staining procedure was that described by McLeish and Sunderland[9] and the measurements were made on an integrating microdensitometer.

From the histograms in Fig. 1 it will be seen in the first place that, contrary to other evidence[10], there is no indication of any appreciable reduction in DNA content associated with the allopolyploidy. In the second place, it will be observed that the predicted value for *AABB* (40·2), where the *BB* values are taken from *Ae. speltoides*, is very close to, and not significantly different from, the observed value for *durum* (38·0). In contrast, when the *BB* value is taken as the mean of *Ae. bicornis* and *Ae. longissima* (which do not differ significantly from one another) the predicted *AABB* value (45·2) lies well outside the *durum* range, and departs significantly from the *durum* value ($P = < 0{\cdot}001$). The conclusion is that *Ae. speltoides* is the more likely contributor of the *BB* genome.

On this assumption, that *BB* derives from *Ae. speltoides*, the predicted and observed *AABBDD* values also show very good agreement, 57·1 and 55·6 respectively. When, on the other hand, *BB* is assumed to have derived from *Ae. bicornis* or *longissima* there is again a convincing departure from expectation ($P = < 0{\cdot}01$).

In brief, these DNA estimates confirm an allopolyploid origin of the cultivated wheats without appreciable change in the DNA content of genomes subsequent to hybridization. The evidence also shows that *Ae. speltoides* is a more likely contributor of the *B* genome than either *Ae. bicornis* or *Ae. longissima*.

More recently the work has been extended by my colleague, Mr. W. I. C. Davies, to include an *Agropyron* species, *A. triticeum*, the other most likely possibility as source of the *B* genome. The evidence was against this possibility, the *Agropyron* DNA values being significantly too low. The *Agropyron*, and the wheat species also, were presented to me by the Plant Breeding Institute, Cambridge, to whose director, Dr. G. D. H. Bell, and cytologist, Dr. R. Riley, I am greatly indebted.

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[1] McFadden, E. S., and Sears, E. R., *Res. Genet. Soc. Amer.*, **13**, 26 (1944).
[2] Kihara, H., *Agric. Hort. Japan*, **19**, 889 (1944).
[3] Sarkar, P., and Stebbins, G. L., *Amer. J. Bot.*, **43**, 297 (1956).
[4] Riley, R., Unrau, J., and Chapman, V., *J. Hered.*, **49**, 91 (1958).
[5] Sears, E. R., *Wheat Inf. Service*, **4**, 8 (1956).
[6] Peto, F. H., *Canad. J. Res. C.*, **14**, 203 (1936).
[7] Wakar, B. A., *Zuchter*, **7**, 199 (1935).
[8] Matsumura, S., *Ann. Rep. Inst. Genet. Japan*, **1**, 22 (1957).
[9] McLeish, J., and Sunderland, N., *Exp. Cell Res.*, **24**, 527 (1961).
[10] Pai, R. A., and Upadhya, M. D., Bhaskaran, S., and Swaminathan, M. S., *Chromosoma*, **12**, 395 (1961).

## A Possible Chemical Term for the Operator-gene

It has been known for a comparatively long time that DNA and proteins of the histone or protamine type are the main components of the chromosomes[1]. The DNA has been the subject of several studies and much knowledge has been gained on its structure and function. Examination of the protein components, however, has been neglected to a large extent. Since the amount of histone protein approximately equals that of the DNA in the nucleus[2], it is apparent that they must play a major part in the cellular processes.

After many years of investigations, Stedman *et al.*[3] suggested that the histones may play a part in the differentiation by functioning as inhibitors of the action of a gene. Qualitative changes of the histones has been noted during spermatogenesis and embryonic development in various animals[4]. Qualitative and also quantitative changes have been encountered during carcinogenesis[3]. Using radioactive indicators, it was shown that syntheses of DNA and of histone are closely associated events[5]. Direct evidence has been obtained recently by Huang and Bonner[2] that the histones are able to suppress DNA-dependent RNA synthesis. These authors showed that the function of the histones is to bind to the DNA. DNA fully complexed with histone was inactive in the support of the DNA-dependent RNA synthesis. Further, it seems probable that only segments of the chromosomes are fully occupied by histones, and that this part is inactive in directing protein synthesis. Thus it seems now to be established that histones interfere with the genetic activity of the DNA; further, that during development they undergo major changes which, in turn, lead us to believe that histones play a deciding part in differentiation.

Jacob and Monod[6] provided us with a theoretical model of the genetic regulation of protein synthesis. The three genetic units involved are: regulator gene, operator gene and structural genes. Only the last one is directly involved in the determination of the protein structure. The operator gene can directly control the structural genes and so indirectly DNA-dependent protein synthesis. Whether the operator locus is actually part of the structural unit or not could not be stated definitely. The regulator gene is able to influence the operator gene and so determine the rate of protein synthesis on the structural genes.

Applying our knowledge of the histones to the Jacob–Monod model, it seems to be possible to substitute the histones instead of the 'operator genes' and so have a chemical expression for this genetic term too. In this case it would be more appropriate to change this term from operator gene to operator. The regulator gene, in this case, could turn the structural genes on and off by controlling the histones. Thus, the Jacob–Monod model would be modified as follows: the regulator gene can interfere with the production of the primary structural-gene product through the histones which are able to stop the production of the DNA-dependent RNA synthesis by combining directly with the responsible structural gene.

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[1] Swanson, C. P., *Cytology and Cytogenetics*, 413 (Prentice-Hall, Inc., 1957).
[2] Huang, R. C., and Bonner, J., *Proc. U.S. Nat. Acad. Sci.*, **48**, 1216 (1962).
[3] Cruft, H. J., Mauritzen, C. M., and Stedman, E., *Nature*, **174**, 580 (1954).
[4] Bloch, D. P., *J. Histochem. Cytochem.*, **10**, 137 (1962).
[5] Prescott, D. M., *J. Histochem. Cytochem.*, **10**, 145 (1962).
[6] Jacob, F., and Monod, J., *J. Mol. Biol.*, **3**, 318 (1961).

# VIROLOGY

## A Simple Method for Purification of Influenza Virus

A method for the purification of influenza viruses by adsorption and elution from barium sulphate has been described by Davenport[1]. This communication is concerned with the use of a modification of that method for the preparation of influenza virus vaccines.

Three strains, *A1/Omachi/1/53*, *A2/Adachi/2/57* and *B/Setagaya/3/56*, which constitute the present influenza virus vaccines in Japan, were selected for this work. Infected allantoic fluids in which merthiolate 1 in 10,000 was added as a preservative were provided by vaccine manufacturers.

Preliminary experiments revealed that barium sulphate to be used for adsorption of virus in infected allantoic fluid had to be fine enough to get good recovery of virus and a homogenized barium sulphate solution (12·5 g/100 ml. of distilled water, sterilized by an autoclave) was used