(These particular experiments were, therefore, not carried out to test the role of a presynaptic effect of kainate (see response by Ferkany *et al.* above).)

The second important element in the proposal of Ferkany *et al.* was that kainate induced the release of glutamate from presynaptic parallel fibre terminals (thereby making this amino acid available for the hypothetical postsynaptic/neurotoxic effects discussed above). However, the dose–response curve for glutamate release by kainate (which covers the range 500 μM–10 mM)[2,5] was found to be so far removed from the concentration range having neurotoxic effects (5–10 μM for the cells innervated by parallel fibres) that a causative relationship was considered unlikely[1]. (In their response, Ferkany *et al.*, for some reason, misquote our results on two counts, first regarding the concentrations of kainate required to kill all neuronal cells (which is 30 μM, that is, well below the minimum glutamate-releasing concentration) and second, with respect to cyclic nucleotide formation: the dose-response curve for the cyclic GMP-stimulating effect of kainate covers the range 3 μM (threshold) to 100 μM (maximum)[6] and is thus very different from the curve describing kainate-induced release of amino acids.)

As a final point, Ferkany *et al.* take exception to our interpretation[1] that the poor cyclic GMP elevations registered in their slices reflect poor cellular preservation (see ref. 7). Assuming the comments made in their response to mean that the postsynaptic elements were, in fact, preserved, this raises additional questions regarding the site and mechanism of glutamate release in the presence of kainate. Within a few minutes of application of neurotoxic concentrations of kainate, neurones become irreversibly depolarized and their membranes cease to resist the free passage of ions[8]. We note that Ferkany *et al.* used 15-min exposures for monitoring amino acid release[5]. It might be considered unrealistic to expect to demonstrate a direct primary effect of kainate on presynaptic terminals when, at the same time, these terminals (together with other neuronal and glial elements) are being subjected to the drastic changes in their ionic, metabolic and electrical environment that would be expected to accompany the postsynaptic neurotoxic action of kainate (which may itself be Ca^{2+}-dependent[9]). The use of synaptosomal preparations for investigating presynaptic kainate receptors would therefore seem more appropriate than slices. However, kainate does not, apparently, cause significant release of glutamate from such preparations[10].

J. GARTHWAITE
G. GARTHWAITE
Department of Veterinary Physiology and Pharmacology, University of Liverpool, Brownlow Hill, PO Box 147, Liverpool L69 3BX, UK

1. Garthwaite, J. & Garthwaite, G. *Nature* **305,** 138–140 (1983).
2. Ferkany, J. W., Zaczec, R. & Coyle, J. T. *Nature* **198,** 757–759 (1982).
3. Foster, G. A. & Roberts, P. J. *Neurosci. Lett.* **23,** 67–70 (1981).
4. Garthwaite, J. & Gilligan, G. J. *Neuroscience* (in the press).
5. Ferkany, J. W. & Coyle, J. T. *J. Pharmac. exp. Ther.* **225,** 399–406 (1983).
6. Garthwaite, J. *Neuroscience* **7,** 2491–2497 (1982).
7. Garthwaite, J., Woodhams, P. L., Collins, M. J. & Balazs, R. *Brain Res.* **173,** 373–377 (1979).
8. Constanti, A., Connor, J. D., Galvan, M. & Nistri, A. *Brain Res.* **195,** 403–420 (1980).
9. Duce, I. R., Donaldson, P. L. & Usherwood, P. N. R. *Brain Res.* **263,** 77–87 (1983).
10. Krespan, B., Berl, S. & Nicklas, W. J. *J. Neurochem.* **38,** 509–518 (1982).

Sequence similarity between putative gene products of geminiviral DNAs

STANLEY AND GAY[1] recently reported the determination of the complete nucleotide sequences of the two circular DNA molecules (DNAs 1 and 2) that make up the genome of cassava latent virus (CLV), a member of the geminivirus group. Several open reading frames (ORFs) capable of encoding proteins of molecular weights greater than 10,000 were identified in both strands of DNAs 1 and 2. Interestingly, two ORFs which are capable of encoding proteins of similar sizes (molecular weights 30,100 and 29,200) are present at equivalent positions on DNAs 1 and 2. We have compared the amino acid sequences of these proteins by a computer-assisted method described previously[2] and found that they are closely related (Fig. 1). Of all the positions compared in the aligned sequences, 43% are occupied by residues that are identical or chemically similar (gaps were considered as substitutions between dissimilar amino acids regardless of their length). Furthermore, a statistical test shows that the similarity between the aligned sequences is highly significant, with a probability of occurrence by chance of 4.3×10^{-6}. The presence of such extensive sequence similarity suggests that like the ORF of DNA 1, which is known to code for the coat protein of CLV (ref. 1 and J. Stanley, personal communication), the ORF of DNA 2 also encodes a functional protein. Although no such extensive sequence similarities were found for other ORFs, the present result, together with the similarity in size of the two viral DNAs and the fact that they share a very similar non-coding segment in common[1], also suggests that the bipartite viral genome has evolved from a single common ancestral DNA.

REIKO KIKUNO
HIROYUKI TOH
HIDENORI HAYASHIDA
TAKASHI MIYATA

Department of Biology, Faculty of Science, Kyushu University, Fukuoka 812, Japan

1. Stanley, J. & Gay, M. R. *Nature* **301,** 260–262 (1983).
2. Toh, H., Hayashida, H. & Miyata, T. *Nature* **305,** 827–829 (1983).

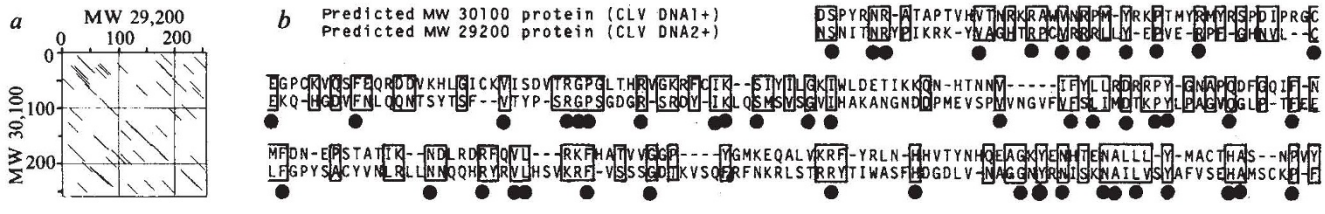

Fig. 1 *a*, Similarity matrix comparison of amino acid sequence of predicted 30,100 MW protein, encoded by the (+) strand of CLV DNA 1 (ordinate), with that of 29,200 MW protein encoded by the (+) strand of DNA 2 (abscissa). A computer program was used to generate diagonal lines indicating segments of 20 residues long that show sequence similarity (see ref. 2). *b*, Alignment of the 30,100 MW and 29,200 MW protein sequences. Aligned regions correspond to nucleotide positions 515–1,174 of DNA 1 and 632–1,327 of DNA 2 (see Fig. 1 of ref. 1) for 30,100 and 29,200 MW proteins, respectively. Boxed residues indicate identities (●) or favoured amino acid substitutions (see ref. 2). Gaps (−) were introduced to maximize similarity.