filled chambers is an important adaptation against whale sonar, it is primarily for locomotor efficiency and only secondarily for anti-sonar defence.

Other obvious defences include jamming, decoying and mimicry. There seems to be little scope for jamming or decoying given the vastly greater sound-producing powers of whales over fishes and squids, and it is hard to imagine how an animal can produce an expendable decoy that resembles it sufficiently on sonar. Perhaps the most promising is mimicry of a distasteful species. Do toxic fish emit ultrasonic cries when they hear whales and do edible fishes make similar calls?

If fishes and squids have sonar counter-measures, have whales kept ahead in the evolutionary arms race by using sonar more efficiently, or even by using it only intermittently as part of a set of techniques, including passive listening for the calls and swimming noises of prey? Some species of bats often use passive listening and vision as well as, or instead of, active sonar¹³, especially when hunting prey which can hear their sonar emissions, and it has already been suggested¹⁴ that sperm

whales lie still at enormous depths, listening for the swimming of giant squids. Another reason for the quietness of whales suggested by Norris and Möhl¹ is to avoid alerting other whales that might want to share the food, or even attack the original whale. □

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Plant molecular biology

Viral RNA in mitochondria?

from David M. Lonsdale

MEMBERS of the largest group of plant viruses contain single-stranded RNA in the '+' or messenger RNA sense. Not all plant viruses induce disease symptoms: the cryptic or temperate viruses, for example, are asymptomatic. Most of these viruses have segmented double-stranded (ds) RNA genomes and virus-like particles can be detected in healthy plants at low levels. In this respect they are similar to dsRNA killer systems in fungi. The presence of dsRNA in healthy plants is often assumed, therefore, to be indicative of a cryptic virus infection¹. However, many apparently healthy plants contain dsRNAs where no inclusion bodies or virus-like particles have been detected². In a recent report³, such cytoplasmically located self-replicating RNAs have once again been highlighted in plants and in particular within the mitochondria of the S cytoplasm of maize.

Cytoplasmically inherited male sterility (CMS), an inability to produce or release functional pollen, results from a mitochondrial-nuclear dysfunction that is common to many higher plant species. In only a few instances, however, have apparently self-replicating dsRNAs been identified in CMS cytoplasm and their role as causative agents of the CMS phenotype has never been established.

Maize has four different cytoplasm types, one (N) is fertile in all nuclear back-

grounds, the remaining three (C, S and T) produce male-sterile plants with certain nuclear genotypes. With one exception, unusual RNAs are limited to the S-cytoplasm group. In the lines W182BN and 2132, two abundant dsRNA species of approximately 2,900 (LBN1) and 900 (LBN2) base pairs were identified by Sisco and co-workers^{4,5}. Analysis of other S-cytoplasm lines, particularly CMS-S(B73 × Mo17) and the two fertile lines R369 (a spontaneous fertile revertant of an S-cytoplasm inbred); and RU (a South American race of maize related to fertile N-cytoplasm types) has revealed two abundant single-stranded RNA species designated S/RU-RNA-a and S/RU-RNA-b (ref. 6).

Hybridization and heat-denaturation experiments demonstrate quite clearly that S/RU-RNA-b hybridizes to LBN2 but not to itself. Following a 60°C formamide denaturation, most LBN2 co-migrates with S/RU-RNA-b. The implication of these results is that LBN2 is the replicative double-stranded form of S/RU-RNA-b. It is probable that a similar relationship exists between LBN1 and S/RU-RNA-a (ref. 4). There is evidence to suggest that these RNAs, LBN1 (S/RU-RNA-a) and LBN2 (S/RU-RNA-b), are related, in contrast Schuster and co-workers⁶ have demonstrated that these RNAs are unrelated to other mitochond-

rial DNA plasmids and to the main mitochondrial genome.

The recent paper by Finnegan and Brown³ confirms the presence of both single- and double-stranded RNAs in the S cytoplasm of maize and establishes that they exist in the mitochondrion and not as ribonucleoprotein particles associated with the mitochondrial fraction. By isolating mitochondria and incubating them in medium that supports RNA synthesis in the presence of actinomycin-D, two major labelled products, the dsRNAs LBN1 and LBN2, can be identified. A low level of incorporation of label is also found in the single-stranded forms (S/RU-RNA-a and b) suggesting that these arise from replication or transcription of the dsRNAs. The structure of these RNAs is unknown — the denaturation studies provide more questions than answers⁶.

The labelling of both the double- and single-stranded RNAs in the presence of actinomycin-D is characteristic of RNA synthesis by plant RNA-dependent RNA polymerase, an enzyme of both healthy and RNA virus-infected plants⁷. In the S-cytoplasm group of maize no inclusion bodies or virus-like particles have been observed, although the nuclear genotype does influence strongly the relative abundance of these mitochondrial RNAs⁵.

The available evidence demonstrates that these RNAs are not causally linked to the S male-sterile phenotype in maize as they are present in at least two fertile cytoplasm, nor are they associated with the presence of specific mitochondrial plasmids^{5,6}.

Because they are not related to other mitochondrial sequences it is probable that these intramitochondrial RNA replicons have an exogenous origin. Many plant viral infections are associated with the organelles, therefore these RNAs could be relics of RNA virus infections or an abortive infection where the whole or part of the viral RNA genome has been sequestered by the mitochondrion and is now being maintained by the plant RNA-dependant RNA polymerase. These RNA replicons constitute a further unusual feature of plant mitochondria in addition to the plethora of circular and linear DNA plasmids which exist and which are unrelated to the mitochondrial genome. □

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