February 3rd, 1942

Dear Hutchinson,

Thanks for your nice long letter about the Crinkle situation. What puzzles me is this: if, starting with a highly inbred Crinkle strain, you back-cross any non-crinkle repeatedly for a number of generations, it is to be presumed that, apart from a region in the neighbourhood of the crinkle locus, the last family will be segregating on a uniform homozygous basis. If, in parallel with these, you have a similar series of back crosses, using the same inbred crinkle line but a different source for non-crinkle, the two final progenies should be similar in all respects, except possibly for the normal allelomorph introduced and a region of the same chromosome. If, therefore, homozygous non-crinkle derived from these two lines are crossed, and the possibly heterozygous offspring back-crossed to the same inbred crinkle line, there should be unifactorial segregation for the two supposedly different non-crinkle alleles. If no such segregation is observable, I cannot see that there is any more sensitive test possible by which the existence of a difference between these alleles could be demonstrated.

If there is considerable variation, but no clear 1:1 segregation, it would, of course, be helpful to have in strictly
parallel culture progenies derived by crossing homozygotes of
the two kinds with the crinkle line, since these would necessarily
be uniform heterozygotes of the supposedly two kinds.

Supposing one found a good 1:1 segregation, or a plausible
one, the question remains whether we have two different normal
alleles of crinkle, or the same allele, with and without a closely
linked modifier. The best evidence of the former against the latter
possibility must, I think, come during the back-crossing process,
in which parallel back crosses might be made for each generation,
say after the 5th, using the highest and lowest grade heterozygotes
respectively. If these always gave equivalent progeny, the evidence
for different alleles is strong; if not, it is certain that the
material is still segregating for at least one factor at another
locus.

What you say about wind-crinkle strongly emphasises the point
that the closest environmental control is needed before scorings
can be trusted, and for this parallel progenies are never really
so good as the same progeny in which to demonstrate a contrast.

I am much puzzled by your statement that Indore crinkle,
Sea-Island crinkle, and Contorta, different mutants of the same
locus, having similar but quantitatively different effects, are not
even similarly affected by modifiers. Evidence from other species
of the bio-chemical similarity of the effect of different mutant
alleles is so overwhelming that, even if the fact were well es-
tablished for one distinct modifier, one would hesitate to believe
that it was also true for others. So far as it goes, it does seem
to suggest that the three mutants differ also in other fact-
presumably also in the same neighbourhood. Is Contorta possibly a deficiency included in crinole locus?

However, I hope you will make all these difficulties clear when you write the thing up, as you say you are on the point of doing. Impatient as I am to have my own ideas put straight on a subject on which so many contradictory statements have been made, I should advise delay rather than run the risk of publishing before any essential point is really demonstrable.

Yours sincerely

I am sending two recent offprints under separate cover.