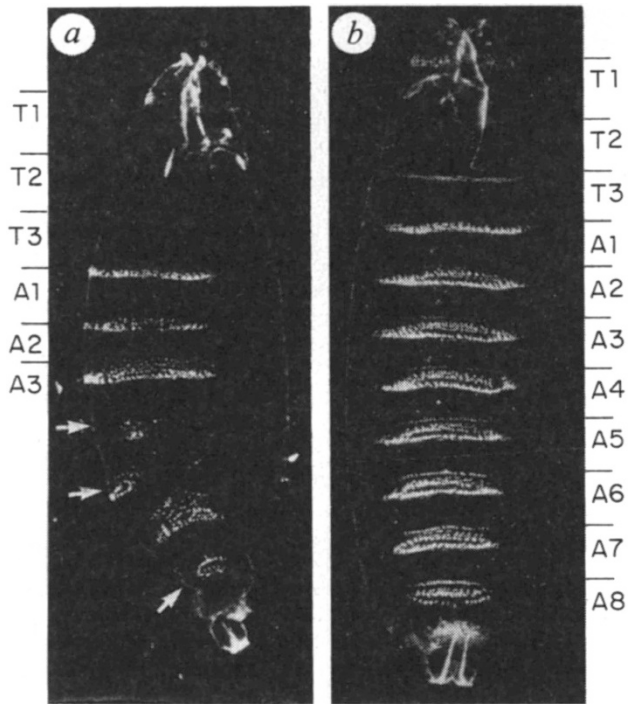

Fig. 5 Ventral cuticular patterns of embryos obtained from crosses of wild-type males with *Dp67A*; *DfB81 Minute* females (*a*), and with *Dp76A*; *DfB81/p[rp49⁺]* non-*Minute* females (*b*). Embryos were fixed and mounted as described previously[38]. For a detailed description of cuticular pattern, see ref. 39. A, abdominal segment; T, thoracic segment. *a*, A characteristic segmentation defect; the abdominal segments posterior to A3 are fused and partially deleted, leaving a remnant of the fused denticle bands. This phenotype is suppressed by the *p[rp49⁺]* insert since unhatched embryos with the segmentation defect are not observed from the *p[rp49⁺]*-bearing females.

deficiency would be expected to have an undetectable, or only a mild phenotype. For genes at the other extreme, that is, those whose mRNA levels are only barely in excess of what is required (almost rate-limiting), a heterozygous deficiency would be expected to have a severe phenotype. Presumably *M(3)99D* falls in this latter class, as the heterozygous deficiency is a strong *Minute* and is not fully rescued in all of the transformed lines, that is, phenotypic rescue by the transduced gene is sensitive to modest position-effect modulation of gene expression.

A primary effect of *Minute* mutations on ribosome assembly would also explain two interesting observations of Schultz[2]: Three wild-type doses of a particular *Minute* gene do not suppress a mutation in a different *Minute* gene; and the phenotype of double or triple *Minute* lines is no more severe than that of a line carrying only the most extreme single *Minute* mutation of the combination. We propose that the mutation giving rise to the lowest ribosomal protein mRNA level is rate limiting for ribosome assembly. The presence of other less severe mutations will have no apparent effect. In this light, Schultz's observations suggest that many *Minute* mutations are effectively deletions which result in reduced levels of ribosomal proteins, and thus retard the rate of ribosome assembly. They may be true deletions or, equally likely, some of them may be missense or nonsense mutations[30,31] which encode mutant ribosomal proteins that cannot assemble.

We thank R. MacIntyre, E. B. Lewis and L. Craymer for fly stocks, and J. A. Lake and J. C. Hall for helpful comments on the manuscript. This work was supported by NSF grant PCM 84-03539 to J.A.L. and J.R.M. and by NIH grants GM23549 and P01GM33205 to M.R.

Received 9 May; accepted 5 August 1985.

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Corrigenda

Primary structure and genomic organization of the histidine-rich protein of the malaria parasite *Plasmodium lophurae*

J. V. Ravetch, R. Feder, A. Pavlovec & G. Blobel
Nature **312**, 616-620 (1984)

Since publication of this article, sequence analysis of the genomic clone 8A using the chemical degradation technique of Maxam and Gilbert has revealed that the M13 clones used to generate the sequence published in Fig. 3 has undergone rearrangement due to the repetitive nature of the sequence cloned. A deletion of 90 nucleotides had occurred in the repeat region 938-1087. In contrast to the 5 published repeats of the sequence APHHHHHHHH, 8 repeats are found in the genomic clone by Maxam-Gilbert sequencing. These are encoded as 3 copies of the sequence GCTCCACACCATCATCACCACCATCACCAT followed by 5 copies of the sequence GCTCCACACCATCATCACCACCAC-CACCAT. Recombination in the M13 clone had occurred between repeat 2 and 5 generating the 3 repeat deletion. Similarly, in the region 1178-1474, encoding 10 copies of the sequence DAHHHHHHHH in the M13 subclones, only 6 copies are found by sequence analysis of the genomic clone using chemical degradation sequencing techniques representing an insertion of 120 bp in this region. Evidence for the presence of an insertion and deletion has been independently obtained from sequence analysis of a partial cDNA clone corresponding to the region 926-1,648 (Irving *et al. Molec. biochem. Parasit.*, in the press). These results reflect the potential difficulty in using subcloning into single-stranded phages to obtain DNA sequence data on highly repetitive genes of this type.

The effect of climate on long-term changes in the crustacean zooplankton biomass of Lake Windermere, UK

D. G. George & G. P. Harris
Nature **316**, 536-539 (1985)

In line 5 of the first paragraph on p. 537 the area of the south basin should read 6.78 km^2 and the last word on line 18 should read copepodites.