the F_1 experiments may be, in general, more sensitive than inbred experiments. Further research is needed to elucidate these points.

W. A. Becker

Washington State University,
Pullman,
Washington.

In comparing the relative sensitivity of genetically different groups of mice in quantitative biological assays, Prof. W. A. Becker has analysed the data published by McLaren and Michie[5] and by me[10,11,18], using the variance ratio F and the tables of Schumann and Bradley[16]. The F statistic is similar to the λ statistic which I suggested applying for the same purpose. The coefficient of regression b of response on dose and the error variance s^2 are involved in both statistics but are used in different ways. The F statistic has the advantage of testing significance between two groups of assay animals, but, as Becker pointed out, the limitation of requiring equal numbers of animals in each dose group.

The results of the analysis by Prof. Becker showed no significant differences in the F values between the genetic groups of mice used. In his computation Prof. Becker used the mean square of deviation of the mean response from the predicted mean, instead of individual responses. This is possibly because he was unable to obtain individual responses in some of the published data, but by so doing some degrees of freedom were lost, and the sensitivity of the test reduced. Prof. Becker has drawn a conclusion concerning the choice between genetically different groups of mice for bioassays in general agreement with mine (ref. 11 and *Nature*, **190**, 894; 1961).

Prof. Becker has proposed using reciprocal recurrent selection and inbreeding hybridization to produce animals for bioassay. The method of inbreeding hybridization involves, I presume, establishing inbred lines and crossing them to produce F_1 hybrids. Production of such F_1 hybrids is practised in animal supply houses, although the parental inbred strains were not developed for use in bioassay. In regard to the reciprocal recurrent selection, a method used in agriculture for improving yield or performance of crops and farm animals, I question whether it is a practical method for producing animals for bioassay by animal supply houses because of the multiplicity of end points. The scope of bioassay has been greatly expanded recently and the physical, chemical, physiological, and pathological end points are numerous. Animals with a genetic constitution suitable for one type of assay may not be at all suitable for other types, a view which I mentioned previously[10] and which Prof. Becker evidently shares.

It is possible that reciprocal recurrent selection could be used in private laboratories for theoretical problems as well as for producing animals for bioassay. It should be kept in mind that reciprocal recurrent selection is aimed at improving the regression of the response on the dose of the assay animals. In comparing these animals with other genetic types, the assay information to be obtained from individuals of a group is based on the balance between the regression and the variation of response.

While waiting for a unique solution to the problem which we are unlikely to reach in the foreseeable future, I suggest that investigators base their choice of the most suitable animal for a given assay on existing information. If none is available, a pilot screening procedure might be used. A small number of each of various types of animals, including inbreds, F_1 hybrids, and possibly animals from closed breeding colonies, would each be given a single dose of the assay material, and the groups with the larger means (likely positively correlated with regression) and smaller variances selected for the bioassay. If desired, a second screening could be applied, giving three or more doses to more animals in each of the groups selected on the basis of the results of the first screening. Using either the F or λ statistic in analysing the results, the investigator could then choose the most suitable types of animals for his particular bioassay.

C. K. Chai

Roscoe B. Jackson Memorial Laboratory,
Bar Harbor,
Maine.

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SYSTEM FOR THE RECOGNITION OF GENETIC TRANSFORMATION IN HÆMOPOIETIC CELLS

By Dr. G. L. FLOERSHEIM

Chester Beatty Research Institute, Institute of Cancer Research,
Royal Cancer Hospital, London, S.W.3

Although genetic transformation in bacteria by deoxyribonucleic acid (DNA) has been known for a considerable time[1], no conclusive evidence of its occurrence in mammalian cells has been recorded so far. A more complex chromosomal reproductory mechanism might be a barrier for its analogy in higher organisms. However, recent information concerning the infective properties of viral nucleic acids and their capacity to penetrate mammalian cells has thrown new light on the possibility of obtaining transformation in non-bacterial cells.

In bacteria, mostly through the use of selective media, transformation can be detected quantitatively and with high sensitivity. A similar approach