

In addition to confirming the hypothetical helical configuration of human chromosomes, this study demonstrated that secondary constrictions are less tightly coiled regions of the chromonemata. Moreover, this technique offers the possibility of a more quantitative analysis of chromosomes at the chromonema level. If a reproducible gyre number is established, coil counts may become a more accurate method of determining arm ratios. The analysis of chromosome breaks or translocations, induced by treatment with chemicals or ionizing radiation, may be described more accurately with partial dissociation of the chromosomes. Quantitative studies regarding the number of helices and the measurement of the length and diameter of the coils are now in progress and will be published elsewhere.

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This communication is dedicated to Prof. Sajiro Makino, Zoological Institute, Hokkaido University, Sapporo, Japan, in honour of his sixtieth birthday on June 21, 1966.

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GENETICS

Chimerical Nature of the Entire-leaf Variant in the Potato Variety 'Majestic'

THE docken, or entire-leaf variation (Fig. 1), like several other variations for leaf shape in potatoes, has not been shown previously to be a chimera. Leaf shape in potatoes is largely determined by the constitution of L_2 (ref. 1), and the two standard methods of investigating potato chimeras, breeding behaviour and eye-excision, give information on L_2 in the variant and not on L_1 . It is thus not possible by these two methods to show that L_1 in a variant is unchanged. Information of L_1 may, however, be obtained by X-ray treatment².

Crossing 'Majestic' docken-leaf with 'Ulster Prince' resulted in a family with a segregation of 23 seedlings with entire leaves: 17 seedlings with compound, pinnate leaves

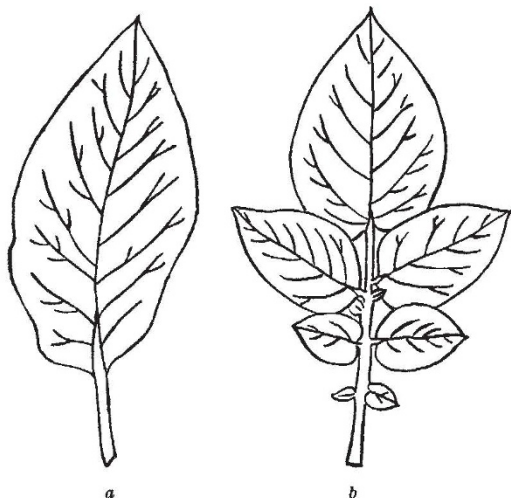


Fig. 1. (a) Docken-leaf and (b) normal, compound pinnate leaf of shoots after X-ray treatment

(the control cross of normal 'Majestic' with 'Ulster Prince' gave 53 seedlings with compound, pinnate leaves and none with entire leaves).

Eye-excision experiments with docken-leaf tubers produced only plants with entire leaves, no normal 'Majestic' plants being obtained. Root buds, produced by the method of Howard³, also resulted only in plants with entire leaves. It thus seems that docken-leaf in 'Majestic' results from a mutation for entire leaves in the L_2 layer and that the L_3 layer also now has the same constitution as that of L_2 ; a similar replacement of L_3 by L_2 cells has been observed in triploid-hexaploid potato chimeras⁴.

Five apical (rose) ends of tubers of docken-leaf 'Majestic' were given an X-ray dosage of 3,500 r. Four of them produced plants and one of the four had a mixture of normal and docken-leaf shoots. The production of the shoots with normal leaves was presumably because in the docken-leaf variant L_1 is still normal, unchanged 'Majestic'. The frequency (about 12.5 per cent) of shoots with all layers with the constitution of L_1 in the variant is similar to that of full 'Red King' from normal 'Red King' and of white from 'Bonte' sports after X-ray treatment².

The finding that the docken-leaf sport is a chimera in which L_1 is still normal 'Majestic' suggests that certain other variants, such as wildings, feathery wildings and bolters, which do not appear to be chimeras from the results of eye-excision experiments, may be chimeras in which L_2 and L_3 have the mutated character but in which L_1 is still unchanged.

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Estimation of the Frequency of Functioning Gametes in Monosomics

WE regret that the estimates of p and q of the functioning male gametes with n and $(n - 1)$ chromosomes respectively given in our recent communication¹ are not consistent. The correct estimates should be as follows.

On applying the maximum likelihood method, the estimate of p may be obtained by taking the positive root of the quadratic equation:

$$p^2[N(p' - q')] + p[q'(a_1 + a_2) - p'(N + a_1)] + a_1p' = 0 \quad (1)$$

and the variance of the estimate will be:

$$V_p = \frac{p^2q^2(p'q + pq')^2}{(p'q + pq')^2(a_1q^2 + a_2p^2) + a_2p^2q^2(q' - p')^2} \quad (2)$$

where a_1 , a_2 and a_3 ($a_1 + a_2 + a_3 = N$) are the observed frequencies of disomic, monosomic and nullisomic respectively and p' and q' ($p' + q' = 1$) are the relative frequencies of the functioning female gametes with n and $(n - 1)$ chromosomes respectively.

The square root of V_p will give the standard error ($S.E.$) of the estimate.

It can be shown that:

$$\text{when } p' = q' = \frac{1}{2} \\ p = \frac{2a_1}{N} \text{ and } q = \frac{2a_3}{N}$$

and the variance of the estimate will be reduced to $\frac{2pq}{N}$.

By using (1) in our numerical example¹, we obtain:

$$-59.28p^2 + 12.08p + 3.12 = 0$$

giving $p = 0.3529$ and $q = 1 - p = 0.6471$.

Similarly, from (2), we have

$$V_p = 0.00324967$$

$$\text{and } S.E. = 0.0570$$

It may be observed that the estimate of p is not significantly different from the experimental results² 0.39.