The lysis of the cell-walls apparently is not related to the mechanism of cell division, and no correlation between the sites of cell budding and the place of the first stages of enzyme digestion before the release of the naked protoplasts was observed.

C. GARCIA MENDOZA
J. R. VILLANUEVA

Instituto 'Jaime Ferrán' de Microbiología,
Velazquez 138, Madrid 6.

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A New Species of *Brucella*: *B. rangiferi*

Two Russian scientists, Zabrodin and Golosow, have isolated *Brucella* strains from reindeers. I obtained from them 24 strains and investigated them by help of taxonomy.

Morphology: typical for *Brucella*; production of hydrogen sulphide—negative, typical for *Br. melitensis* or *Br. suis*, type II. Urease production: 10–15 min (characteristic for *Br. suis*). Bacteriostatic action of thionine and basic fuxine: thionine (+), fuxine (±). That is rather similar to *Br. suis*. Receptors analysis mono-specific sera: *Br. melitensis* and *Br. abortus*.

My own *Brucella*-phage No. 371 (XXIX), dose 1 RTD, 100 RTD, 1,000 RTD and 10,000 RTD shows the results obtained from 24 strains (Fig. 1). The picture is similar to *Br. suis*, dose 1 RTD. With dose 10,000 RTD, the picture resembles *Br. suis* somewhat, but is much weaker in the phage-lysis. I obtained a similar picture when applying further my own 5 *Brucella*-phages; Russian phages (Tb, P, 3, 6, 7) and van Drimmelen's phages (10).

24 *Brucella* strains, isolated by Zabrodin and Golosow in the far north of Russia, behave almost identically and showed similar features to *Br. suis* (hydrogen sulphide urease, thionine, fuxine, *Brucella*-phages) and somewhat similar to *Br. melitensis* (receptors analysis). So it is clear

that we have here a uniform but separate group of *Brucella*, which one may call *Brucella rangiferi*.

J. PARNAS

Department of Medical Microbiology,
Academy of Medicine,
Lublin, Poland.

GENETICS

Inheritance of Seed Weight in *Ricinus communis* L.

THE cross investigated was Brazilian large seeded, *L* (mean seed weight 913 mg), by Peruvian small seeded, *S* (mean seed weight 147 mg). The method followed was that of continuous back-crossing of heterozygotes to one of the parent varieties, *S*, with the object of isolating bimodal curves indicating monohybrid segregation. Once this was achieved the new homozygous genotypes could be combined in various ways to elucidate the genetical architecture of a typical quantitative character. Since the mode of inheritance proved to follow a geometric rather than an arithmetic pattern, it is convenient to express the results in terms of log seed weight.

A summary of the results follows:

Family	Log seed weight	Expected on G.M. basis
<i>L</i>	960	
<i>S</i>	167	
<i>F</i> ₁	568	564
<i>F</i> ₂	575	564
First <i>B.C.</i> to <i>L</i>	773	774*
First <i>B.C.</i> to <i>S</i>	368	378†
Second <i>B.C.</i> to <i>S</i>	290	288‡
Third <i>B.C.</i> to <i>S</i>	224	226§

* 762 using G.M. of parents as *F*₁ value.

† 366 using G.M. of parents as *F*₁ value.

‡ Calculated from mean of first *B.C.* parents used for crossing.

§ Calculated from mean of second *B.C.* parents used for crossing.

Apart from minor complications caused by probable slight heterosis effect in *F*₁, and an unavoidable non-randomization of the parents used for the second and third back-crosses, it is clear that successive back-crosses to *S* approach the latter by a series of geometric means, the mean value for any back-cross being the geometric mean of the previous back-cross and *S*. This rule is also obeyed in the first back-cross to *L*.

Does this continued geometric approach to *S* continue until the frequency distributions are statistically indistinguishable from that of *S* itself, or will bimodal curves begin to appear, indicating the existence of monohybrid segregation. The answer to this question is not yet clear. One family in the second back-cross points to the segregation of a single factor for seed weight linked with *B* (waxy bloom). In the third back-cross one or more families may indicate monogenic segregation. On the assumption of 8 factors for seed weight acting geometrically, the results are close to expectation.

S. C. HARLAND

Plant Breeding Station,
Box 2580,
Lima, Peru.

Genetic Controls of Allelic Recombination in *Neurospora*

MAPS of the fine structure of genes are intended to exhibit the positions relative to one another, and to other genetic markers, of the sites of difference from the normal of a series of allelic mutants. Commonly, in their construction, most reliance is placed on the frequencies of prototrophs observed to arise in repulsion phase crosses between pairs of alleles. It is assumed that the order of the sites may be deduced from these values of prototroph frequency by application of the additivity rule. This is that any pair, *m*¹ and *m*², shows a value which is approximately the sum or difference of the values shown by each

Fig. 1. *Brucella rangiferi* and *Brucella*-phage No. 371 (XXIX) in 1, 100, 1,000 and 10,000 RTD