WHEAT

Contested Parentage

from a Correspondent

NEW interest in the evolutionary origins of the common wheat of agriculture, *Triticum aestivum*, has been stimulated by the discovery that some of its diploid relatives, in the genus *Aegilops*, contain genetic variation which affects meiotic chromosome pairing. *T. aestivum* is a hexaploid which contains the complete sets of chromosomes—known respectively as the A, B and D genomes—of three distinct diploid species. It has long been accepted that the A and D genomes were derived respectively from close ancestors of the contemporary diploids *Triticum monococcum* and *Aegilops squarrosa*. More uncertainty surrounds the origin of the B genome.

It should first be pointed out that in each genome of wheat the chromosomes relate genetically to corresponding, or homoeologous, chromosomes in each of the other genomes. Homoeologous chromosomes do not normally pair at meiosis, being prevented from doing so (Wall, Riley, Chapman and Gale, *Genet. Res.*, **18**, 311 and 329 ; 1971) by the activity of a single locus (*Ph*) which is distantly located on the long arm of chromosome 5B. The genotypes of *speltoides* and *mutica* have the capacity, in hybrids with *T. aestivum*, to suppress the activity of the *Ph* locus. Dover and Riley (*Nature New Biology*, **235**, 61 ; 1972) and Kimber and Athwal (*Proc. US Nat. Acad. Sci.*, **69**, 912 ; 1972) have now described the existence of genetic variation which affects the occurrence of homoeologous meiotic pairing in hybrids between *T. aestivum* and *Ae. mutica* and *Ae. speltoides* respectively.

Ae. speltoides, for reasons based on karyotype, gross plant morphology and geographical distribution, has been considered to be a strong candidate for recognition as the donor of the B genome. Kimber and Athwal now interpret the patterns of meiotic chromosome pairing observed in wheat–*Ae. speltoides* combinations, in which the *Ph* activity is apparently not suppressed, as implying no closer relationship between wheat and *Ae. speltoides* than that between wheat and many other *Aegilops* species, so reducing the likelihood of *Ae. speltoides* being the source of the B genome. The essence of Kimber and Athwal's argument is that, even if homoeologous pairing cannot occur, there should still be pairing between chromosomes of the B genome and their full homologues in the *Ae. speltoides* genome.

The strength of this case will ultimately depend on the cause of the low-pairing behaviour in the critical wheat–*Ae. speltoides* hybrids. It might be the result merely of a form of asynapsis, and this could be tested by making hybrids in which one wheat chromosome was disomic as a result of the cross *T. aestivum* tetrasomic for one chromosome × *Ae. speltoides*. If Kimber and Athwal are correct in their interpretation, the disomic chromosomes should pair normally, pairing being prevented only between homoeologues. Conclusions, based on other criteria, that *Ae. speltoides* was involved in the parentage of wheat would then be more deeply undermined.

Another question that might be resolved using the newly recognized pairing variants, as proposed by Dover and Riley, is the nature of the origin of the *Ph* allele of *T. aestivum*. Because no activity similar to that of *Ph* is known among the diploid relatives of wheat, it has long been thought that this allele must have arisen by mutation after chromosome 5B had been incorporated in polyploid wheat. The genotypes of *Ae. speltoides* and *Ae. mutica* that, in hybrids with wheat, result in low levels of meiotic pairing, may, however, carry alleles corresponding to that on chromosome 5B, in which case, as Dover and Riley suggest, there would be low pairing in similar hybrids lacking chromosome 5B because the presence of the diploid genome would compensate for its absence. This question, however, has still to be resolved.

The course of evolution of wheat is still a controversial issue. Clearly, difficulty is created by attempts to demonstrate parentage experimentally, with contemporary material, several thousands of generations of evolution subsequent to the hybridization event and there will always be uncertainty. Crop plant evolutionists now, however, have a better specification of the characteristics of the B genome donor than formerly, when such bizarre proposals were made as that the B genome came from *Agropyron triticeum*, in spite of the fact that all the chromosomes of this species have subterminal centromeres and those of the B genome are median or submedian.

VIROLOGY

Captive Genomes

from our Cell Biology Correspondent

REOVIRUS places several claims for attention on virologists. For one thing, its genome is unusual; it comprises ten segments of double stranded RNA. For another, the virus particles contain an RNA transcriptase which, once the outer of the two capsids has been removed *in vitro* by proteolytic enzymes, will transcribe one of the two strands of each of the ten double stranded segments of the genome, all of which are themselves conserved.

These so-called sub-viral particles are an interesting source of messenger RNAs, and their properties at least raise the possibility that *in vivo* during the infectious cycle the reovirus genome, unlike the genomes of most

Selective Inhibition of RNA Synthesis

INFORMATION about new drugs or new ways to exploit tried and tested drugs, which allow experimentalists to probe further into the metabolic processes of eukaryotic cells, is always welcome and no doubt the suppliers of camptothecin can look forward to a boom in demand as a result of what Abelson and Penman have to say in *Nature New Biology* next Wednesday (May 31). They show that camptothecin, which is known to induce breakages in cellular DNA, also selectively interrupts the synthesis of high molecular weight RNAs in HeLa cell nuclei.

Abelson and Penman have confirmed that when HeLa cells, growing in suspension, are exposed to 1 μg/ml. of the drug, DNA and RNA synthesis are both markedly inhibited whereas protein synthesis is hardly affected. Closer analysis of the small amount of RNA made in the presence of the drug reveals its selective effect. Although the average size of the molecules in ribosomal RNA precursor and heterogeneous nuclear RNA fractions is very much smaller than in controls the synthesis of 4S RNA is only slightly impaired and 5S RNA synthesis seems to be completely unaffected by the drug at this and higher doses. Furthermore, whereas the truncated ribosomal RNA fractions made in the presence of the drug are rapidly degraded within the nucleus, the aberrant heterogeneous nuclear RNA is comparatively stable; it persists in the nucleus, being neither degraded nor exported to the cytoplasm.

How, at the molecular level, camptothecin brings about these changes remains to be elucidated ; it is not apparently simply a matter of slowing down the rate of growth of RNA chains, and whether or not the drug inhibits RNA synthesis because it causes breaks in the template DNA is as yet an open question.

Abelson and Penman confirm one thing, however; camptothecin can be used to inhibit selectively synthesis of ribosomal and messenger RNAs without concomitantly blocking the synthesis of 4S and 5S RNAs or RNA synthesis in mitochondria. It will therefore increasingly find a place on the laboratory shelf.

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