Expression of Yeast L-A Double-Stranded RNA Virus Proteins Produces Derepressed Replication: a ski^- Phenocopy

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The plus strand of the L-A double-stranded RNA virus of Saccharomyces cerevisiae has two large open reading frames, ORF1, which encodes the major coat protein, and ORF2, which encodes a single-stranded RNA-binding protein having ^a sequence diagnostic of viral RNA-dependent RNA polymerases. ORF2 is expressed only as ^a Gag-Pol-type fusion protein with ORF1. We have constructed ^a plasmid which expresses these proteins from the yeast PGK1 promoter. We show that this plasmid can support the replication of the killer toxin-encoding M_1 satellite virus in the absence of an L-A double-stranded RNA helper virus itself. This requires ORF2 expression, providing ^a potential in vivo assay for the RNA polymerase and single-stranded $RNA-binding activities of the fusion protein determined by ORF2. ORF1 expression, like a host ski^- mutation,$ can suppress the usual requirement of M₁ for the $MAX11$, $MAX18$, and $MAX27$ genes and allow a defective L-A (L-A-E) to support M_1 replication. These results suggest that expression of ORF1 from the vector makes the cell a ski⁻ phenocopy. Indeed, expression of ORF1 in a wild-type killer makes it a superkiller, suggesting that a target of the SKI antiviral system may be the major coat protein.

Saccharomyces cerevisiae carries three double-stranded RNA (dsRNA) viruses (35, 36), several retroviruses (2), and ^a single-stranded circular RNA virus (21a). The plus strand of the 4.5-kb L-A dsRNA virus has two open reading frames (19). The ⁵' open reading frame ORF1 encodes the 80-kDa major coat protein (5, 18, 19), and a combination of ORF1 and the ³' ORF2 encodes the 180-kDa Gag-Pol fusion protein (Fig. 1) (13, 19). The C-terminal domain of the fusion protein has single-stranded RNA (ssRNA)-binding activity (13) and an amino acid sequence pattern diagnostic of viral RNAdependent RNA polymerases (19). Within the 130-bp overlap of ORF1 and ORF2 is a "slippery site" at which ribosomal frameshifting occurs (5a, 19) by a mechanism similar or identical to that described for retroviruses in forming their Gag-Pol fusion proteins (17, 20, 21).

In addition to providing these proteins for its own replication, L-A can support one of several satellite dsRNA viruses, called M_1 , M_2 , etc., each of which encodes a secreted protein toxin and immunity to that toxin (reviewed in references ³ and 36). L-A can also support the replication of smaller deletion mutants derived either from L-A itself or from M_1 (8, 9). While L-A particles contain only one L-A dsRNA molecule per particle, those containing a satellite genome (M or ^a deletion mutant of M or L-A) contain one to eight dsRNA molecules per particle. In each case, the plus strand is the species packaged to form new particles and replication occurs until the particle is full ("head-full replication"). Then new plus strands are all extruded from the particles (6, 8, 10-12).

The yeast SKI genes are an antiviral system that are essential for host growth at high and low temperatures only in the presence of M dsRNA $(7, 23, 24, 26, 27)$. The SKI proteins repress replication of M_1 , M_2 , L-A, and L-BC dsRNAs (1, 24, 27) as well as the single-stranded circular 20S RNA virus of yeast (21a).

The interactions of L-A and its natural variants with the M satellite genomes have been studied genetically. A variant of L-A (L-A-E) unable to support M_1 or M_2 in a wild-type host has been previously described (24, 25, 33). L-A-E can, however, support M in a ski^- host. This defect can be complemented from a normal L-A, and this activity is called [HOK] (helper of killer) or just H, as in L-A-H (24, 39). $[NEX]$ (or N) is another L-A trait $(15, 33, 34)$.

Replication or maintenance of M dsRNA requires the products of at least ³⁰ host genes, called MAK (maintenance of killer) genes (31, 32, 37, 38). Of these genes, only three, MAK3, MAKIO, and PET18, are needed for L-A replication (25, 39). Certain variants of L-A can bypass M_1 's usual requirement for many of the MAK gene products. This trait is called [B] (bypass), and L-As carrying it are designated L-A-B, or L-A-HNB if they have [HOK] and [NEX] activity as well (1, 27, 30). It was from such an L-A-HNB that we isolated our cDNA clone (19). M_1 's requirement for most MAK genes is also suppressed in a ski^- host (29).

In order to dissect the molecular mechanisms of expression of L-A-encoded information, L-A replication, and the L-A genetics, we have constructed an L-A expression vector and studied its biological activities. This work has led us to the hypothesis that one target of the antiviral SKI genes is the L-A major coat protein.

MATERIALS AND METHODS

Media and strains. The media used for growth of yeast and assay of the killer phenomenon were as described elsewhere (31). The yeast strains used are listed in Table 1. Escherichia coli HB101 was the host for most plasmid manipulations. E. $coli$ CJ236 (F⁺ dut ung) and MV1190 (F⁺ dut⁺ ung⁺), obtained from Bio-Rad, were used for oligonucleotide-directed, site-specific mutagenesis by following the Bio-Rad Mutagene kit instructions.

Construction of mutable L-A expression vector. pTIL05

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FIG. 1. Expression of coding information from L-A plus strands (modified from reference 19). ORF1 encodes the major coat protein. ORF1 and ORF2 are fused by ribosomal frameshifting to encode the 180-kDa minor viral coat protein. IRE, Internal replication enhancer.

(19) is the Bluescript vector SK^+ with the entire L-A sequence (except for 8 bp at the ³' end that are downstream of the coding region) inserted in the SmaI site. p375 is a derivative of YEpIPT (16) into which a multiple cloning site has been inserted in the unique EcoRI site (15a). In order to carry out localized mutagenesis, we inserted the fl ori on a 0.52-kb Sall fragment from pDM1 (22) into the unique Sall site in the tet gene of p375, forming p12. The L-A sequence on an XhoI-Sstl fragment from pTIL05 was inserted between the XhoI and SstI sites of p375 and of p12, forming pTIL131 (pORF1+2) and pI2L2, respectively. From pTIL131 a NotI fragment that included nearly all of ORF2 (from base 2580 of

FIG. 2. Plasmid for expressing L-A-encoded proteins in S. cerevisiae.

the L-A plus strand to the ³' end) was removed. The remaining plasmid was ligated to form pTIL141 (pORF1). M2, M10, and Mll were constructed by oligonucleotidedirected localized mutagenesis of pI2L2 (Table 1).

Testing for suppression of *mak* mutations. Plasmids were introduced into trpl mak hosts, and then L-A and M_1 were introduced by cytoduction using the karl mutant defective in nuclear fusion (4). When a karl strain mates, binucleate cells carrying the cytoplasmic elements (viruses, mitochondria, etc.) of both parents are formed. The nuclei fail to fuse and separate at the next cell division. When a karl strain carrying L-A, M_1 , and mitochondrial DNA ([rho^+]) is used to mate with a mak M-o $[rho^0]$ strain, the net effect is to transfer cytoplasmic elements from the karl parent (called the donor) to the mak parent (called the recipient). Cytoductions were performed as described previously (39), except that cytoduction mixtures were plated on media that simultaneously selected for retention of the plasmid and against the cytoduction donor.

RESULTS

L-A expression vector. The expression vector, p375, has the PGK1 promoter, a multiple cloning site, the 2μ m DNA replication origin, the yeast TRP1 gene, and pBR322 sequences. In order to be able to do site-directed mutagenesis and express the mutated L-A sequence in yeast cells, we inserted the fl origin of replication into the yeast expression vector p375 (Fig. 2). The L-A sequence was inserted between the PGK1 promoter and the 2μ m DNA terminator to make $pORF1+2$ ($pTIL131$).

[HOK] activity requires only ORF1. To test whether the L-A information was being expressed, pORF1+2 was put into a $S\chi I^+$ L-o strain, and the transformants were crossed with a ski2-2 L-A-E M_1 strain (Table 2). The diploids formed were $S K I^+$ and would have lost M_1 if L-A information had not been expressed from the clone, since L-A-E is defective in its ability to maintain M_1 . However, the diploids were all stable killers as long as selection for the expression plasmid pORF1+2 was maintained. Allowing the plasmid to be lost by growth on nonselective medium showed that loss of the L-A expression plasmid resulted in the loss of M_1 . Thus, $pORF1+2$ has [HOK] activity, the ability to provide M_1 with the helper function that is deficient in the natural variant L-A-E. The same result was obtained when pORF1 was used instead of pORF1+2, indicating that the ssRNA-binding RNA polymerase domain (ORF2) is not necessary for [HOK]. When we introduced an ochre mutation in place of amino acid 20 of ORF1, the resulting plasmid (p ORFloc+2) had no [HOK] activity, indicating that the protein encoded by ORF1 and not just the RNA was essential for [HOK]. As expected, introducing an ochre mutation in ORF2 in place of the third amino acid after the end of ORF1 (pORF1+2oc) did not interfere with [HOK] activity.

[B] activity requires only pORF1. Certain isolates of L-A, called L-A-HNB and including that from which our cDNA clone was isolated, make several MAK genes, such as $MAX11$, dispensable for $M₁$ replication or maintenance (30). When $pORF1+2$, $pORF1$, and $p375$ (vector alone) were transformed into a makl1-1 strain and L-A-HN and M_1 were then introduced by cytoduction, the same pattern as for [HOK] activity was seen, namely, only ORF1 was needed for [B] activity and ORF1 RNA was not sufficient; an ochre mutation early in ORF1 prevented expression of [B] from the vector (Table 3).

pORFi suppresses makl8 and mak27 mutations. While many mak mutations are suppressed by L-A-HNB (1), mutations in mak18 and mak27 are among those which are not suppressed. We found, however, that expression of L-A proteins from pORF1+2 or from pORF1 suppress both makl8 and mak27 mutations (Table 4). These results could suggest that the MAK18 and MAK27 products are concerned with the expression of L-A proteins, particularly the major coat protein encoded by ORF1. Alternatively, since makl8 and *mak27* mutations are suppressed by *ski* mutations, these results could mean that expression of pORF1 makes the cells a ski^- phenocopy.

pORFl makes cells superkillers. Introduction of pORFi into the wild-type killer strains 2604 and 2928 made them

TABLE 2. [HOK] requires only ORF1 protein^a

Plasmid	Insert	Characteristics of diploids formed by crossing with:		
		4219-2A (ski2-2 $L-A-E M_1$	4219-2C (ski2-2 $L-A-E M_1$	
None p375 pTIL131 pTIL141 M ₁₀ M11	None None $ORF1 + ORF2$ ORF1 ORFloc + ORF2 $ORF1 + ORF2oc$	All K^- All K^- All K^+ All K^+ All K^- All K^+	All K^- All K^- All K^+ All K^+ All K^- All K^+	

^a Plasmids were transformed into strain 2966 (L-A-o M-o), and transformants were mated with the $ski2-2$ L-A-E M_1 strains. Finding that all diploids were killers (K^+) indicated that the plasmid was expressing [HOK] activity. At least 10 diploid single colonies were isolated on plates lacking $Trp (-Trp)$ to ensure retention of the plasmid and tested for \tilde{K}_1 . Subcloning on YPAD resulted in frequent loss of the expression plasmid and concomitant loss of M₁. Subcloning on -Trp plates of diploids carrying pTIL131 or pTIL141
yielded only K⁺ single colonies. K⁻, Nonkiller.

Donor charac- teristics ^a	Recipient characteristics ^b	Characteristics of cytoductants	No. of cyto- ductants
$L-A-HN M$	$mak11-1$ L-A-HN	All K^-	>500
L -A-HNB M_1	$makII-I L-A-HN$	All K^+	15
$L-A-HN M_1$	$mak11-1$ L-A-HN p375 (vector)	All K^-	>30
$L-A-HN M1$	$mak11-1$ L-A-HN pORF1+ORF2	All K^{+c}	20
L -A-HNB M_1	mak11-1 L-A-HN pORF1+ORF2	All K^+	>15
$L-A-HN M$,	mak11-1 L-A-HN pORF1	All K^{+c}	
$L-A-HNB$ $M1$	mak11-1 L-A-HN pORF1	All K^+	>15
$L-A-HN M_1$	$mak11-1$ L-A-HN pORF1+2oc	All K^+	>20
$L-A-HN M$	$mak11-1$ L-A-HN pORF1oc+2	All K^-	>20

TABLE 3. [B] requires ORF1 only

^a Cytoduction donors were strains 1101 (L-A-HN M_1) and 1368 (L-A-HNB M_1).

^b Cytoduction recipients were strain 2128 (makl^l -I L-A-HN M-o) carrying one of the L-A expression plasmids. Cytoductions were done on SD agar containing His and uracil to keep in the L-A expression plasmid and plated on SD agar containing uracil to select against donor cells and retain the plasmid.

Subcloning these cytoductants on $-Trp$ plates to retain the plasmid produced only K^+ subclones. Subcloning on YPAD to allow loss of the L-A expression plasmid produced only K^- and a few weak killer (K^w) subclones.

superkillers, as judged by their zone of killing of a sensitive strain at 30°C. In contrast, the vector p375 or the vector pORFloc+2, which has an ochre mutation early in ORF1, had no such effect.

 $mak10-1$, but not mak3-1, is suppressed by $pORF1+2$. The MAK3, MAKIO, and PET18 genes are needed for L-A replication (25), although Toh-e and Sahashi (28) have shown that PET18 is needed only at temperatures above 30°C. The loss of M_1 by *makl0-1* strains was suppressed by $pORF1+2$, as shown by both meiotic crosses (Table 5) and cytoduction experiments (Table 6). However, pORFi did not detectably suppress $mak10-1$. To determine whether $pORF1+2$ allowed replication in the maklO-J host of the L-A virus itself, the mak10-1 pORF1+2 M_1 strains (Table 6) were mated with either of two trpl mak3 L-A-o strains (1717 and 1720) and the diploids were examined to determine whether they were killers before and after mitotic loss of pORF1+2. Since the mak3 and mak10 mutations complement each other, and since mak3 mutants lack L-A, the diploids, after loss of $pORF1+2$, are expected to be killers only if $pORF1+2$ allows replication of L-A in the mak/O host. In each case, all

TABLE 4. Suppression of mak27-1 and makl8-1 by pORF1 or pORF1+2

Donor characteristics $(karl-1)^a$	Recipient characteristics ^b	Cvtoductant characteristics	
$L-A-HN M_1$	mak27-1	All K^-	
$L-A-HNB M_1$	mak27-1	All K^-	
$L-A-HN M_1$	$mak27-1 pORF1+2$	All K^{+c}	
L -A-HNB M_1	$mak27-1 pORF1+2$	All K^+	
$L-A-HN M$	$mak27-1$ pORF1	All K^{+c}	
L -A-HNB M_1	mak27-1 pORF1	All K^+	
$L-A-HN M_1$	mak18-1	All K^-	
$L-A-HN M_1$	$mak18-1$	All K^-	
$L-A-HN M_1$	mak18-1 p375	All K^-	
L -A-HN M_1	mak18-1 pORF1	All K^{+c}	
$L-A-HN M_1$	$mak18-1 pORF1+2$	All K^{+c}	

 a Cytoduction donors were strains 1101 and 1074 (L-A-HN M_1) and strains 1368 and 2629 (L-A-HNB M_1).
 h_2 The mak27-1 recipient was

The mak27-1 recipient was strain 2057, and the mak18-1 recipient was strain 3012.

 c Four cytoductants from each of these cytoductions were subcloned on $-$ Trp plates, and all were stably K⁺. Subcloning the same cytoductants on YPAD plates showed that all Trp⁻ mitotic segregants had become K⁻, showing that the suppression of mak27-1 or of mak18-1 depended on the L-A expression plasmid.

diploids were stable killers while pORF1+2 was present and nonkillers when pORF1+2 was lost. The same result was obtained by examination of isolated viral particles for L-A dsRNA by Northern (RNA) blot hybridization (Fig. 3). This shows that pORF1+2 did not allow the replication of L-A-HN in the the makJO background and suggests that MAKIO is needed for the replication or maintenance of L-A independent of the supply of L-A-encoded proteins. Even though the proteins are being supplied in amounts sufficient for M_1 , L-A cannot replicate. This result also indicates that $M₁$ does not need the L-A genome itself for its replication but needs only the products of L-A. It also suggests that the MAKIO product is not necessary for the translation of L-A products. These results also show that pORF1+2 can maintain M_1 in a wild-type host. In contrast, crosses carried out with $mak3-1$ and $pORF1+2$ showed no evidence of suppression (Table 5).

DISCUSSION

We report the establishment of an expression system for the information encoded by the L-A dsRNA virus of yeast. That both open reading frames are in fact expressed from this clone is shown by its maintenance of M_1 in a makl0 strain (or in a wild-type strain) in the absence of the L-A dsRNA genome, an activity dependent on both ORF1 and ORF2. This activity proves that our clone of L-A encodes biologically active proteins. That our sequences of three complete independent cDNA clones of L-A were, except for a single nucleotide, in complete agreement with each other also supports this conclusion (19).

Using this expression system, we have begun to examine the molecular basis of several phenomena we have previously described. L-A-E can support M_1 only in a ski⁻ host defective in the antiviral system. [HOK] is the ability of many L-A isolates to supplement L-A-E in supporting M_1 in a wild-type host. That [HOK] activity is expressed from pORF1+2 and requires only ORF1, which encodes the major coat protein, indicates that the defect in L-A-E is in the major coat protein and is either qualitative or quantitative. L-A-E must, however, be supplying the fusion protein. Since [HOK] is needed only in a $SKI⁺$ host, this suggests that one function of the major coat protein is to protect M_1 (and presumably L-A as well) from the SKI antiviral system.

[B] is the ability of certain L-A natural variants (called L-A-HNB) to support M_1 in certain *mak*⁻ hosts from which it would otherwise be lost. [B] suppresses many mak muta-

TABLE 5. pORF1+2 suppresses mak10-1 but not mak3-1

Parents	Segregation ^{a}	No. of tetrads
1717 (mak3-1 L-oM-o) \times 4224-8B (pORF1+2 L-A-E M ₁)	$2K^-:2K^+$	10
2956 (<i>mak10-1</i> L-oM-o) \times 4224-8B (pORF1+2 L-A-E M ₁)	$4K^+:0$	
2957 (mak10-1 L-oM-o) \times 4224-5A (pORF1+2 L-A-E M ₁)	$4K^{+}$:0	12
2604 (L-A-HN M_1) \times 2955(pORF1+2) (<i>mak10-1</i> L-o pORF1+2)	$4K^{+}$:0	
2604 (L-A-HN M_1) \times 2955(pTIL141) (<i>mak10-1</i> L-o pORF1)	$2K^{+}$:2K ⁻¹	

^a All crosses were carried out, diploids were sporulated, tetrads were dissected, and spores were germinated in the absence of tryptophan in order to insure the continued presence of pTIL131. The dependence of M_1 in the segregants on pTIL131 was demonstrated by streaking each spore clone of three tetrads of the cross $2957 \times 4224-5$ A on either $-Trp$ plates or on YPAD plates. All the single colonies on $-Trp$ plates were killers, while all those on the YPAD plates were either nonkillers⁻ or weak killers.

FIG. 3. Maintenance of M_1 but not L-A in a *makl0-l* strain by pORF1+2. Viral particles were prepared as previously describe d(6, 8, 13, 14) from stationary-phase cells of strain 2955(pORF1+2) which L-A-HNB and M_1 from strain 2629 had been cytoduced. The final step in the purification was a CsCl gradient. RNAs were extracted from each fraction of the gradient and analyzed on a nondenaturing agarose gel. Ethidium bromide staining of the gel is shown in the upper panel. The the RNAs were denatured in the gel, blotted onto a nylon sheet, and hybridized with a 34 P-labeled L-A-specific probe. An autoradiogram of the sheet is shown in the lower panel. Lanes 1 to 14 are the CsCl gradient fractions, with lane 1 being the bottom fraction and lane 14 being the top fraction. Lanes and L-A show λ HindIII markers and purified L-A dsRNA, respectively. The positions of L-A and M_1 dsRNAs are shown as L and M_1 , respectively, on the right. Note that there are two types of M_1 viral particles (6); one, which contains two M_1 dsRNA molecules per particle (M_1-H) , forms a band at fraction 4, and the other, which contains one M_1 dsRNA molecule per particle (M_1-L) , forms a band at fraction 7. The expected density of mature L-A particles is th at of fraction 3. The dsRNA with the same mobility as that of L-A seen throughout the gradient is L-BC.

tions but not makl8-1 or mak27-1. The expression of [B] from our cDNA clone requires only ORF1. Furthermore, the same pORF1 suppresses at least two *mak* mutations not normally suppressed by [B] (Table 7). That pORF1 suppresses mutations in many MAK genes is consistent with the notion that these genes are concerned with the efficiency of L production of the major coat protein from L-A transcripts. Alternatively, since these mak mutations are also those which are suppressed by *ski* mutations, they could be involved in M_1 's defense against the *SKI* antiviral system or be one of the actual targets of the SKI system.

A unifying hypothesis to explain the interactions of [HOK], [B], pORF1, MAK genes, and SKI genes. The SKI products reduce the copy numbers of M_1 , M_2 , L-A, and L-BC dsRNAs, and this function is essential or at least important for cell growth, depending on the temperature and other cytoplasmic elements in the strain (7, 24, 27). However, the precise target of SKI gene action is not yet known. L-A-E's defect in maintaining M_1 is suppressed by ski mutations or by supplying major coat protein from a normal L-A ([HOK] function) or from pORF1. This is consistent with the major coat protein being the target of the SKI antiviral system or L with the coat protein protecting the actual target (genomic RNA?) from the SKI system. L-As carrying [B] make many M_1 MAK genes dispensable for M_1 , and the same L-A maintains M_1 at a higher-than-normal copy number (30). Here we show that pORF1 is sufficient for [B] and for the suppression of two mak mutations not suppressed by [B]. However, all the mak mutations suppressed by pORF1 are suppressed by ski mutations. If the target of the SKI system were the major coat protein, then its overproduction by pORFi might swamp the SKI system, making the cell a ski phenocopy.

TABLE 6. L-A expression vectors allow M_1 replication in a mak10-1 strain

Characteristics of donor strain $2629 (karl-l)$	Characteristics of recipi- ent strain 2955rho ⁰	Killer phenotype of cytoductants ^a		
L-A-HNB M.	$mak10-1$	All K^-		
L-A-HNB M ₁	mak10-1 p375	All K^-		
L-A-HNB M.	$mak10-1 pORF1+2$	All K^+		
L-A-HNB M.	$mak10-I$ pORF1	All $K-$		
L-A-HNB M,	mak10-1 pORF1fus2	$All K-$		
L-A-HNB M.	$mak10-1$ pORF1oc+2	All $K-$		
L-A-HNB M-	$mak10-1$ pORF1+2oc	All $K-$		

^a Cytoduction mixtures were plated on media selecting against the cytoduction donor and for retention of the L-A expression plasmid. Clones were tested for growth on minimal medium (to screen out diploids), for growth on glycerol plates (to identify clones that had received donor cytoplasm), and for killing of a sensitive strain. At least 10 cytoductants from each cytoduction were scored.

Trait	Definition		Suppression by:		
		ski ⁻	pORF1	$pORF1+2$	
[B]	Ability of an L-A to make $MAXII$ dispensable for $M1$ replication				
[HOK]	Ability of an L-A to complement defective L-A-E in supporting M_1 in a $S K I^+$ host				
mak18, mak27	Lose M_1 but not L-A or L-BC				
mak10	Lose M_1 and L-A but not L-BC				
mak3	Lose M_1 and L-A but not L-BC				

TABLE 7. Comparison of effects of pORF1, pORF1+2, and ^a ski mutation

This would have the effect of suppressing many *mak* mutations and allowing L-A-E to support M_1 replication.

In fact, introduction of pORF1 into a wild-type killer strain makes it a superkiller, as predicted by this model. This finding is most easily explained if the major coat protein is the target or the first molecule recognized by the SKI products. Supplying an excess of this target would titrate out the SKI products, allowing unrestrained replication of M_1 , and all of the genetic consequences of the cell's being skiwould follow. L-A-B could be interpreted, in accord with this model, as a variant of L-A that produces more major coat protein and as a result has a partial Ski⁻ phenotype. L-A-B both suppresses some (but not all) of the mak mutations suppressed by ski mutations and produces a partial superkiller phenotype (with larger killing zones and higher M_1 copy number than wild-type strains). An alternative model would have the excess of major coat protein providing better protection of M_1 from the SKI products.

pORF1+2 support of M_1 in a mak10-1 host provides an in vivo assay for ORF2 functions. $pORF1+2$ supported M₁ replication in a maklO-1 host. Both genetic and biochemical tests showed that L-A was lost from the strain. Subsequently making the strain MAK^+ by mating it with a mak3 strain produced wild-type cells in which pORF1+2 was maintaining M_1 in the absence of L-A. This indicates that M_1 depends on the products of L-A for its replication but not on the presence of a replicating L-A genome. Moreover, M_1 does not directly require the MAKIO product for its replication; MAKIO is needed only because L-A products are needed and L-A needs $MAX10$. Since pORF1 did not support M₁ in a makl0-1 host, M_1 needs both ORF1 and ORF2. An ochre mutation early in ORF1 and an ochre mutation in ORF2 just after the end of ORF1 both eliminate the ability of pORF1+2 to maintain M_1 . This provides a simple in vivo assay for the activity of ORF2 which can be used to study the role of the RNA polymerase consensus sequence in ORF2 (19) and the ssRNA-binding activity of ORF2 (13).

That pORF1+2 allows M_1 , but not L-A, to replicate in a mak10 host points again to the distinction between the mechanisms of replication of the L-A replicon and those of its satellites, M_1 , M_2 , and X (a deletion mutant of L-A). Biochemical studies indicate that both follow the same replication cycle, except for the head-full replication mechanism shown by the smaller replicons, the fact that M_1 and X require many MAK genes not needed by L-A, and the fact that M_1 and X must borrow coat proteins synthesized by L-A. pORF1+2 also supports M_1 in a wild-type host (in the absence of L-A), showing that this is not a phenomenon peculiar to mak10 strains. Previous studies of L-A replication in a makl 0^{ts} host showed that L-A dsRNA-containing particles were unstable, although L-A ssRNA particles were apparently unaffected (11). If that difference were due to the L-A dsRNA-containing particles being full while the L-A ssRNA-containing particles were not, then the present results would not be unexpected. This is consistent with the MAK10 product being essential for the stability of full viral particles but not for that of particles that are only partially filled.

While pORF1+2 supported M_1 in a *mak10* host, it did not do so in ^a mak3 host. This suggests that the MAK3 product is more directly needed for M_1 replication, not simply through its being needed for L-A as in the case of MAKIO.

The availability of a complete, expressed clone of L-A makes possible the detailed dissection of the role of L-Aencoded proteins in the replication process and in interaction with satellite genomes and with the host. Since viral plus strands are the species packaged to make new viral particles, plus strands made from the vector with the correct ends should replicate. This "launching" of L-A from the vector should allow its use as an RNA virus expression vector.

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