ated sperm, and in four experiments all four possible combinations of the two curve shapes were observed. In each of these cases, however, the terminal portion of the recovery curve for the fertilized eggs was steeper. Therefore, it appears, that the kinetics of the recovery processes before and after fertilization of irradiated eggs from the same animal differ and that the post-fertilization recovery process is somewhat more efficient.

The cleavage delay induced by exposing the gametes of *Arbacia* to radiation has been interpreted as the time required for the zygote to repair or replace some constituent (of the nucleus) destroyed by radiation, which was necessary for cell division (*3*). Since recovery from this delay was demonstrated in unfertilized eggs but not in sperm, it was postulated that some cytoplasmic component was essential for repair. The current experiments confirm this view since they demonstrate that recovery can take place in irradiated sperm if the sperm is inside the egg where it can presumably mobilize the resources required for repair. It has also been shown that the recovery mechanism which operates in the irradiated unfertilized egg is not necessarily the same in the zygote (*4*).

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Heterokaryon-Incompatibility Factor Interaction in Tests between Neurospora Mutants

Abstract. Studies on presumably isogenic *ad-3A* and *ad-3B* mutants of the ascomycete *Neurospora crassa* derived from the same wild-type strain have revealed that the negative heterokaryon tests shown by certain pairwise combinations can be attributed to interaction of incompatibility factor mutations.

Heterokaryon tests on mutants with identical biochemical requirements induced in the same or isogenic wild-type strains of *Neurospora* have been used widely to group such mutants into series of presumptive alleles, and to test within each group for allelic complementation. Since such mutants are essentially isogenic, it is generally assumed that they are fully heterokaryon-compatible (*1*) and that a negative test is indicative of functional allelism (*2*). Mutation of genes affecting both heterokaryon formation and subsequent growth can be expected to occur simultaneously with mutation of genes governing nutritional requirements in some percentage of the mutants recovered from forward-mutation experiments. Heterozygosity for incompatibility-factor mutations can be generally recognized by the failure of a given mutant isolate to show positive heterokaryon tests with both allelic and nonallelic testers induced in the same genetic background (*3*).

In the present experiments evidence has been found for incompatibility-factor mutations with more subtle effects, which do not prevent positive heterokaryon tests when they are heterozygous individually but which do prevent positive heterokaryon tests when they are present in some heterozygous combinations.

Previous data from crosses and heterokaryon tests (*4*), tetrad analysis (*5*), an insertional translocation (*6*), and x-ray-induced recessive lethal mutation in the *ad-3* region (*7*) have shown that the *ad-3A* and *ad-3B* mutants are functionally distinct and in separate cistrons. In extensive tests on samples of *ad-3* mutants induced in mating type *A* wild-type strains by x-ray or ultraviolet treatment, no mutants were found that gave negative heterokaryon tests with all *ad-3A* or *ad-3B* testers. However, some mutants were found that gave negative heterokaryon tests only with certain *ad-3A* and *ad-3B* testers so that they were represented initially on the complementation map of the *ad-3* region as partial overlaps into the a*d-3A* or *ad-3B* cistrons. The existence of such a class of mutants in the absence of a class noncomplementing with all *ad-3A* and *ad-3B* testers was not expected. Because of this, experiments were planned to determine whether the negative tests, given by those mutants represented as partial overlaps, could be explained on any other basis. If, for example, such negative heterokaryon tests were due to the presence of incompatibility-factor mutations at other loci, segregation would be expected in the F_1 progeny from a cross of such a mutant to wild type.

The interaction patterns of three *ad-3A* mutants, three *ad-3B* mutants, and of mating type *A* F_1 progeny from a cross of each mutant to wild-type strain 74-OR8-1a (mating type *a* strain essentially isogenic with 74A) are given in Table 1. Three types of tests were made as described previously (*4*): (i) original isolate + original isolate, (ii) F_1 progeny + original isolate, or (iii) F_1 progeny + F_1 progeny. Under these conditions three of the nine combinations involving the original isolates gave a weak but positive response. Heterokaryon formation in such cases was delayed for many days and subsequent growth was at less than wild-type rate. Marked variation in the ability to form heterokaryons was also observed among the F_1 progeny from each cross. In some instances, the F_1 progeny gave either a negative test or a vigorous positive test, but in most crosses those combinations giving positive tests showed variation both in the time of heterokaryon formation and the type of response. By selection among the F_1 progeny, however, derivatives of each of the six mutants were obtained that gave vigorous heterokaryon tests (no delay in heterokaryon formation and growth at wild-type rate) for all of the *ad-3A* + *ad-3B* mutant combinations recorded as negative in the same type of test on the original isolates.

This analysis shows that the failure to obtain positive heterokaryon tests in certain pairwise combinations of presumably isogenic *ad-3A* and *ad-3B* mutants can be attributed to the interaction of extrinsic factors affecting heterokaryon formation and subsequent growth. Studies on known incompatibility factor mutations in *Neurospora* (*1, 8, 9*) have shown (i) that there are many different stages involved in the formation and subsequent growth of heterokaryons that can be affected by mutation, and (ii) that incompatibility is found only when the tested strains are heterozygous for such incompatibility mutations. If there are a large number of incompatibility loci in the *Neurospora* genome, then the presence of incompatibility mutations in large samples (> 100) of allelic mutants as a consequence of simultaneous mutational events is not unexpected. The mutations encountered in this study are somewhat atypical of those previously described, in that none prevent hetero-

Table 1. Number of positive heterokaryon tests obtained with various pairwise combinations of mating type *A ad-3A* and *ad-3B* mutants and their mating type *A* F_1 progeny (from a cross to wild type) on minimal medium. Symbols: ±, weak positive response; +, vigorous positive response; −, negative response.

ad-3B mutant	*ad-3A* mutant					
	1-230-0200		1-230-0049		3-010-0194	
	Original	F_1 progeny	Original	F_1 progeny	Original	F_1 progeny
2-017-0095						
Original	−	10/18	−	14/25	−	6/27
F_1 progeny	4/25	+*	4/25	+*	7/17	+*
1-152-0068						
Original	±		−	16/24	−	7/16
F_1 progeny		+*	6/16	+*	2/17	+*
1-155-0055						
Original	±		±		−	14/16
F_1 progeny		+*		+*	21/25	+*

* At least one pairwise combination was made of heterokaryon-compatible F_1 progeny from each cross.

karyon formation with the majority of tester strains when heterozygous individually. Negative heterokaryon tests were obtained only when such mutations were present in certain doubly or multiply heterozygous combinations as shown in Table 1. Apparently the effect of heterozygosity for mutations with marginal effects is cumulative and only in some cases is the net effect extreme enough to prevent completely a positive heterokaryon test.

It is important to note that the incompatibility factor interactions found in the present experiments with relatively isogenic strains may be even more frequent among the so-called "heterokaryon-positive" derivatives of allelic mutants induced in unrelated wild-type strains as well as isolates of "isogenic" allelic mutants derived from outcrosses to other strains. The existence of such subtle interactions between incompatibility factor mutations suggests that a note of caution is advisable in the interpretation of negative heterokaryon tests. It seems possible that the basis for some of the nonlinear complementation maps (or mutants that do not map as a continuous straight line on a linear map) is the failure to recognize that apparent "functional identity" may be due to an incomplete or inadequate heterokaryon test.

The unsuspected interaction of such incompatibility factor mutations may in fact be the explanation for the greater sensitivity reported (*10*) for the pseudo-wild type (PWT) test in studies on allelic complementation. The generally accepted hypothesis for the formation of PWT's is that they result from nondisjunction of homologous chromosomes during meiosis and the formation of an unstable disomic (*11*). Thus in the PWT test, homologous chromosomes carrying nonidentical allelic mutations are present initially in the same nucleus, whereas in the heterokaryon test they are present in different nuclei in the same cytoplasm. The marked difference in sensitivity has been attributed to more favorable nuclear ratios in the heterokaryons derived from the breakdown of the disomic in PWT ascospores than in the heterokaryons obtained by direct mixing of conidia from vegetative cultures. This is undoubtedly true, but the basis for the greater sensitivity is not just a greater likelihood of forming a heterokaryon having equal numbers of two types of mutant nuclei (*10*). Even though there may be a 1 : 1 nuclear ratio in the PWT ascospore, the nuclear ratio in the hyphae emerging from opposite ends of germinating PWT ascospores may vary over a very wide range (0 to 100 percent) (*12*). The most plausible basis for the greater sensitivity of the PWT test is the elimination of any influence of heterozygosity for incompatibility factor mutations that could either prevent heterokaryon formation or cause marked departures from a 1 : 1 nuclear ratio (*9*) in the heterokaryon test. Furthermore, in at least some of the heterokaryons resulting from breakdown of the disomic, heterozygosity for very closely linked incompatibility factor mutations would even be eliminated by crossing over in addition to nondisjunction (*2*).

If the effect of heterozygosity for such mutations is always cumulative, however, then their presence in heterokaryon tests on samples of unknown mutants may be more readily detectable by the inclusion of the appropriate strain, such as 2-017-0095 or 3-010-0194, as an "incompatibility-factor control." In contrast with the other four strains studied (Table 1), all combinations of the mutations present in either of these two strains produced an effect extreme enough to completely prevent a positive test. In this way it seems possible to detect mutations with marginal effects on heterokaryon formation and to simplify the interpretation of an otherwise simple and straightforward test for allelism.

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Blood Clotting: The Force of Retraction

Abstract. The force of blood clot retraction was measured and found to be at least 10^4 dyne/cm^2; this is sufficient to deform many soft tissues and to allow clots to retract in vivo.

During the clotting of blood the platelets increase in size; they clump and aggregate at the interstices of the developing fibrin network (*1*). At this time the platelets exhibit rapid glycolysis and a sharp increase and subsequent fall in their content of adenosine triphosphate (ATP). Contraction follows, presumably due to the shortening of a constituent protein similar to actomyosin (*2*). This process results in marked reduction in the size of the clot (*3*). The biological significance of clot retraction is not entirely clear. Its role in hemostasis, wound healing, and in recanalization of thrombosed vessels has often been suggested (*4*). Budtz-Olsen concluded that the force of clot retraction is so weak that clot retraction does not occur at all in vivo and that this characteristic of blood represents an evolutionary vestige without usefulness in the human (*4*).

The present study was undertaken to measure the force of clot retraction in order to determine whether or not this