on either side of the rosy locus were used to determine whether a crossover or gene conversion event was responsible for generating the ry^+ progeny. Examination of these strains to determine whether they have the XDH electrophoretic mobility characteristic of the maternal or paternal parent can then be used to map the site responsible for the electrophoretic variation. In effect, the ry mutant sites are selected markers in these crosses and the sites responsible for electrophoretic mobility comprise unselected markers.

The electrophoretic (e) sites mapped in two clusters, one at each end of the region identified by rosy mutations. This leaves open the possibility that the structural information for XDH might be located in two elements separated by some distance. By using a cis/trans test, however, Gelbart et al. demonstrated that e sites at both extremes appear to fall within the same protein-coding element. This is consistent with the observation that the enzyme XDH consists of a dimer of two identical subunits of about 130,000 daltons; this should require a coding length of a little more than 3,000 base