alleles in common, or, if the same genes are involved, then they are being expressed in quite a different fashion.

One possible explanation for the different modes of inheritance could be different time scales used in the 2 experimental situations. However activity in the one-way vial apparatus does not change significantly during the test period. Both types of apparatus provide measures of the amount of walking done by flies introduced into a novel situation. Despite this superficial similarity the results show that the stimulus situation presented to the flies in the 2 instances must be quite different.

The purpose of these preliminary studies was behavioural rather than genetical and the data was collected in such a manner as to facilitate scoring rather than in a form from which the maximum amount of genetical information could be extracted. For example in the one-way vial apparatus the activity of groups of flies rather than that of individuals was scored. It is not therefore possible in this case to estimate the number of segregating units involved in these behavioural characters. It is however possible to design experiments so that a full analysis could be made. Further, animals could be tested in the same apparatus under a variety of experimental conditions. This would allow one to assess the genetical contribution towards each of the variables in terms of direction of action, mode of interaction and possibly also the number of segregating units. The technique outlines in this paper could be used to analyse behavioural characters other than activity[10].

Zusammenfassung. Eine Methode zur Abschätzung dreier Maßstäbe von Lokomotionsaktivität bei *Drosophila melanogaster*, die unter gemeinsamer genetischer Kontrolle stehen, wird beschrieben. Es wird wahrscheinlich gemacht, dass die Kontrolle des einen Maßstabes von einem besonderen Teil des Gen-Komplementes ausgeübt wird, während die andern mehrere kontrollierende Gene gemeinsam besitzen.

A. W. EWING

Department of Zoology, University of Edinburgh (Scotland), 28th October 1966.

[10] *Acknowledgments*: My thanks are due to Dr. A. MANNING and Dr. B. CLARKE for their helpful criticism of the manuscript.

The Control of Wheat Gluten Synthesis at the Genome and Chromosome Levels

Since aneuploid wheat samples have become available, a powerful tool has been added to studies on the genetic control of wheat gluten synthesis. It is well known that gluten is a complex mixture of proteins all characterized by their carrying a relatively low charge over a wide range of pH. That genotype determines the distribution and identity of the individual gluten proteins has been known for some years. No genes have been specifically associated with individual protein components and little has been done at the chromosome level.

One of the most powerful tools for the study of gluten protein composition ('profile') is gel electrophoresis. This communication reports the results of starch gel electrophoretic studies on some aneuploid lines of the wheat variety 'Chinese Spring', on another hexaploid wheat 'Canthatch' and a tetraploid derivative of it, together with 3 reconstituted Hexaploids.

Materials and methods. Wheat samples used included ditelocentric lines of the variety 'Chinese Spring' where one pair of arms of one of each of the 21 pairs of chromosomes had been removed. Of the 42 possible ditelocentrics only 22 were available for study. Samples of the variety 'Canthatch', a hexaploid ($2n = 42$) with A, B, and D genomes and a tetraploid derivative, 'Tetracanthatch' ($2n = 28$) of it with the D genome removed (KERBER[1]) were also examined together with reconstituted hexaploids in which 3 varieties of *Aegilops squarrosa* L. ($2n = 14$) had contributed a D genome to the A and B genomes of 'Tetracanthatch'. Protein was extracted from crushed single grains of wheat with 0.4 ml $2M$ aqueous urea. Starch gel electrophoresis in aluminium lactate buffer, pH 3.1, containing $2M$ urea was conducted according to the method of GRAHAM[2]. Only gluten or storage proteins were examined.

Results. The ditelocentric lines of 'Chinese Spring' showed the most dramatic change from the parent when one arm of the 1D chromosome was removed. The effect of this is shown in Figure 1. Only 7 of the 22 samples

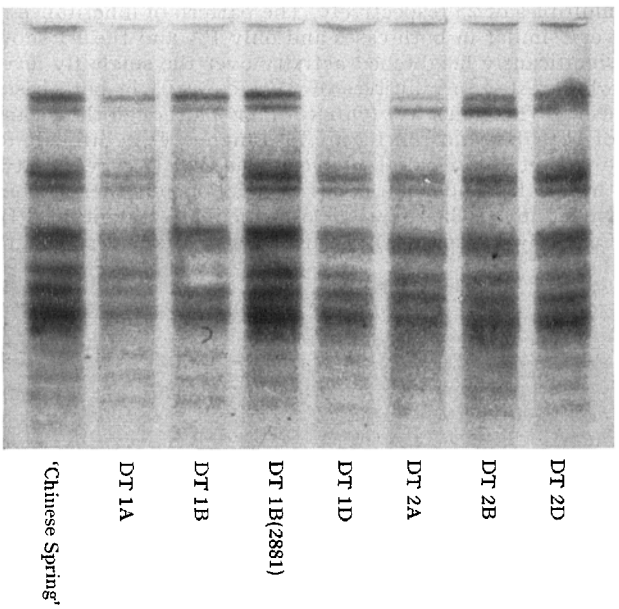

Fig. 1. Starch gel electrophoretic patterns of gluten proteins from ditelocentric lines of the hexaploid wheat variety 'Chinese Spring'.

[1] E. R. KERBER, Science *143*, 253 (1964).
[2] J. S. D. GRAHAM, Aust. J. biol. Sci. *16*, 342 (1963).

examined are shown here with the normal disomic parent. Minor changes in gel pattern were observed in some of the other ditelocentric lines but in this communication we are only concerned with those lines illustrated. It can readily be seen that removing the arm of the 1D chromosome of 'Chinese Spring' results in the disappearance of 2 slow-moving bands. Apparent quantitative differences in these bands are observable in the proteins extracted from other ditelocentric lines but only the 1D chromosome appears to be associated with their complete removal. It is of interest to note that WELSH and HEHN[3] in studies with monosomics, found that the 1D chromosome had the greatest influence on flour dough quality as measured on the 'Farinograph' and fermentation time.

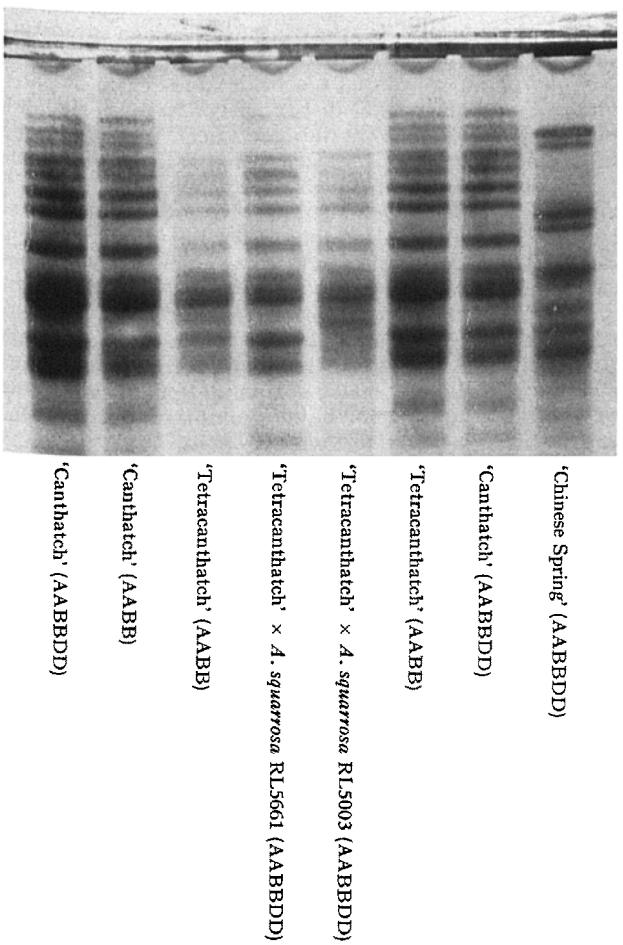

Fig. 2. Starch gel electrophoretic patterns of gluten proteins from related hexaploid and tetraploid wheats.

Figure 2 shows the starch gel patterns obtained with the hexaploid wheat 'Canthatch' together with its tetraploid derivative 'Tetracanthatch'. Protein patterns from hexaploids reconstituted from 'Tetracanthatch' and 3 varieties of *A. squarrosa* L. are shown together with that of 'Chinese Spring' for comparison. It is quite obvious that removal of the complete D genome from 'Canthatch' has had no observable effect on starch gel pattern. The proteins from reconstituted hexaploids show some differences in pattern but unavoidable differences in the amount of protein loaded into the gel make comparison of these samples difficult.

There is no doubt that individual protein components in gluten represent heritable characters. In a polyploid like wheat it appears that the genetic information controlling the synthesis of many of these proteins may be duplicated on different genomes. The only clear-cut example of single chromosome control shown in these studies is for the 1D chromosome of 'Chinese Spring'. There are 2 obvious interpretations of the results with 'Canthatch' and its tetraploid derivative where the removal of the D genome had no effect on protein pattern. The first explanation is simply that the chromosomes on the D genome are not controlling the synthesis of any of the proteins examined. Perhaps a more likely explanation is that the genes in the D genome controlling protein synthesis are duplicated in the A and B genomes. The fact that A, B and D genomes are all believed to have arisen from a single progenitor lends more credence to the latter explanation. The apparent contradiction of the results with 'Chinese Spring' where removal of part of a chromosome on the D genome caused a definite change in the protein 'profile' and the observation that removal of the whole D genome from 'Canthatch' caused no change, emphasises the complexity of the inheritance of these characters.

Résumé. L'hérédité des composants protéiques du gluten a été étudié au moyen de l'électrophorèse en gel d'amidon. Une branche du chromosome 1D de la variété du blé dit «Chinese Spring» est en corrélation avec la présence de 2 composants protéiques. Le composant du gluten n'a aucun effet lorsqu'on prélève le génome D entier à la variété «Canthatch».

W. J. R. BOYD and J. W. LEE

Institute of Agriculture, University of Western Australia, Nedlands (Western Australia), and Wheat Research Unit, C.S.I.R.O. North Ryde (N.S.W. Australia), 19th December 1966.

[3] J. R. WELSH and E. R. HEHN, Crop Science *4*, 320 (1964).

Hydrolysis of Human Leucocyte Phospholipids by Snake Venoms

The A-phospholipases of *Vipera palestinae* (VP) and *Naja naja* (NN) venoms do not split the phospholipids of intact erythrocytes, but are able to do so in the presence of a lytic factor (LF) in NN venom, a basic protein[1]. These venom phospholipases differ in their ability to attack the phospholipids in platelets[2], osmotic erythrocyte ghosts[1] and mitochondria[3,4], hydrolysis occurring with NN phospholipase but not with VP phospholipase. In the present study, the action of these venom components on leucocyte phospholipids was investigated.

Leucocytes were separated from normal blood according to the procedure described by BERGMEYER[5]. Venom phospholipases and LF were prepared as described pre-