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**Biosynthesis of deoxyamphotericins and deoxyamphoteronolides by engineered strains of *Streptomyces nodosus*.**

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**Summary**

Amphotericin B is an antifungal antibiotic produced by *Streptomyces nodosus*. The macrolactone core of amphotericin B is assembled from acetate and propionate units by a large modular polyketide synthase. This macrolactone then undergoes three tailoring modifications: oxidation of a methyl branch to a carboxyl group, mycosaminylation, and hydroxylation. Gene disruption was undertaken to investigate the order in which these modifications

occur and to engineer the biosynthesis of novel amphotericin analogues.

Initial disruption experiments targeted the *amphDIII* gene which encodes a GDP-D-mannose 4,6-dehydratase involved in biosynthesis of the mycosamine sugar of amphotericin. Analysis of polyene products by mass spectrometry and NMR indicated that the *amphDIII* mutant produced 8-deoxyamphoterolides A and B as major products. These results suggest that glycosylation with mycosamine normally precedes C-8 hydroxylation and that formation of the exocyclic carboxyl group can occur prior to both these modifications.

Inactivation of the *amphL* cytochrome P450 gene gave a mutant strain that produced novel tetraene and heptaene compounds in much reduced yields. Analysis by electrospray mass spectrometry indicated that these compounds had masses appropriate for 8-deoxyamphotericins A and B, as well as homologues containing additional methyl groups.

The 8-deoxyamphoterolides had reduced antifungal activity but could be useful for glycosylation engineering. The 8-deoxyamphotericins had antifungal activity comparable to that of amphotericin B and may be useful new antibiotics.

## **Introduction**

The heptaene macrolide amphotericin B (**1a**) (Figure 1) is a medically important antifungal agent that is produced by *Streptomyces nodosus* in combination with the tetraene amphotericin A (**1b**). The antifungal activity of polyenes results from specific interactions with ergosterol, the predominant sterol lipid in fungal membranes. Polyene-sterol complexes associate to form transmembrane channels that allow unregulated loss of ions and small molecules causing cell death [1]. Amphotericin B has very high activity and is the most effective drug for the treatment of life-threatening systemic fungal infections [2], and resistance still has not emerged as a serious problem even after more than forty years of regular clinical use. However, amphotericin B does have severe side-effects that include nephrotoxicity, cardiotoxicity and neurotoxicity, due to low water-solubility and interactions with cholesterol in mammalian cell membranes [3]. As the incidence of life-threatening fungal infections is increasing [4], there is an urgent need to develop effective new polyene-based antibiotics with reduced toxicity.

Numerous amphotericin analogues have been made by chemical modification of the carboxyl and amino groups [5, 6]. Some of these analogues show improved antifungal specificity, particularly

amphotericin B methyl ester. This indicates that more extensive structural alterations could further improve the therapeutic index. However, it has proved difficult to chemically modify the macrolactone ring. An ability to understand and manipulate the biosynthetic pathway would enable production of large numbers of new analogues with alterations on the macrolactone and the sugar, any of which may prove to be a clinically important alternative to the toxic amphotericin B.

The biosynthesis of the amphotericins has been investigated by feeding experiments with  $^{13}\text{C}$ -labelled precursors [7] and the biosynthetic gene cluster has been characterised [8]. A sluggish enoyl reductase (ER5) is believed responsible for the co-formation of amphotericins A and B (**1b**, **1a**). The macrolactone core (**1i**, **1j**) is assembled from acetate and propionate units by a large modular polyketide synthase encoded within the gene cluster, as are enzymes that assemble the mycosamine sugar from GDP-D-mannose, and the glycosyl transferase to attach the sugar to the ring. The cluster also contains genes for two cytochrome P450 monooxygenases that are thought responsible for hydroxylation at C-8 and oxidation of the C-16 methyl branch to a carboxyl group. Techniques have been developed for replacement of *S. nodosus* genes to allow the engineered biosynthesis of amphotericin analogues [8]. Here, these developments are exploited to disrupt genes involved in the late steps of amphotericin biosynthesis. The results provide the first insights into the order in which these tailoring modifications occur and also generate previously unavailable analogues of amphotericins for therapeutic testing.

## Results

### Disruption of the *amphDIII* gene

A 2091 base-pair region of the amphotericin cluster (nucleotides 3474 - 5565 [8]) containing the *amphDIII* gene was amplified by PCR using oligonucleotides designed to introduce unique *Bam* HI and *Pst* I sites at opposite ends of the product. These sites were used to clone the amplified DNA into pUC118. The resulting plasmid was digested with *Bgl* II, which cuts a single site approximately in the centre of the *amphDIII* gene. The cohesive ends were repaired with T4 DNA polymerase and ligated to create a frameshift mutation. The removal of the *Bgl* II site was verified by restriction analysis. The *Bam* HI- *Pst* I fragment was cloned into

KC515 and recombinant phage were identified by PCR using primers specific for the insert. The KC515-*amphDIII* phage was propagated on *S. nodosus* and three thiostrepton-resistant lysogens were isolated and purified. One of the lysogens was cultured in the absence of thiostrepton to allow prophage excision and gene replacement to occur. The mycelial cells were converted to protoplasts to generate single cell units. After protoplast regeneration, single colonies were tested for thiostrepton sensitivity to identify clones in which a second cross-over event had excised the prophage. Nineteen thiostrepton-sensitive revertants were obtained from 208 clones. Genomic DNA was isolated from these revertants and the *amphDIII* region was amplified by PCR and subjected to restriction analysis. Two of the revertants gave PCR products which lacked a *Bgl* II site and were identified as *amphDIII* mutants. Figure 2 shows restriction analysis of the *amphDIII* region PCR products amplified from *S. nodosus* ATCC14899 and one of the replacement mutants.

#### **Analysis of polyenes made by *amphDIII* mutant**

The *amphDIII* mutant was grown on fructose-dextrin-soybean medium [7], and was shown by UV spectrophotometry to produce tetraenes (50-250 mg/L culture broth), and lower levels of heptaenes, predominantly in the sedimentable mycelial fraction of the cultures. This mycelial sediment was extracted with methanol and the tetraenes were partially purified by selective precipitation (removing some heptaene and more polar polyene products). Analysis by ESMS indicated that the major products present were 8-deoxyamphoteranolides along with some amphoteronolides. Figure 3 shows spectra obtained with a sample enriched in 8-deoxyamphoteranolide A (**1f**) with some amphoteronolide A.

The partially purified 8-deoxyamphoteranolides were converted to methyl esters (**1g**) and (**1h**) and a fraction containing mainly tetraene products further purified by normal phase HPLC, from which two tetraenes were isolated, both with the expected molecular weight (778.4). Analysis of one of these components by proton, carbon and proton-proton 2D NMR gave spectra consistent with methyl 8-deoxyamphoteranolide A (**1h**) (Figure 4A) [9]. Preliminary NMR analysis of the second component gave spectra consistent with either methyl 37-*epi*-8-deoxyamphoteranolide B or methyl 36-*epi*-8-deoxyamphoteranolide B (Figure 4B). This assignment is based upon a large upfield shift of H-37 in the proton and 2D NMR spectra from 5.2 in (**1h**) (coupled to methyl doublet at 1.2 ppm) to 4.0 ppm (coupled to

methyl doublet at 1.2 ppm) in the epimer. These compounds are undergoing further characterisation (B. J. Rawlings, unpublished data). Molecular modelling indicates that epimerisation at either C-36 or C-37 results in a major change in macrolactone conformation. The stereochemistry at these centres is determined by module 1 of the amphotericin PKS. Literature evidence suggests that this module uses a (2*S*)-methylmalonyl extender unit (**2a**) and upon condensation with acetyl CoA initially generates a (2*R*)-2-methyl-3-oxoacyl chain (**2b**) [10, 11] that can readily epimerise at C-2. Based on the stereochemistry observed in amphotericin B, the Amph KR1 appears to select the 2-epimerised (2*S*)-2-methyl-3-oxobutanoyl thioester intermediate (**2c**), and to carry out stereospecific anti reduction to form the (2*S*,3*S*)-3-hydroxy-2-methylbutanoyl thioester intermediate (**2e**) (Figure 5). 37-*epi*-8-Deoxyamphoteronolides would result from KR1 generating the opposite alcohol stereochemistry to form (**2f**). 36-*epi*-8-Deoxyamphoteronolides would arise from the selection by KR1 of the unepimerised substrate (**2b**), with ketoreduction to form (**2d**). (Figure 5). The data do not exclude the possibility that anti reduction still occurs but on the unepimerised substrate, to give the bis-epimer (2*R*, 3*R*)-3-hydroxy-2-methylbutanoyl thioester. The literature to date is consistent with all of these possible mechanisms. Complete structural characterisation of the products should help to resolve the issue.

*epi*-Amphoteronolides have not been reported and their formation suggests that although the remaining extension modules can tolerate an "incorrect" *epi*-diketide, and extend it to form the epimerised macrolactone, and that the AmphN cytochrome P450 efficiently oxidises the C-41 methyl to a carboxyl group (*vide infra*), the mycosaminyltransferase does not efficiently recognise the *epi*-8-deoxyamphoteronolide as substrate. *S. nodosus* ATCC14899 was subsequently found to produce a minor polyene with chromatographic properties identical to those of the putative *epi*-8-deoxyamphoteronolide (B. J. Rawlings, unpublished data). This indicates that these compounds are normally generated at low levels by the amphotericin PKS but were only detected during characterisation of 8-deoxyamphoteronolides formed by the *amphDIII* mutant. This is the first known example of a natural (non-chimaeric) polyketide synthase in which a lapse in programming fidelity results in production of epimeric macrolactones.

Polyenes were also detected in culture supernatants of *amphDIII* strains, and more polar polyene fractions were obtained when mycelial

extracts were chromatographed. These polyenes may represent analogues of amphotericin that are modified with alternative sugars. The absence of the 'normal' glycosylation (which would allow rapid export from the cell), resulting in a slow build up of polyenes in the cell, may allow other relatively slow conversions to now occur to the macrolactone. In the absence of GDP-mycosamine, the AmphDI mycosaminyl glycosyl transferase might be capable of using GDP-D-mannose, dTDP-D-glucose or even dTDP-L-rhamnose as substrate to convert a fraction of the aglycone to polar glycosylated minor products, with mannosyl, glucosyl or rhamnosyl residues attached at C-19. Indeed, a minor compound with a mass appropriate for hexosyl-amphoteronolide A ( $M - H^+ = 941.5$ ) was routinely detected in extracts from the *amphDIII* mutant (Figure 3B). To investigate this compound further, a polar tetraene fraction was methylated and purified further. Analysis by positive ion ESMS showed a large peak at 979.4, corresponding to the sodium adduct of desmycosaminyl O-mannosylamphotericin A methyl ester, or the O-glucosyl isomer, with no evidence of the 8-deoxy analogues (data not shown). Presumably the AmphL cytochrome P450 recognises the corresponding hexosyl 8-deoxy intermediate, and hydroxylates it.

NDP-deoxysugar flexibility in macrolide glycosyltransferases has been documented. An oleandrosyltransferase OleG2, that normally utilises dTDP-L-oleandrose, when introduced into *Saccharopolyspora erythraea* EryBV mutant (lacking dTDP-L-oleandrose), was shown able to complement the missing EryBV mycarosyltransferase activity, but by attaching rhamnose to form 3-L-rhamnosyl-6-deoxyerythromycin B [12, 13]. The dTDP-L-rhamnose is believed to be present in the cytoplasm as a cell-wall building block.

As 8-deoxyamphoteronolides may exist in *amphDIII* mutant cells for several days, other adventitious glycosylation processes may very slowly occur during this time, resulting in the glycosylation of other hydroxyl groups. The polyenes nystatin A3 and candidoin each have an additional dideoxyhexose sugar residue attached at the position corresponding to C-35 of amphotericin [14].

The polyenes produced by the *amphDIII* mutant were tested for antifungal activity in agar diffusion assays with *Saccharomyces cerevisiae* as an indicator organism. No inhibition zones were detected when extracts containing 14  $\mu\text{g}$  total tetraene and 6  $\mu\text{g}$  total heptaene per ml were assayed (data not shown). The amphoteronolides and their hexosyl analogues had dramatically reduced activity compared to amphotericins A and B extracted from wild-type *S.*

*nodosus*. This observation is consistent with previous findings that a positive charge on the amino group of mycosamine is essential for significant antifungal activity [5].

### **Disruption of *amphL* gene**

The amphotericin cluster contains two cytochrome P450 genes, *amphL* and *amphN*. The AmphN protein shows a high degree of sequence identity with the NysN, PimG and CanC proteins that are thought to function in formation of exocyclic carboxyl groups in nystatin, pimaricin and candicidin [15]. The AmphL protein is homologous to the NysL P450 which is thought to introduce the C-10 hydroxyl group of nystatin [16] and to PimD which introduces the epoxide in the polyol chain of pimaricin. Aparicio *et al.* disrupted *pimD* to produce a novel pimaricin, de-epoxypimaricin [17]. These considerations suggest that AmphL functions to introduce the C-8 hydroxyl group of amphotericin.

The *amphL* gene contains two *Sac* I sites flanking the 1053 base-pair region between nucleotides 56903 and 57956 of the amphotericin cluster. This internal *Sac* I fragment of *amphL* was cloned between the *Sac* I sites of KC515. Recombinant phage were identified by PCR using oligonucleotide primers specific for the insert. Since the *amphL* gene appears to be located at the end of a transcription unit, insert-directed integration of this phage into the chromosome was not expected to have polar effects on transcription of any other genes. A single cross-over event would be sufficient to bring about gene disruption. The recombinant phage was plated on *S. nodosus* and lysogens were selected by overlaying plates with soft agar containing thiostrepton. A typical lysogen was isolated and genomic DNA was analysed for the presence of prophage DNA by Southern hybridisation and by PCR. Analysis of hybridising restriction fragments indicated that gene disruption had occurred as anticipated. A typical experiment is shown in Figure 6. Homologous recombination between the phage and chromosomal sequences resulted in loss of the 4.8 kb *Xho* I fragment that contains *amphL*, and appearance of 3.4 and 43 kb junction fragments.

### **Analysis of polyenes made by *amphL* mutant**

The *amphL* mutant produced heptaene and tetraenes that were found predominantly in the mycelial fraction of the culture. The yields were greatly reduced (2-5 mg/L) compared to amphotericin production by *S. nodosus* ATCC14899 [7] or 8-deoxyamphoteronolide

production by the *amphDIII* mutant. The mycelium was extracted with methanol to give multigram quantities of extract, from which partially purified polyenes were obtained by selective precipitation and column chromatography for analysis by electrospray mass spectrometry. Analysis in negative ion mode gave compounds with masses of 906.2 and 920.2 (Figure 7; all compounds show an M:M+1:M+2 ratio of ca. 6:3:1 due to isotopic natural abundance) The M - H<sup>+</sup> of 906.2 is in good agreement with that expected for 8-deoxyamphotericin B (**1c**) (M = 907.5). The peak with a mass of 920.2 suggests the presence of a homologue with an additional methyl group. Analysis in positive ion mode yielded masses of 930.3 and 932.3, 944.3 and 946.3, consistent with the masses of sodium ion (M+23)<sup>+</sup> adducts of 8-deoxyamphotericins A and B and homologues. NMR analysis of these samples revealed resonances indicating at least two polyenes present in large quantities of glycerides and an unidentified aromatic metabolite. Adequate purification of these compounds was hampered by their low abundance in mycelia and their relative resistance to extraction with alcoholic solvents. The deoxyamphotericins that were extracted were contaminated with overwhelming amounts of membrane lipids and other non-polyenic material. Despite considerable effort, it has not so far been possible to obtain material pure enough for structural characterisation by NMR. Therefore, the designation of these compounds as 8-deoxyamphotericins rather than 16-descarboxyl-16-formylamphotericins is based on the homology between AmphL and PimD (*vide supra*). The presence of methyl homologues of these deoxyamphotericins may be due to the use of propionate as a starter unit, however as the corresponding homologues were not detected in the *amphDIII* mutant, an alternative explanation is that the 8-deoxyamphotericins undergo O-methylation on the sugar residue, possibly as a detoxification procedure. Methyl homologues of amphotericins A and B were not reported in cultures of wild type *S. nodosus*.

The 8-deoxyamphotericins retained antifungal activity in agar diffusion tests. The inhibition zone diameters were comparable to those of amphotericin B at equivalent total heptaene concentrations (data not shown). A partially purified fraction containing 8-deoxyamphotericin B and its methyl homologue was tested against liquid cultures of *S. cerevisiae*. With this material, a total heptaene concentration of 1.25 µg per ml was sufficient to inhibit growth of the yeast cells. The minimum inhibitory concentration for purified amphotericin B was estimated as 0.3125 µg per ml. These

results indicate that 8-deoxyamphotericins have a slightly lower activity than amphotericin B.

## Discussion

Manipulation of biosynthetic genes is yielding novel polyene macrolides. Aparicio and co-workers have produced de-epoxypimaricin [17] and Zotchev *et al.* [18] have produced a hexaene derivative of nystatin as well as trace levels of a heptaene analogue. This study describes the first amphotericin analogues that have been generated by engineered biosynthesis, and provides the first insights into the order in which the late stages of amphotericin biosynthesis occur.

The *amphDIII* mutant produced 8-deoxyamphoterionolides as major products indicating that C-8 hydroxylation is impaired in the absence of glycosylation. The failure of the AmphL P450 to hydroxylate the 8-deoxyamphoterionolides may result from their reduced solubility, or from strict molecular recognition of glycosylated polyene substrates.

The C-16 carboxyl group was present in all the polyenes isolated from the *amphDIII* mutant, with no evidence for the formation of 16-descarboxyl-16-methylamphoterionolides. This indicates that oxidation of the C-16 methyl branch occurs efficiently in the absence of the other two modifications. Thus it seems likely that 8-deoxyamphoterionolides are normal biosynthetic intermediates that are substrates for glycosylation. Taken together, these results indicate that the late stages of amphotericin biosynthesis can occur in the following order: exocyclic carboxyl group formation, glycosylation with mycosamine, and finally C-8 hydroxylation.

It is important to mention preliminary data that suggests that this sequence of events may not be obligatory in all circumstances. We have recently disrupted the *amphN* gene after numerous unsuccessful attempts (M. Carmody and P. Caffrey, unpublished data). Although purification and chemical analyses have not yet been carried out, the *amphN* mutant produces low yields of heptaenes and tetraenes that retain antifungal activity. This raises the possibility that glycosylation can occur in the absence of exocyclic carboxyl group formation. Gene disruption studies may not be sufficient for determining whether these two steps occur in a preferred order. On the other hand, this approach promises to yield several amphotericin analogues rather than the few that could be generated from a single linear pathway.

The 8-deoxyamphoterionolides had reduced water-solubility and diminished antifungal activity. However, the *amphDIII* mutant could

be useful in glycosylation engineering experiments aimed at altering the sugar residue of amphotericin B. A wide range of aminodeoxysugars are derived from dTDP-glucose, and several groups are constructing gene cassettes for their *in vivo* synthesis in streptomycetes. Similar cassettes can be introduced into *S. nodosus*. In addition, the *amphDI* gene could be subjected to error-prone PCR or DNA shuffling to develop glycosyltransferases that can recognise the polyene aglycone and other dTDP-glucose derived amino sugars. Successfully redesigned glycosyltransferases could be detected by screening for restored antifungal activity.

The detection of epimeric 8-deoxyamphoteronolides is interesting and suggests that the amphotericin system may be useful for determining how PKS modules determine alkyl stereochemistry in nascent chains.

The *amphL* mutant produced 8-deoxyamphotericins although the yields were significantly lower than the yields of 8-deoxyamphoteronolides from the *amphDIII* mutant. This may reflect regulatory phenomena or feedback mechanisms that are not yet understood. The 8-deoxyamphotericins were less soluble than amphotericin B. However, they retained activity and could be tested as antifungal drugs. Polyenes are also active against *Leishmania* parasites, enveloped viruses, prion proteins [6], and hepatocellular tumours [19]. These additional biological activities appear to result from interactions of the polyene with sterol-rich membranes. Some of the amphotericin analogues could be useful for some or all of these potential medical applications.

### **Significance**

These results show that formation of the exocyclic carboxyl group of amphotericin B can occur prior to glycosylation with mycosamine. The second hydroxylation, at C-8, appears to be inefficient in the absence of prior glycosylation. One possible order of the macrolactone tailoring steps is: exocyclic carboxyl group formation, mycosaminylation and C-8 hydroxylation.

The *amphDIII* mutant produced 8-deoxyamphoteronolides that had little antifungal activity. However, this mutant strain can now be used as a host in engineering experiments to glycosylate the amphoteronolide macrolactone with a wide range of (amino)deoxysugars any of which may significantly improve the therapeutic properties over those of amphotericin B.

Disruption of the *amphL* gene gave novel deoxyamphotericins that retained good antifungal activity in preliminary tests. These are the first amphotericin analogues that have been produced by engineered biosynthesis. Further work should reveal whether these compounds or their derivatives have any clinical significance as antifungal antibiotics or as antiviral, antiparasitic or antiprion agents.

## **Experimental Procedures**

### **Genetic procedures**

PCRs were carried out with *Taq* or *Vent* DNA polymerases as described [20] using a Perkin Elmer GeneAmp 2400 thermocycler. The oligonucleotide primers were synthesised by GenoSys, Cambridge, UK. The oligonucleotides used to amplify the *amphDIII* region were 5' CCGAGGATCCGCACCAGATGCAAAACGAC 3' and 5' TAAACTGCAGGACAGCACGCTGCCGGTGTTG 3'. The oligonucleotides used to detect the *amphL* phage were 5' GCGGGATCCTAGCTGAAGCAGCTGCTGCAC 3' and 5' CAGGTCGACATGGGTGGCAAC 3'

Methods for DNA manipulation were as described by [20]. *Escherichia coli* strain XL1-Blue MR was used as a host for propagation of plasmids. Plasmid DNA was isolated using the alkaline-SDS procedure. Restriction enzyme digestions and ligations were carried out using standard procedures. Competent *E. coli* cells for transformation were prepared by the calcium chloride method.

Methods for preparation of streptomycete spores and protoplasts were those described by Hopwood *et al.* [21]. *Streptomyces lividans* 66 (John Innes strain 1326) was used for propagation of phage KC515 [22]. Phage KC515 DNA was isolated using the small-scale method [21]. DNA fragments ligated to KC515 DNA were introduced into *S. lividans* 66 protoplasts by transfection [21]. Recombinant phage were identified by PCR using primers specific for the cloned inserts.

*S. nodosus* ATCC 14899 was used as the parent strain for gene disruptions. To obtain lysogens, recombinant phage were plated on *S. nodosus* spores to give near confluent lysis. After overnight incubation, plates were overlaid with soft nutrient agar containing thiostrepton (50 µg/mL). Thiostrepton-resistant lysogens resulting from integration of the phage were streaked on tryptone soya (TS) agar containing thiostrepton. Lysogens were cultured in the absence of thiostrepton then protoplasts were allowed to regenerate. Regenerated protoplasts were toothpicked onto TS agar and TS agar

containing thiostrepton to identify thiostrepton sensitive revertants.

Labelling of probes with digoxigenin-dUTP and detection of hybridising DNA were carried out using a Boehringer Mannheim DIG DNA labelling and detection kit. For Southern hybridisation, DNA fragments were transferred to nylon membranes by capillary transfer [20].

### **Production and analysis of polyenes**

For polyene production, *S. nodosus* was grown on fructose-dextrin-soybean medium [7]. 100  $\mu$ l samples of culture (containing suspended mycelia) were mixed with 900  $\mu$ l volumes of butanol and sonicated for 20 min. The extract was centrifuged and the supernatant was diluted with methanol. Amphotericin B gives four specific UV absorption peaks at 346, 364, 382 and 405 nm with  $\epsilon = 1.7 \times 10^5 \text{ M}^{-1}\text{cm}^{-1}$  at 405 nm [23]. Amphotericin A absorbs at 280, 292, 305 and 320 nm, with  $\epsilon = 0.78 \times 10^5 \text{ M}^{-1}\text{cm}^{-1}$  at 318 nm. Amphotericin B standard was obtained from Sigma.

Bioassays were carried out with *S. cerevisiae* NCYC 1006 as an indicator organism. A 100 mL volume of molten cooled yeast agar medium (3g yeast extract, 3g/L malt extract, 5g/L peptone, 10g/L dextrose, 15g/L agar) was mixed with approximately  $10^6$  yeast cells and poured into petri dishes. Test samples were pipetted into wells punched in the solidified agar. Plates were incubated at 30°C for 20 hours and inhibition zones were measured. Alternatively, 1 ml volumes of liquid yeast medium containing varying concentrations of polyenes were each inoculated with  $10^3$  yeast cells. Tubes were incubated with shaking at 30°C for 20 h and growth was assessed by measuring the absorbance (turbidity) at 540 nm.

### **Chemical methods**

UV spectrophotometry was performed using a Hewlett Packard 8452A diode array spectrophotometer using 1 cm path length. Electrospray mass spectrometry was performed on a Micromass Quattro LC. Nuclear Magnetic Resonance (NMR) spectroscopy was performed on a Bruker DRX 400 spectrometer. HPLC was performed on a Shimadzu LC-4A with a UV detector.

For preparative-scale production and purification of polyenes, a glycerol deep (1 mL) was added to GYE media (100 mL; 10 g/L yeast

extract; 10 g/L glucose, pH 7) and shaken in an orbital incubator shaker (New Brunswick Series 25) at 28°C for 48 h at 160 rpm. Portions (10 mL) of the resulting growth were each transferred to eight 500 mL production media (fructose 20 g/L, dextrin 60 g/L, soybean flour 30 g/L, CaCO<sub>3</sub> 10 g/L) and shaken at 28°C for 72 h at 160 rpm. The growth was centrifuged (Sorvall RC-5B), and the finely divided mycelial fraction added to methanol (4 L) with occasional shaking for 48 h. Yields varied from 50 mg/L to 500 mg/L of tetraenes by UV assay with smaller amounts of heptaenes. The supernatant was collected, and reduced in volume *in vacuo* to ca. 200 mL (largely aqueous). Centrifugation yielded a yellow precipitate that was shaken in methanol (80 mL) and the solid removed by centrifugation to yield a clear yellow solution whose polyene content was mainly tetraene (> 90%), but still contained gram quantities of non-polyene material (membrane components) and an unknown yellow metabolite. Addition of excess ethereal diazomethane resulted in ca. 50% of the polyene material present now having an R<sub>f</sub> of 0.45 to 0.5 with the yellow impurity at R<sub>f</sub> 0.7, and some polyene material remaining on the baseline (CH<sub>2</sub>Cl<sub>2</sub> : MeOH 9:1). Purification by flash chromatography (CH<sub>2</sub>Cl<sub>2</sub> : MeOH 9:1) gave a pure mixture of tetraenes, which were further purified by normal phase HPLC (MeOH : EtOAc, 1:19), to yield 8-deoxyamphoteronolide A, an epimer, and a third peak containing a mixture of compounds whose RMM corresponded to 8-deoxy- and amphoteronolide A. Similar procedures were used for the growth of the *amphL* mutant, with extraction of the mycelia using methanol or butanol followed by selective precipitation and column chromatography.

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### Figure legends

Figure 1. Structure of amphotericin B and analogues.

Figure 2. Targeted inactivation of the *amphDIII* gene. (A) A double cross-over recombination event results in replacement of the *amphDIII* gene with a form containing a frameshift mutation and lacking a *Bgl* II site. K and Bg denote the unique *Kpn* I and *Bgl* II sites within the 1035 base-pair *amphDIII* gene. The star denotes the frameshift mutation. The small arrows represent the primers used to amplify the *amphDIII* region. (B) Analysis of a typical replacement mutant. The *amphDIII* region was amplified from *S. nodosus* ATCC14899 and from the

*amphDIII* mutant using the oligonucleotide primers described in the text. The 2091 bp PCR products were treated with *Bgl* II or *Kpn* I. The region amplified from wild type *S. nodosus* was cut by *Bgl* II to give the expected 973 and 1118 bp fragments (lane 1) whereas the product amplified from the mutant was resistant to cleavage by *Bgl* II (lane 3). The DNA amplified from both strains gave the expected 446 and 1645 bp fragments when digested with *Kpn* I (lanes 2 and 4).

Figure 3. Analysis of extract from *amphDIII* mutant by ESMS in positive ion mode (panel A) and negative ion mode (panel B) showing presence of 8-deoxyamphoteronolide A (1f). A sodium adduct was detected in positive ion mode. A lesser amount of amphoteronolide A ( $M + Na^+ = 803$ ) was detected by positive ion ESMS only. Detection in this mode could be more sensitive for the 8-hydroxylated amphoteronolides if  $Na^+$  co-ordinates to the 1,2 diol present in these compounds.

Figure 4. A. Proton NMR (400 MHz) spectrum of methyl 8-deoxyamphoteronolide A (1g) showing the C-37 proton at 5.2 ppm (▲) and the coupled doublet at 1.2ppm (\*). B. Proton NMR spectrum of methyl *epi*-8-deoxyamphoteronolide A showing the C-37 proton at 4.0 ppm (▲) and the coupled doublet at 1.2ppm (\*). Residual 8-deoxyamphoteronolide H-37 proton indicated (Δ).

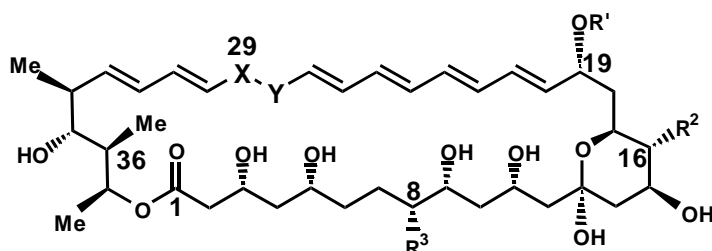
Figure 5. Proposed routes for production of *epi*-amphoteronolides by the amphotericin PKS.

Figure 6. Targeted disruption of the *amphL* gene. (A) Schematic diagram showing integration of the KC515 *amphL* phage into the chromosomal *amphL* gene. This results in loss of the 4.3 kb *Xho* I fragment containing the *amphL* gene and formation of 3.4 and 43 kb fragments containing the 5' and 3' regions. (B) Analysis of *Xho* I digests of genomic DNA from an *amphL* mutant (lane 1) and *S. nodosus* ATCC14899 (lane 2) by Southern hybridisation using an *amphL* gene probe.

Figure 7. Analysis of polyenes produced by the *amphL* mutant by ESMS in positive ion mode (A) and negative ion mode (B) showing the presence of 8-deoxyamphotericins B **1c** and **1d**. As explained in the text, each of these compounds is represented by three peaks due to

isotopic natural abundance. The third of the peaks corresponding to **1c** overlaps with the first of the **1d** peaks.

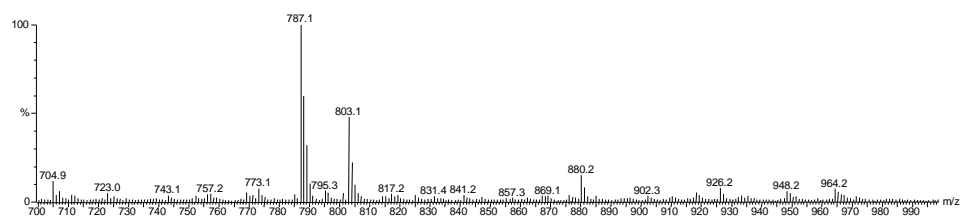
# Figure 1



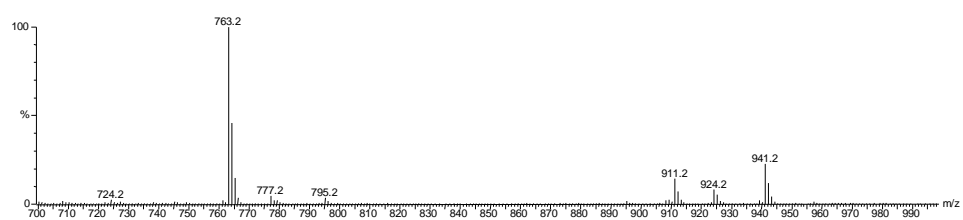
	R <sup>1</sup>	R <sup>2</sup>	R <sup>3</sup>	X-Y	RMM	Name
1a		-COOH	-OH	-CH=CH- <sup>E</sup>	923.5	Amphotericin B
1b		-COOH	-OH	-CH <sub>2</sub> CH <sub>2</sub> -	925.5	Amphotericin A
1c		-COOH	-H	-CH=CH- <sup>E</sup>	907.5	8-Deoxyamphotericin B
1d		-COOH	-H	-CH <sub>2</sub> CH <sub>2</sub> -	909.5	8-Deoxyamphotericin A
1e	-H	-COOH	-H	-CH=CH- <sup>E</sup>	762.4	8-Deoxyamphoteronolide B
1f	-H	-COOH	-H	-CH <sub>2</sub> CH <sub>2</sub> -	764.4	8-Deoxyamphoteronolide A
1g	-H	-COOMe	-H	-CH=CH- <sup>E</sup>	776.4	Methyl 8-deoxyamphoteronolide B
1h	-H	-COOMe	-H	-CH <sub>2</sub> CH <sub>2</sub> -	778.4	Methyl 8-deoxyamphoteronolide A
1i	-H	-Me	-H	-CH=CH- <sup>E</sup>	732.4	8-Deoxy-16-descarboxyl-16-methylamphoteronolide B
1j	-H	-Me	-H	-CH <sub>2</sub> CH <sub>2</sub> -	734.4	8-Deoxy-16-descarboxyl-16-methylamphoteronolide A

# Figure 3

A

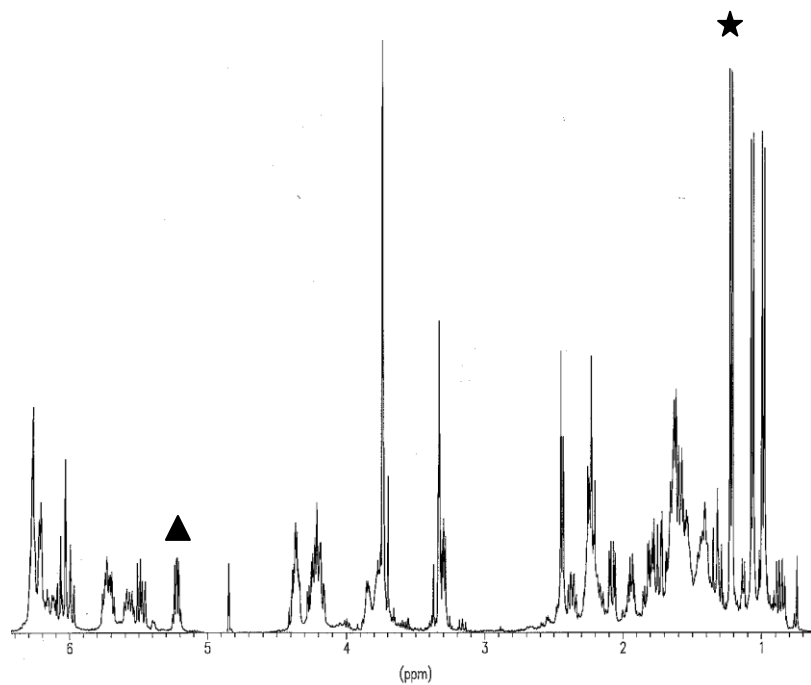


B

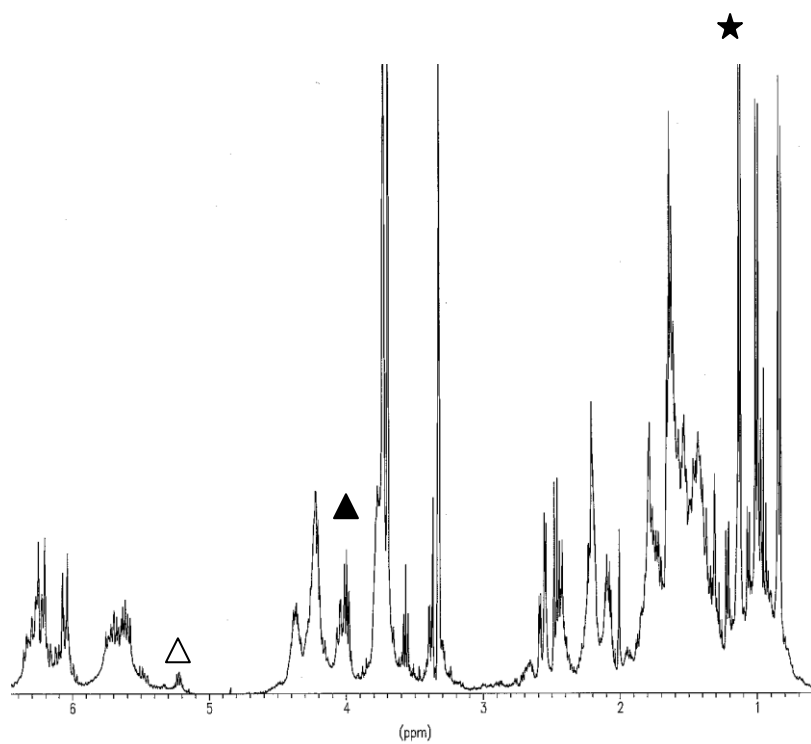


## Figure 4

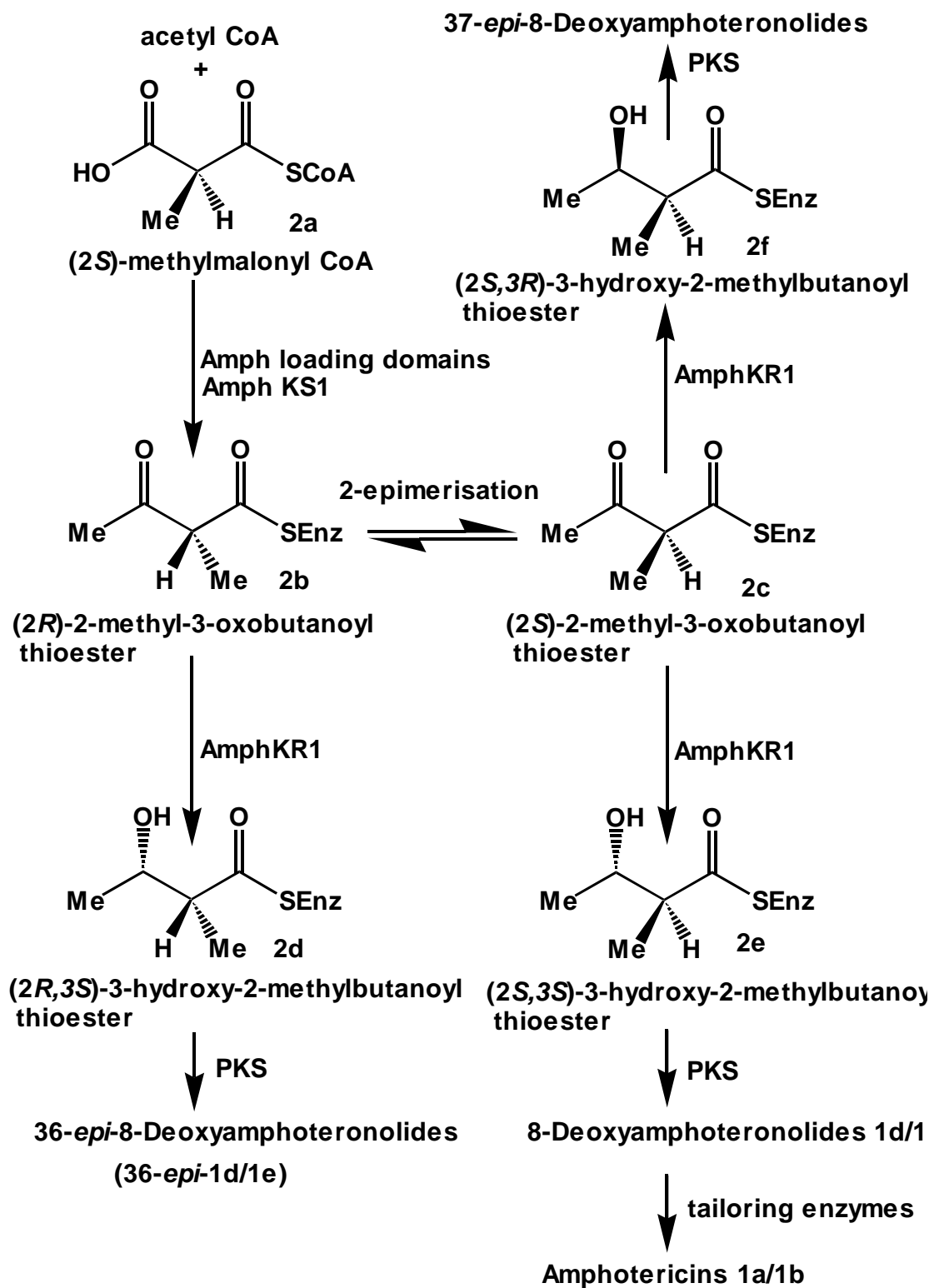
### A. Methyl 8-deoxyamphoterone A



### B. Methyl *epi*-8-deoxyamphoterone A

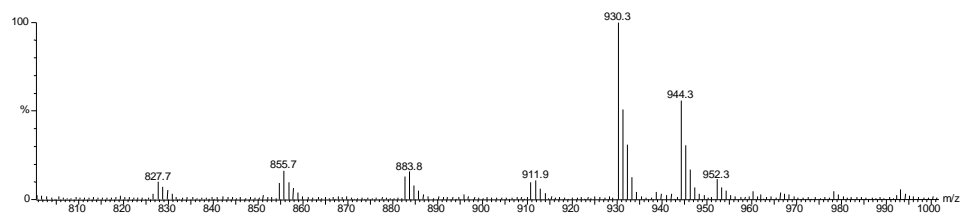


**Figure 5**

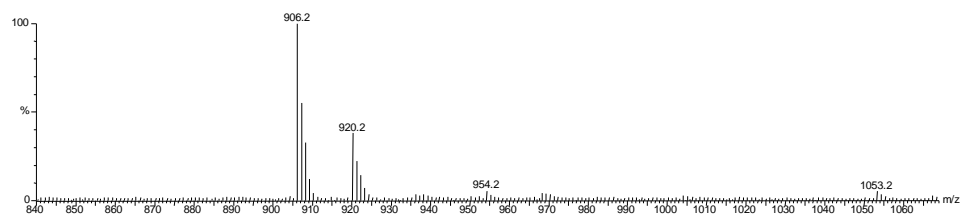


# Figure 7

A



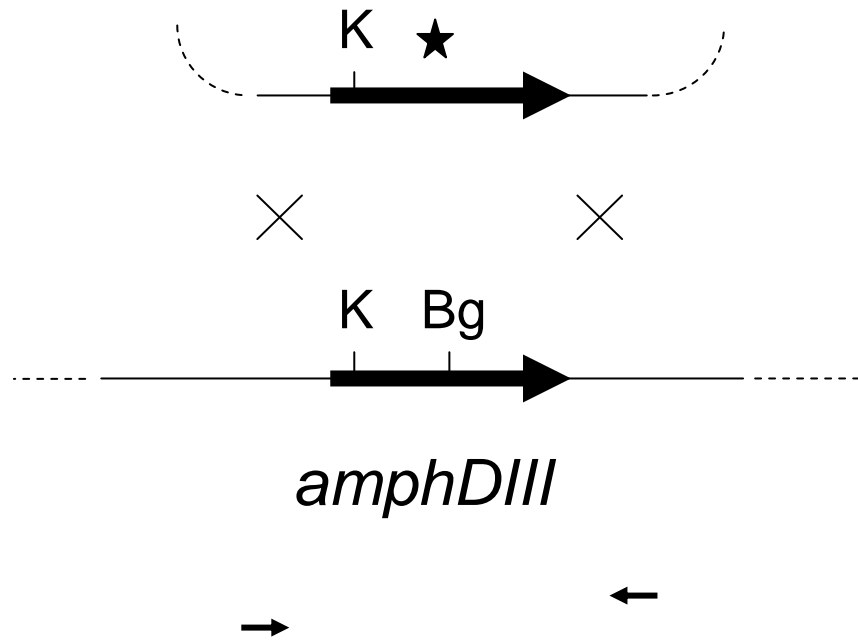
B



# Figure 2

## A

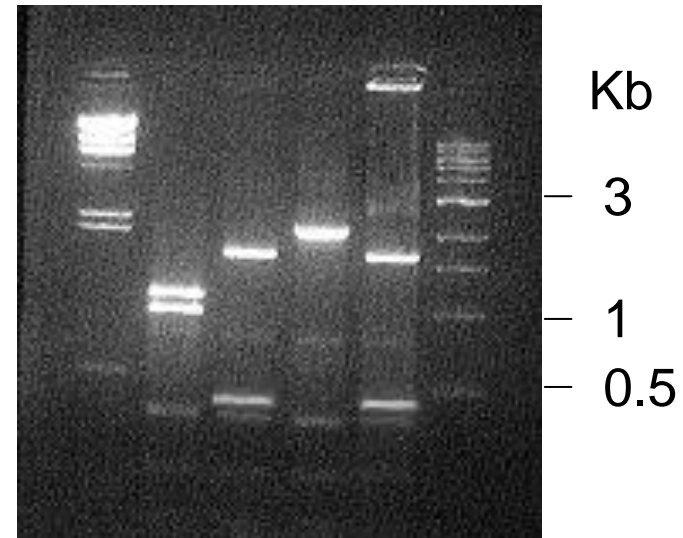
KC515-*amphDIII*



*S. nodosus* chromosome

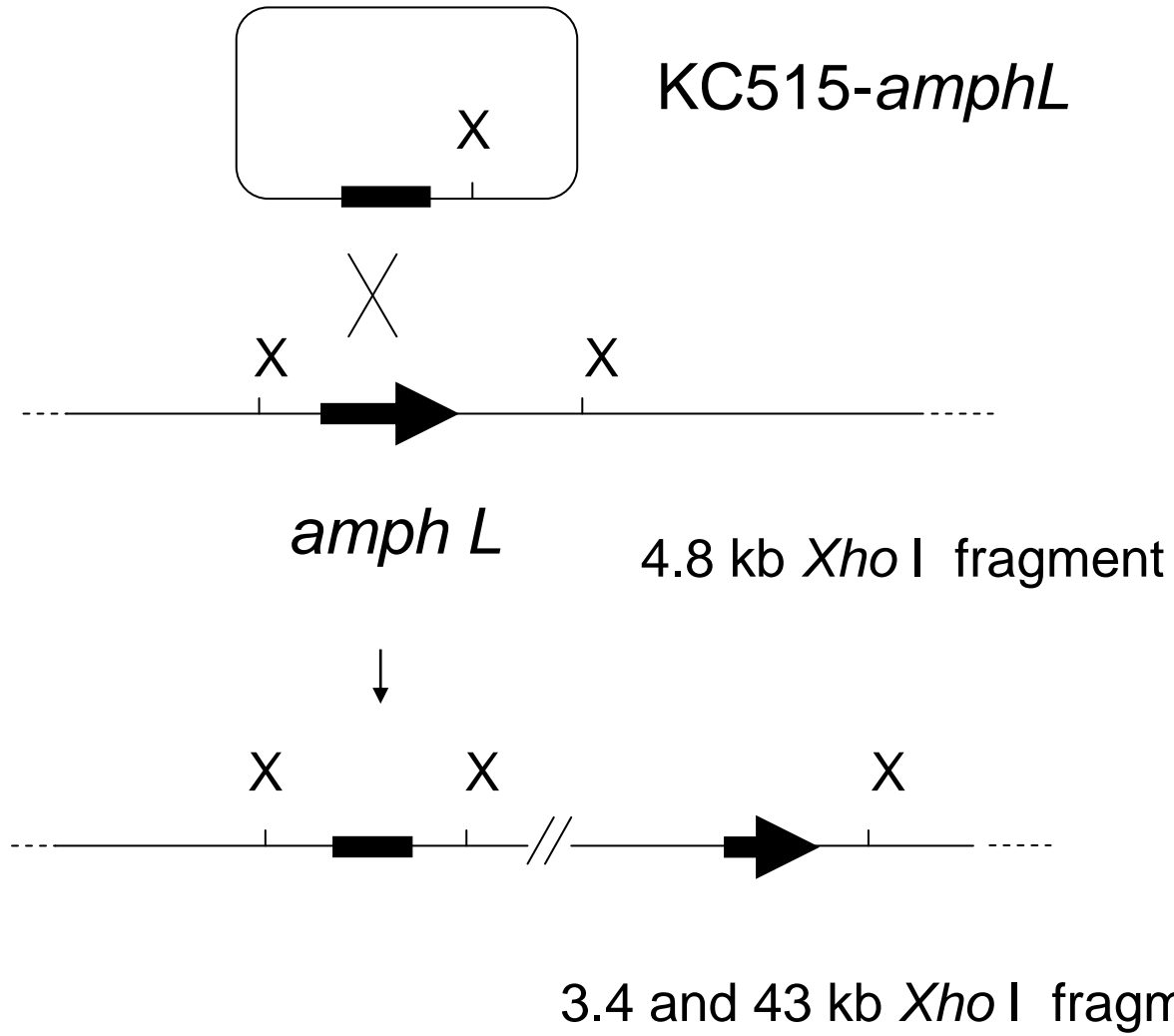
## B

M1 1 2 3 4 M2



**Figure 6**

**A**



**B**

