# MINI-REVIEW

 $F.$  Meinhardt  $\cdot$  R. Schaffrath  $\cdot$  M. Larsen Microbial linear plasmids

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Abstract While plasmids were originally considered to be generally *circular* until almost two decades ago, *linear* elements were reported to exist as well. They are now known to be common genetic elements in both, pro- and eukaryotes. Two types of linear plasmids exist, the socalled hairpin plasmids with covalently closed ends and those with proteins bound to their 5' termini. Hairpin plasmids are common in human-pathogenic Borrelia spirochetes, in which they are instrumental in escape from the immunological response; cryptic hairpin elements are present in mitochondria of the plant pathogenic fungus Rhizoctonia solani. Plasmids with 5' attached proteins constitute the largest group. In actinomycetous bacteria they are conjugative and usually confer advantageous phenotypes, e.g. formation of antibiotics, degradation of xenobiotics, heavy-metal resistance and growth on hydrogen as the sole energy source. In contrast, the majority of linear plasmids from eukaryotes are cryptic, with only a few exceptions. In some yeasts a killer phenotype may be associated, the most thoroughly investigated elements being those from Kluyveromyces lactis killer strains. In Neurospora spp. and in Podospora anserina, senescence and longevity respectively are correlated with linear plasmids. This review focuses on the biology of linear plasmids, their environmental significance and their use as tools in molecular and applied microbiology.

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## Introduction

During replication, any linear DNA molecule faces a severe problem: in contrast to covalently closed circular DNA it requires specific mechanisms to circumvent progressive shortening during each replication round. In eukaryotes, chromosome shortening is prevented by the ribonucleoprotein enzyme telomerase, which compensates for reduction of the termini by repeatedly adding short sequence motifs (telomeric repeats) to the ends of the chromosomes. It is regulated such that telomeric DNA lengths are kept within defined bounds (McEachern and Blackburn 1995). However, the termini of both pro- and eukaryotic extrachromosomal linear DNA are different from those of telomeres. Microbial extrachromosomal linear DNA elements either carry covalently closed ends (hairpins) or proteins covalently attached to both 5<sup> $\prime$ </sup> ends, similar to viral and phage genomes.

Linear plasmids were detected only some 20 years ago, the relatively late discovery being partly due to the fact that they are not regularly present but are associated with specific strains, such as kalilo in Neurospora intermedia (Bertrand et al. 1985) or pAL2-1 in Podospora anserina (Hermanns and Osiewacz 1996). In eukaryotes, most of them are associated with mitochondria and, in addition, the presence of 5' covalently attached proteins resulted in removal of the plasmids along with deproteinization steps routinely applied in isolation procedures. Many giant linear plasmids could only be detected when nucleic acid samples were submitted to pulsed-field gel electrophoresis, which was developed and frequently applied only a decade ago.

Hairpin plasmids

*Borrelia* spirochetes  $-$  among them the agents causing relapsing fever, B. hermsii and Lyme disease, B. burg $dorferi - have linear chromosomes approximately$ 1000 kbp in size. In addition, they harbour numerous

circular and linear plasmids, which can comprise onethird of the total genome. Their linear plasmids as well as their chromosomes have short terminal inverted repeats (TIR) and covalently closed hairpin loops at both termini (Barbour and Garon 1987; Hinnebusch and Barbour 1991). For further details see a review by Girons et al. (1994).

The genes for major surface proteins, namely  $ospA$ and ospB of B. burgdorferi and the vmp gene family of B. hermsii are located on linear plasmids. Two of the linear plasmids of B. hermsii each carry a nonexpressed *vmp* gene coding for a variable major surface protein. On an additional plasmid, one copy of these genes is governed by an expression signal. Recombination between the *vmp* genes located on the different plasmids causes antigenic variation, allowing the bacterium to escape the immunological response of its host (Plastkerk et al. 1985). The mitochondria of an isolate of the phytopathogenic fungus Rhizoctonia solani were reported to contain short linear plasmids (2.7 kbp) that have hairpin loops and TIR at both ends (Hashiba et al. 1984; Miyashita et al. 1990). It has been postulated that these plasmids might be instrumental in determining avirulence or virulence (Hashiba et al.1984; Hashiba 1987; Hongo et al. 1994). Meanwhile, the occurrence of small linear extrachromosomal elements, ranging in size from 2.2 kbp to 7.0 kbp, seems common in R. solani, because plasmids were found in a great number of randomly chosen isolates (Miyasaka et al. 1990; Jabaji-Hare et al. 1994). The fact that plasmid-containing strains were as virulent as plasmid-less isolates indicated that plasmids do not play a role in pathogenicity (Jabaji-Hare et al. 1994). These findings are supported by extensive investigations, conducted in various laboratories in Canada, Spain and Japan (for details see a review by Rubio et al. 1996). A replication model was proposed for Rhizoctonia plasmids by analogy to viral systems, and it involves nicking the DNA at the beginning of the loops (Miyashita et al. 1990). Recent investigations in Borrelia led to the suggestion that circular intermediates are involved in replication of linear hairpin plasmids. Circularization occurs presumably by the cutting of opposite strands at identical positions close to the TIR, followed by unfolding and hybridization of the terminal inverted repeats. The same mechanism, acting in reverse, converts the circular molecules back to linear elements (Ferdows et al. 1996).

### Linear plasmids with 5<sup>'</sup> attached polypeptides

DNA plasmids with proteins covalently linked to their 5'ends constitute the largest group of extrachromosomal linear elements. Along with viruses having structurally similar linear genomes and with transposons they are also known as invertrons (Sakaguchi 1990). Linear plasmids of this kind exist in bacteria, particularly in Actinomycetes; in plants and fungi they are located in organelles, usually in mitochondria (reviewed by Meinhardt et al. 1990; Meinhardt and Rohe 1993; Griths 1995). Yeast linear plasmids, however, are located in the cytoplasm (reviewed by Stark et al. 1990; Gunge et al. 1995). Figure 1 shows examples of linear plasmids representing the different types.

Besides linearity and 5' attached proteins, all elements have terminal inverted repeats, varying in size from 44 bp in SLP2 of Streptomyces lividans (Chen et al. 1993), 95 kbp in pPZG 101 in Streptomyces rimosus (Gravius et al. 1994). Since the structure of linear plasmids is reminiscent of adenoviruses and linear phages, a viral mode of replication via protein priming has repeatedly been suggested (Paillard et al. 1985; Meinhardt et al. 1986; Sakaguchi 1990). Replication is initiated by covalent attachment of a deoxynucleotide monophosphate moiety to a free molecule of terminal protein, thereby providing the -OH group necessary to start polymerization. By forming a complex with the viral DNA polymerase the charged terminal protein binds to the TIR, allowing DNA synthesis to start. Unidirectional 5' to 3' DNA chain elongation results in

Fig. 1 Schematic representation of a selection of linear plasmids with 5<sup>'</sup> attached proteins. Arrows open-reading frames; directions correspond to the orientation of the respective gene. Black triangles the terminal inverted repeats; black circles terminal proteins. (References: pSCL1: Wu and Roy 1993, pClK1: Oeser and Tudzynski 1989, pGKL1: Hishinuma et al. 1984, Stark et al. 1984, pGKL2: Tommasino et al. 1988)



displacement of the parental strand. The displaced strand forms a panhandle-shaped structure due to hybridization of the self-complementary TIR, which then acts as the start site of a new replication round, such as occurs in adenoviruses (Desiderio and Kelly 1981), phage  $\Phi$ 29 (Hermoso and Salas 1980) or phage PRD1 (Bamford et al. 1983). Experimental evidence that replication of linear plasmids is due to a similar mechanism exists for pAI2 of the ascomycetous fungus Ascobolus immersus. It could be shown that a radioactive label was preferentially incorporated from the 5' termini (Kempken et al. 1989).

#### Prokaryotic elements

For the only linear plasmid so far reported to exist in a gram-negative bacterium (pKO2 of Klebsiella oxytoca, Stoppel et al. 1995) it is not known whether proteins are attached. No function is known either, as is also true for elements from the gram-positive Lactobacillus gasseri (Roussel et al. 1993) and Bacillus polymyxa (Rosado and Seldin 1993).

However, while in eukaryotes most linear plasmids are also cryptic (see below), a phenotype can be attributed to many bacterial elements, particularly to those from Actinomycetes (Table 1). In the nocardioform 331

genus Rhodococcus several large linear plasmids were found that confer advantageous abilities on their hosts. The genus comprises nutritionally versatile soil bacteria, many of which are known to degrade a wide array of xenobiotics, such as phenol, insecticides, acrylamines, anilines, and also halogenated alkanes. Rhodococcus sp. (MR11 and MR22), formerly designated Nocardia opaca, have the ability to grow autotrophically on hydrogen as the sole energy source. This character, denoted  $Aut^+,$ can be transferred to non-autotrophic strains and a number of other heterotrophic *Rhodococcus* species (Reh and Schlegel 1981). The ability to grow as an aerobic hydrogen bacterium is encoded on a giant linear plasmid, about 270 kbp in size. Recombination between different giant linear conjugative plasmids led to the formation of a new linear genetic element with tremendously enhanced transfer frequency (up to 1000-fold compared to the original situation; Kalkus et al. 1990, 1993).

Other members of the genus, e.g. Rhodococcus erythropolis BD2 have the ability to utilize isopropylbenzene as the sole carbon and energy source. The latter strain was shown to contain a giant linear plasmid (approx. 210 kbp); loss of the plasmid was accompanied by the loss of isopropylbenzene and trichlorethene degradation. In addition, resistance to arsenite and also mercury was shown to be plasmid-encoded in this

Table 1 Selection of microbial linear plasmids with 5' attached proteins

Organism	Plasmid	Size (kbp)	Phenotype attributed	Reference
Bacteria				
Rhodococcus sp.	pHG201	270	Autotrophy	Kalkus et al. 1990, 1993
(formerly Nocardia opaca)	pHG204	180	Thallium resistance	
	pHG205	280	Autotrophy	
Rhodococcus erythropolis	pBD2	210	Isopropylbenzene and trichlorethene catabolism, arsenite and mercury resistence	Dabrock et al. 1994; Kesseler et al. 1996
Rhodococcus fascians	pFiD188	200	Induction of fasciation	Crespi et al. 1992; 1994
Streptomyces clavuligerus	pSCL1	11.7	Cryptic	Wu and Roy 1993
Streptomyces coelicolor	SCP <sub>1</sub>	350	Methylenomycin synthesis	Kinashi et al. 1987, 1993
Streptomyces fradiae		420	Tylosin synthesis	Kinashi and Shimaji 1987
Streptomyces lasaliensis	pKSL	520	Lasalocid A synthesis	Kinashi et al. 1987
Streptomyces parvulus		520	Actinomycin D synthesis	Kinashi and Shimaji 1987
Streptomyces rimosus	pPZG101	387	Cryptic	Gravius et al. 1994
Streptomyces venezuelae		130	Chloramphenicol synthesis	Kinashi and Shimaji 1987
Yeasts				
Debaromyces hansenii	pDHL1	8.4	Associated with osmotolerance	Gunge et al. 1993
	pDHL2	9.2		
	pDHL3	15.0		
Kluvveromyces lactis	pGKL1	8.9	Killer	Gunge et al. 1981
	pGKL2	13.5		
Pichia acaciae	$p$ Pac $1-1$	13.6	Killer	Worsham and Bolen 1990
	$p$ Pac <sub>1</sub> -2	7.3		
Pichia inositovora	pPin11	18	Killer	Ligon et al. 1989
	pPin12	13		
	pPin13	10		
Saccharomyces kluyveri	pSKL	14.2	Cryptic	Hishinuma and Hirai 1991
Filamentous fungi				
Claviceps purpurea	pCLK1	6.8	Cryptic	Oeser and Tudzynski 1989
Neurospora crassa	Maranhar	7.1	Senescence	Court et al. 1991
Neurospora intermedia	Kalilo	9.0	Senescence	Bertrand et al. 1985, 1986
Podospora anserina	$pAL2-1$	8.4	Longevity	Hermanns and Osiewacz 1996

bacterium (Dabrock et al. 1994). Conjugational transfer to a cured strain restored the resistance as well as the degradation abilities.

R. fascians is a phytopathogenic representative of the genus, which induces fasciation, i.e. leafy galls, on dicots and several monocots. Strain D188 was reported to contain a conjugative, 200-kbp linear plasmid. Cured strains were avirulent, but virulence was restored by reintroduction of the linear 200-kbp plasmid by conjugation. It was proven that at least three virulencerequiring regions (*fas*, fasciation; *att*, attenuation;  $hvp$ , hypovirulence) are located on the plasmid (Crespi et al. 1992, 1994). The fact that all virulent strains of  $R$ . fascians, so far investigated, contained similar linear genetic elements may indicate that the conjugative ability of linear plasmids facilitates their dissemination amongst the genus and other related actinomycetes.

Linear plasmids of the gram-positive genus Streptomyces range in size from approximately 12 kbp to several hundred kbp (see Table 1). The replication mode of Streptomyces linear replicons was shown to be different from the strand-displacing mechanism outlined above for the adenoviral and phage systems. DNA synthesis of pSLA2, a 17-kbp linear plasmid of Streptomyces rochei occurs by bidirectional replication extending outward from a centrally located origin toward the ends of the plasmids (Chang and Cohen 1994). Since the chromosomes of several Streptomyces spp. are also linear with proteins and highly conserved inverted repeats at their termini (Lin et al. 1993), a similar replication mode was suggested. Support for this assumption came from experiments in which the linear S. lividans chromosome was circularized by joining both ends either by artificial targeted recombination or by spontaneous deletion spanning both inverted repeats (Lin et al. 1993).

Large plasmids, commonly over 50 kbp in size, are often referred to as giant linear plasmids; some of these have known phenotypes, and they particularly carry antibiotic biosynthesis genes (see Table 1). Irrespective of whether actinomycete linear plasmids contribute to the formation of antibiotics or not, all linear plasmids detected so far are conjugative (Hopwood and Kieser 1993). In addition, Streptomyces conjugative plasmids (linear and circular) are associated with pocks, macroscopically visible, circular areas of retarded growth that develop around colonies growing from individual plasmid-carrying spores seeded in a lawn of plasmid-free spores.

Conjugation provides bacteria with the ability for horizontal gene transfer, which is in most cases limited to one species or at least to closely related organisms. Among Actinomycetes, i.e. Rhodococcus and Streptomyces, there are several lines of evidence that conjugative transfer of DNA might cross the species barrier. Plasmid pBD2 of Rhodococcus erythropolis carries genes for isopropylbenzene and 3-isopropylcatechol dioxygenases, which exhibit a  $55\% - 78\%$  identity to analogous enzymes from gram-negative bacteria (Dabrock et al. 1994; Kesseler et al. 1996). The corresponding enzymes of the gram-negative bacteria all contain the same type of redox components and are functionally and evolutionarily related (Mason and Cammack 1992). Mating is possible between different Streptomyces species. Transfer of DNA was observed in combinations of S. bambergiensis and S. lividans, the latter contained a 42-kbp linear conjugative plasmid that is derived from a giant linear 640 kbp plasmid (pSB1) of the former (Zotchev et al. 1992). The linear plasmid SLP2 could be transferred from S. lividans to S. coelicolor and S. parvulus and vice versa. Consistent with these results is the fact that the inverted terminal repeats of many Streptomyces linear plasmids are almost identical (Chen et al. 1993). It is not yet clear whether plasmid-mediated conjugation is as promiscuous as that brought about by conjugative transposons of the gram-positive bacteria (Scott and Churchward 1995); however, actinomycetous soil bacteria may have the ability to share  $-\nu$  via conju $gation - useful genetic material, such as heavy-metal$ resistances, production of and resistance to antibiotics, degradation of xenobiotics, and possibly the ability to exist as a plant pathogen.

Linear plasmids of filamentous fungi

The number of eukaryotic linear plasmids with 5' attached proteins identified in various species is continuously growing, and they have been the subject of many reviews (e.g. Meinhardt et al. 1990; Meinhardt and Rohe 1993; Schründer and Meinhardt 1995a; Griffiths 1995; Kempken 1995a), to which we refer for further information. Table 1 lists a selection of elements, known to have associated phenotypes; upon request a complete list of linear plasmids reported so far is available.

In spite of the DNA sequence data available for many of them, very little is known about specific gene functions. In particular, most mitochondrial plasmids of filamentous fungi appear to be cryptic in function, thus representing selfish DNA. In general, linear plasmids of filamentous fungi and also plants appear to be simple and uniform in structure. A typical mitochondrial linear plasmid (pClK1 of Claviceps purpurea) is shown in Fig. 1. It only encodes viral-like DNA and RNA polymerases. Mitochondrial linear plasmids shown to affect their hosts, i.e. kalilo, maranhar and pAL2-1, are the exceptions of this rule. Kalilo and maranhar are involved in the control of senescence in certain strains of the genus Neurospora. It has been shown that senescence was induced by integration of a copy of the plasmids into the mitochondrial DNA and by subsequent accumulation of the defective mitochondrial genome (for details see Griffiths 1995). In contrast to *Neurospora*, longevity is induced by the integration of plasmid pAL2-1 into the mitochondrial genome of Podospora anserina (Hermanns and Osiewacz 1992; Hermanns et al. 1994). Transformation and other genetic experiments using such elements are largely hampered by their mitochondrial localization, and that is why data are rather scarce.

Nevertheless, experimental evidence exists, that mitochondrial linear plasmids can be transferred between Claviceps strains by protoplast fusion (Gessner-Ulrich and Tudzynski 1994) and even the horizontal transfer of a linear plasmid from Ascobolus immersus to Podospora anserina has recently been reported (Kempken 1995b). However, stable propagation in the new host was not possible, leading to gradual plasmid loss. In compatible pairings of Neurospora strains, plasmids can readily spread out (Debets et al. 1994). Since there is a plasmid that is closely related to the kalilo DNA in Gelasinospora, this might be indicative that even intergeneric distribution of such elements is possible (Wei et al. 1996). Thus, although evolutionary calculations suggest that these elements are descended from a common ancestor and coevolution with their hosts (Rohe et al. 1992), horizontal transfer of mitochondrially inherited linear plasmids cannot be excluded a priori (Kempken et al.1992).

### Yeast linear plasmids

A recent survey of plasmids among 1800 yeast strains covering about 600 species revealed that linear DNA plasmids can be found at a frequency of about  $1\% - 2\%$ (Fukuhara 1995). Linear plasmids of yeasts differ from all other eukaryotic plasmids in some aspects. They are located in the cytoplasm and encode additional proteins other than viral-like DNA and RNA polymerases; furthermore, some confer an advantageous phenotype on their hosts (see Table 1).

The best-characterized yeast system is the killer plasmid pair pGKL1 and -2 of the dairy yeast Kluyveromyces lactis (see Fig. 1 for the structure). Originally detected by Gunge et al. (1981), they were also described by Wesolowski et al. (1982a,b,c) and termed k1 and k2 respectively. The killer system has been the subject of a number of reviews to which we refer for further citations of the original literature (Stark et al. 1990; Schründer and Meinhardt 1995a; Gunge 1995).

Killer plasmid pGKL1 gene functions are mainly understood. Open-reading frame ORF1 codes for the plasmid-specific DNA polymerase, ORF2 and ORF4 specify subunits  $\alpha$ ,  $\beta$ ,  $\gamma$  of the heterotrimeric killer toxin and ORF3 is essential for toxin immunity. The toxin causes an irreversible arrest of sensitive yeast cells in the unbudded (G1) phase of the cell cycle (Sugisaki et al. 1983). Toxicity exclusively resides within the  $\gamma$  subunit since intracellular ORF4 expression mimicked the effect of exogenously applied native toxin (Tokunaga et al. 1990, Butler et al. 1991a). The  $\alpha$  subunit shows chitinase activity, inhibition of which by allosamidin in vivo abolishes activity of the holotoxin (Butler et al. 1991b). Since the  $\beta$  subunit is remarkably hydrophobic, both  $\alpha$ and  $\beta$  subunits are considered to be instrumental in binding and/or uptake of the  $\gamma$  subunit.

pGKL2 appears to play a fundamental role in the killer system by providing essential functions for gene expression and maintenance of both plasmids within the same cell. pGKL1 is strictly dependent on pGKL2, which carries ten genes: ORF1 is not essential for killer plasmid replication and maintenance (Schaffrath et al. 1992); ORF2 encodes the plasmid-specific DNA polymerase as well as the terminal protein of the plasmid (Schaffrath et al. 1995b; Takeda et al. 1996); no function is known for ORF3; ORF4 exhibits similarities to a viral helicase (Stark et al. 1990); ORF5 has been shown to be essential and functionally interchangeable between both plasmids and is presumably involved in plasmid stability (Schaffrath and Meacock 1995, 1996); ORF6 encodes the plasmid-specific RNA polymerase, considered to be instrumental in transcription of both plasmids (Schaffrath et al. 1995a, b); ORF7 might encode a subunit of the latter (Schaffrath et al. 1997); for ORF8 and ORF9 functions are not known; ORF10 encodes TRF1, a terminal recognition factor, likely to be involved in plasmid replication initiation (Tommasino 1991; McNeel and Tamanoi 1991).

When artificially transferred to different yeast species, such as Saccharomyces cerevisiae, Kluyveromyces fragilis and Candida pseudotropicalis, the killer plasmids are stably maintained and confer the killer phenotype on their new hosts (Gunge and Sakaguchi 1981; Gunge et al. 1982; Sugisaki et al. 1985; Tokunaga et al. 1990). However, in S. cerevisiae the plasmids are only stable in haploid  $\rho^-$  strains (Gunge and Yamane 1984, Gunge et al. 1990).

The killer plasmids have all the parameters needed for yeast vectors: broad host range, a high copy number of 50-100/cell, ensuring a high gene dosis, extreme mitotic stability without selective pressure (Kämper et al. 1991), and cytoplasmic localization making them independent from nuclear control in terms of replication and transcription.

First attempts to manipulate linear plasmids pGKL1 and pGKL2 genetically in vitro involved nuclear Saccharomyces cerevisiae genes as selectable traits and resulted exclusively in the formation of circular vectors replicating in the nucleus (de Louvencourt et al. 1983; Fujimura et al. 1987). In vivo experiments, aimed at integration of the nuclear *LEU*2 gene into the killer toxin gene, also resulted in nucleus associated hybrid plasmids (Kämper et al. 1989a, b, 1991). Cytoplasmic linear hybrid plasmids could, however, be obtained by fusing the 5<sup>'</sup> non-coding region of ORF2 (killer toxin gene) to selectable marker genes  $[LEU2, K\$ ämper et al. 1989b; HIS3, Gallo and Galeotti 1990; G418 resistance (*aph*), Tanguy-Rougeau et al. 1990]. There is at least one non-essential locus on each plasmid that is dispensable and not neccessary for plasmid maintenance, i.e. the killer toxin ORF2 of the smaller plasmid pGKL1 and ORF1 of the larger plasmid  $pGKL2$  (Schaffrath et al. 1992). Thus, these loci represent potential target sites for integration of foreign DNA.

DNA sequence and transcript analysis revealed that all 14 plasmid genes are transcribed independently (Romanos and Boyd 1988; Tommasino et al. 1988) and preceded by a cytoplasmic promoter, also known as the upstream conserved sequence (Stark et al. 1990). Transcription in general appears to be rather weak, as judged from an assay based on the bacterial glucose dehydrogenase reporter gene (Schründer and Meinhardt 1995b). Applying this reporter system made it evident that the level of expression can vary upto 12-fold depending on the upstream conserved sequence motif used. Sequences further upstream do not influence expression, whereas deletion of the upstream conserved sequence motifs lead to complete loss of expression (Schaffrath et al. 1996; Schickel et al. 1996). Since linear plasmids presumably have evolved from a postulated viral ancestor (Meinhardt et al. 1990; Rohe et al. 1992; Kempken et al. 1992) this balanced low level of expression evidently ensures both stable plasmid propagation and viability of the host cell.

Several heterologous genes, including biotechnologically relevant enzymes (Schründer et al. 1996), have been expressed using killer plasmids as vectors (Kämper et al. 1991; Gallo and Galeotti 1990; Tanguy-Rougeau et al. 1990; Meinhardt et al. 1994; Schaffrath et al. 1995b). Expression, in general, occurred at a low level, thus the main application of linear yeast plasmids remains, for the present, in the area of basic research. For biotechnological exploitation it is necessary to increase efficiency of expression, e.g. by site-directed mutagenesis and promoter optimization. As exemplified by the K. lactis killer plasmids (pGKL1, pGKL2) and plasmid pSKL of Saccharomyces kluyveri (Hishinuma and Hirai 1991) these elements constitute a closely related group (Rohe et al. 1992). Further investigations on the K. *lactis* killer plasmids should thus be highly encouraged, as this will contribute to our understanding of these widely distributed genetic traits.

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