*Table 1.* Number of breaks in colcemid treated cells

100 cells scored for each concentration

| Conc. $\times 10^{-6}$ mol/l | Total number of breaks and gaps | Cells with breaks or gaps | Breaks or gaps per affected cell |
|---|---|---|---|
| 10 | 26 | 15 | 1.73 |
| 7 | 15 | 8 | 1.88 |
| 5 | 20 | 11 | 1.82 |
| 2.5 | 25 | 11 | 2.27 |
| 1.4 | 22 | 12 | 1.83 |
| HBSS | 19 | 15 | 1.27 |
| Control | 6 | 6 | 1.00 |

tude as that of butyl mercury bromide, which was determined to 0.05–0.1 $\times 10^{-6}$ M by FAHMY (1951). The response of Chinese hamster cells to organic mercury compounds would be expected to approximately the same, judging from the results of FISKESJÖ (1971), who found similar threshold concentrations for other mercury compounds in different test systems. The threshold value of HMB for c-mitosis in Chinese hamster cells was somewhat higher than corresponding values in the *Allium* test.

The strength of the effects decreased with falling concentrations. Fig. 1 shows that there was a correlation between the concentration of HMB and the manifestation of cell damage. Toxic and c-mitotic cells were found mostly in the strongest concentrations. The transitions was gradual between c-mitosis and normal mitosis. The number of chromosome breaks was clearly elevated both in the treatments with HMB and with HBSS. This effect was probably due to the starvation the cells were submitted to during the treatment. In the affected cells, however, the number of breaks and gaps per cell was higher in the HMB treatment, both relative to the HBSS treatment and the untreated controls. The increase was not significant statistically.

*Acknowledgments.* - This work has been supported by grants from the Nilsson-Ehle foundation. My sincere thanks are due to prof. A. Levan for valuable help and criticism.

Institute of Genetics, University of Lund, Sweden

*Literature cited*

BOYER, P. D. 1959. Sulfhydryl and disulfide groups of enzymes. — In *The Enzymes 2 ed. (Eds.* BOYER, LARDY and MYRBÄCK), *Vol. 1, Acad. Press, New York*, p. 511—588.

FAHMY, F. Y. 1951. Cytogenetic analysis of the action of of some fungicide mercurials — *Ph. D. Thesis, Inst. Genet., Lund, Sweden.*

FISKESJÖ, G. 1969. Some results from *Allium* tests with organic mercury halogenides. — *Hereditas 62*: 314—322.

—— 1970. The effect of two organic mercury compounds on human leukocytes in vitro. — *Ibid. 64*: 142—146.

—— 1971. The effect of two mercury compounds on lysogenic *E. coli* K39 (λ). — *Ibid. 69*: 135–138.

KRISTOFFERSSON, U. 1971. The effect of cyclamate and saccharin on the chromosomes of a Chinese hamster cell line. — *Ibid. 70*: 271–282.

LEVAN, A. 1971. Cytogenetic effects of hexyl mercury bromide in the *Allium* test. — *J. Indian Bot. Soc. 50A*: 340—349.

RAMEL, C. 1969. Genetic effects of organic mercury compounds I. Cytological investigation on *Allium* roots. — *Hereditas 61*: 208—230.

RAMEL, C. and MAGNUSSON, J. 1969. Genetic effects of organic mercury compounds II. Chromosome segregation in *Drosophila melanogaster*. — *Ibid. 61*: 231—254.

RUNNSTRÖM, J. and MINELLI, H. 1964. Induction of polyspermy by treatment of sea-urchin eggs with mercurials. — *Exp. Cell Res. 35*: 157–193.

STEINEGGER, E. and LEVAN, A. 1947. Constitution and c-mitotic activity of iso-colchicine. — *Hereditas 33*: 385—396.

Ulf Kristoffersson
Institute of Genetics
S-223 62 Lund, Sweden

## O. HALKKA, L. HALKKA, R. HOVINEN, M. RAATIKAINEN and A. VASARAINEN; Genetics of *Philaenus* colour polymorphism: the 28 genotypes

(Received January 13, 1975)

In a recent article on the genetic basis of colour polymorphism in the meadow spittlebug, *Philaenus spumarius* (L.) (Homoptera), a hypothetical scheme of the dominance and co-dominance relationships was presented (HALKKA et al. 1973). The results of the crosses performed in 1972 and 1973 were not then available; they corroborate practically all the relationships proposed in the

*Table 1.* Allele combinations and the corresponding phenotypes in *Philaenus spumarius*. The subscripts denote:

| ♂ \ ♀ | $p^T$ | $p^M$ | $p^L$ | $p^F$ | $p^C$ | $p^0$ | $p^t$ |
|---|---|---|---|---|---|---|---|
| $p^T$ | $tri^1$ / $tri^1$ | $tri^4$ | tri | tri | $tri^4$ | tri | tri |
| $p^M$ | tri | $mar^1$ / $typ^1$ | mar | $mar^5$ | $mar^6$ | $mar^6$ | mar |
| $p^L$ | tri | typ | $lat^1$ / $typ^1$ | $mar^5$ | $mar^6$ | $lat^6$ | lat |
| $p^F$ | tri | typ | typ | $fla^0$ / $typ^0$ | fla | $fla^1$ | fla |
| $p^C$ | tri | typ | $typ^7$ | $typ^7$ | $lce^{0(2)}$ / $typ^0$ | $lce^2$ | $lce^2$ |
| $p^0$ | tri | $typ^7$ | $typ^7$ | $typ^7$ | $typ^7$ | $lop^{0(3)}$ / $typ^{0(7)}$ | $lop^3$ |
| $p^t$ | tri | typ | typ | typ | typ | typ | typ / typ |

0) experimental evidence lacking
1) experimental evidence considered insufficient
2) genotype also expressed (or believed to be expressed) as *fla* and *gib* in most individuals with appropriate modifier genes
3) genotype also expressed (or believed to be expressed) as *qua* and *alb* in most individuals with appropriate modifier genes
4) median stripe often truncated at anterior end
5) the *fla* dots, or at least the anterior dots are present in most individuals as indentations in the pale elytral margins
6) the *fla* or *qua* dots (see also notes 2 and 3), or at least the anterior dots are present as indentations in the pale elytral margins in some individuals with appropriate modifier genes
7) genotype also expressed (or believed to be expressed) as *qua*

scheme. In these years, 186 successful crosses were performed. They produced a total progeny of 3799 individuals.

With seven alleles, as in *Philaenus*, there are 28 possible genotypes (7 homozygotes and 21 heterozygotes). In Table 1, all the possible combinations are shown separately for males and females. As explained in detail in the previous article (HALKKA et al. 1973), the same genotype often produces dissimilar phenotypes in the two sexes.

In the table, the names of the phenotypes are abbreviated as in our earlier paper (see HALKKA et al. 1973 for the full names). If no superscript is attached to the phenotype designation, the genotype-phenotype correspondence (g–p) has been verified by Mendelian $F_2$ ratios and backcrosses. Superscript "0" means that there is no firm experimental evidence for the g–p presented. In these instances, the phenotype suggested is hypothetical, the evidence being circumstantial.

Other superscripts imply that the evidence for the g–p presented is based on insufficient evidence (e.g., Mendelian ratios from small progenies), or that complexities of penetrance or expression exist. Some of the complexities are caused by non-allelic modifier genes (see HALKKA et al. 1973). The effect of some of the modifiers on pigmentation is dissimilar in different geographical regions, and forms of expression not mentioned in the table may occur in some natural populations.

Such details do not obscure the fact that, with the help of Table 1, it is possible to calculate allele frequencies from practically every sample collected from natural populations in northern Europe, Asia and North America. In Southern and Central Europe, many additional phenotypes are found, but most of them occur at very low frequencies (RAATIKAINEN 1971). In most of the populations investigated throughout the world so far the three homozygotes with unidentified phenotypes (superscript "0") in Table 1 are very rare. Their frequencies usually are within the range 0.005–0.0001. In fact, all the combinations except $p^t/p^t$ can be considered infrequent in natural populations. In Denmark, Finland, Norway and Sweden the frequency of the allele $p^t$ is often as high as 0.9. Very high $p^t$ frequencies are similarly found in other parts of Europe, and in Asia and North America. As the sexes are equal in number in newly emerged *Philaenus* adults, significant inaccuracy is not introduced if only the female sex is used in determinations of allele frequencies for the whole species. This is often necessary, because many of the alleles are expressed only in the females.

Ten years ago, HUTCHINSON (1964) wrote on *Philaenus* that "- - - no clear understanding of the whole situation, which may well prove to be one of the most dramatic examples of polymorphism, will be possible without genetic knowledge - - - -". Although the "genetic knowledge" called for by HUTCHINSON will not cover the most minute details for many years, the information presented in Table 1 signifies a decisive breakthrough in the understanding of polymorphic equilibria in the spittlebug. The many complexities of genetic determination revealed by the table are less deterrent than they seem. This is so because in most natural populations the "clear" genotypes stand for well over 90% of the gene pool.

*Acknowledgments* — Most of the work was performed at the Department of Pest Investigation, Agricultural Research Centre, Tikkurila, Finland. Without the facilities generously provided by the former and present Heads of this Department, Professors Veikko Kanervo and Martti Markkula, the work would not have been possible. In various phases of the work, we have been aided by Simo Hovinen and Tarja Kohila The study has been supported by grants from the University of Helsinki and from the National Research Council for Sciences of the Academy of Finland.

Department of Genetics, University of Helsinki, (M.R.) Department of Biology, University of Jyväskylä and (A.V.) Department of Pest Investigation, Agricultural Research Centre, Tikkurila, Finland

## *Literature cited*

HALKKA, O., HALKKA, L., RAATIKAINEN, M. and HOVINEN, R. 1973. The genetic basis of balanced polymorphism in *Philaenus* (Homoptera). — *Hereditas 74*: 69—80.

HUTCHINSON, G. E. 1964. A note on the polymorphism of *Philaenus spumarius* (L.) (Homopt., Cercopidae) in Britain. — *Entomol. Monthly Mag. 99*: 175—178

RAATIKAINEN, M. 1971. The polymorphism of *Philaenus spumarius* (L.) in northern Italy. — *Ann. Entomol. Fenn. 37*: 72—79.

Olli Halkka
Department of Genetics
P. Rautatiekatu 13
SF-00100 Helsinki 10, Finland