Aggregation of Virus Particles

EVIDENCE confirming the description[1] by Bawden *et al.* of the shape of the tobacco mosaic virus particle appears in Best's recent photograph[2] of virus protein forming long threads after it has been precipitated from solution. Further evidence that virus particles, even in dilute solutions, may form chain aggregates is obtained from experiments on the relation between dilution of virus and number of infections caused.

Certain carefully purified preparations of virus[3] gave, on dilution, infection series which agreed closely with an equation of the form $y = N(1 - e^{-pn_1x})$, where y is the number of infections produced by an inoculum of relative concentration x, N is the asymptotic number, n_1 is the number of virus particles in the undiluted preparation, and p is the small probability of any one particle entering one of the N points in the plant tissue to cause an infection.

In the example given of a dilution series for a purified sample of tobacco mosaic virus (ref. 3, Table 1) there was a significant divergence from the values calculated from the equation; and the results since published by Stanley[4,5] for crystalline tobacco mosaic and aucuba mosaic proteins are widely divergent from calculated values. The number of infections increases less rapidly with concentration of virus than would be expected. In attempting to explain such divergences, we assumed that the virus particle was capable of combining reversibly with a particle of impurity to give an inactive complex. The relation between the concentration of effective virus particles, n_1x, and the total concentration, v_1x, is given by

$$(n_1x)^2 + n_1x\{k - v_1x(1 - q)\} - v_1xk = 0,$$

where q is the ratio of the number of particles of impurity to the number of virus particles and k is the dissociation constant of the complex. The special form of the equation which fitted the results was that when $q = 1$. This seemed to be a highly unlikely state of affairs. Search for a more likely hypothesis revealed the fact that the same equation is obtained if it is assumed that virus particles can join end-to-end to form chains, single particles or aggregates being infective units. If r is the number of junctions between particles, then using the above nomenclature,

$$r = v_1x - n_1x;$$

and if k_1 and k_2 are independent of chain length

$$k_1(n_1x)^2 = k_2r = k_2(v_1x - n_1x)$$
$$(n_1x)^2 + kn_1x - kv_1x = 0.$$

The infection-dilution data for a number of experiments with viruses of the tobacco mosaic group and Stanley's results with purified virus proteins[4,5] have been tested by applying this modifying equation. The former were obtained with virus preparations at various stages of purification, but in all cases the agreement between observation and calculation is sufficiently accurate to render it likely that end-to-end aggregation is the main cause of the divergence of the results from expectations based on the simpler picture of separate virus particles.

It may be expected that the modified picture will apply only to the tobacco mosaic group of viruses, which are thought to consist of rod-shaped particles[6], and this has so far been borne out by experiment.

These results are described more fully in a paper to be published in the *Australian Journal of Experimental Biology and Medical Science*.

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[4] Stanley, W. M., *J. Biol. Chem.*, **117**, 325 (1937).
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Production of Mutations by Neutrons

IN experiments to determine the possibility of producing mutations by treatment with neutrons, adult males of *Drosophila melanogaster* were subjected to a neutron bombardment derived from a 485 gm. block of beryllium exposed to the γ-rays from 4 gm. of radium. It is known that beryllium thus exposed produces neutrons of two velocities, the fast ones having an energy of 0·60 million electron-volts and the slow of 0·16 million electron-volts. Fast neutrons were used in one series of experiments, the very slow ones being excluded by means of a cadmium plate. In a second series, the fast neutrons were slowed down by passage through paraffin, so that only slow neutrons were used. In a third series, serving as a control, paraffin was substituted for the beryllium block, so that the flies received no neutrons but did receive the same gamma radiation and secondary radiation from the radium source as in the first two series. In these three series, a thick lead block was used to remove most of the radium γ-radiation. Finally, in a fourth series, serving as a second kind of control, the flies were not irradiated artificially in any way.

The ClB method of breeding was used, and the occurrence of all sex-linked lethals was noted. The table below gives the summarized results of the examination of the F_2 groups of flies (15,352 fertile cultures in all).

Series	No. of Groups of F_2	No. of lethals	Observed frequency of lethals
1. Fast neutrons plus escaping radium radiation	4312	44	1 in 98
2. Slow neutrons plus escaping radium radiation	1504	5	1 in 301
3. Escaping radium radiation without neutrons	4764	19	1 in 250
4. No irradiation	4772	12	1 in 398

It will be seen that although the radiation escaping from the radium source may have caused a few mutations, this by no means accounts for all the mutations arising in the flies treated with fast neutrons. On the other hand, the slow neutron series did not have an appreciable number of mutations produced in it, although, from a theoretical point of view, some production of mutations by this means also is to be expected.