A physical map for *Mycoplasma capricolum* Cal. kid with loci for all known tRNA species

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Submitted December 18, 1990

Macro-restriction maps for *Mycoplasma capricolum* Cal kid ATCC 27343 were presented (1, 2) at a recent meeting of the International Organisation for Mycoplasmology. For the 1070 kbp map of Whitley *et al.* (2), shown in Fig. 1, restriction sites for *Apa*I (*Ap*), *Asp*718I (*As*) = *Kpn*I (*Kp*), *Bgl*I (*Bg*), *Bss*HII (*Bs*), *Sal*I (*Sl*), *Sma*I (*Sm*) and *Xho*I (*Xo*) were located as previously described for *M. mycoides* (3) and *Ureaplasma urealyticum* (4), whereas the *Bam*HI sites were mapped relative to *Bgl*I sites by reciprocal 2D-PFGE (5). This map agreed with the map of Miyata and Fukumura (1) except our map showed 3 extra *Asp*718I (=*Kpn*I) sites (AsA, E and F, Fig. 1) defining additional fragments of 26, 4 and 3 kbp. We have observed that *M. capricolum* Cal kid from another source (NCTC 10133) lacks the site (AsA in Fig. 1) defining the 26 kbp fragment. Lu *et al.* reported at the IOM meeting (6) that the replication origin was within fragments *Bam*HI-H or -I and the terminus within *Bam*HI-C. The loci listed in Table 1 and shown in Fig. 1 were mapped by probing with appropriate cloned genes as described previously (3, 7). They included the complete set of tRNA genes (thirty) identified for this organism as well as a gene encoding msRNA, a new small RNA from *M. capricolum* (8). The latter has a potential secondary structure with features common to eukaryotic 7SL RNA, eubacterial 4.5S- and scRNA and archaebacterial 7S RNA (9). The gene for a closely similar RNA has been recently cloned from *M. mycoides* subsp. *capri* (10). The two rRNA operons (*rrn*A, *rrn*B) were differentiated by a sequence upstream

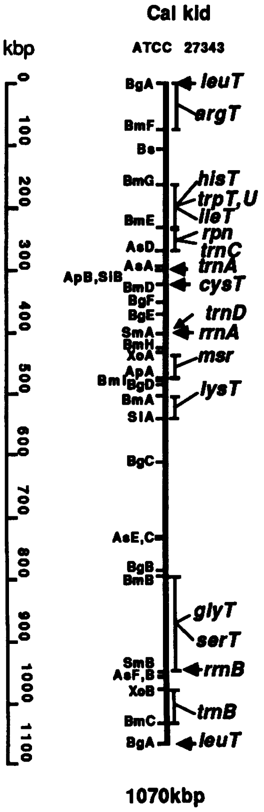

Figure 1. Genetic map for *M. capricolum* (ATCC 27343) with restriction sites for various endonucleases labelled by abbreviations as defined in text. Designation of sites with the suffices A, B, C, D etc is used in relation to the single digest restriction fragment which lies below a site on the map. The circular genome is shown linearised from the *Bgl*I site within *leuT*. Symbols identifying the loci are defined in Table 1. Symbols: ←, probe hybridized with fragments on both sides of the indicated cleavage site; I, hybridisation with the probe was confined to sequences between the restriction sites at the ends of the vertical line.

Table 1. Loci placed on the genomic map of *M. capricolum* ATCC 27343 by use of cloned DNA probes containing sequences for defined genes previously described in [a] (7) and [b] (8).

Locus	Defined gene product in cloned DNA probe
rrn[a]	rRNA
rpn[a]	13 ribosomal proteins
trnA[b]	9 tRNA cluster
trnB[b]	5 tRNA cluster
trnC[b]	4 tRNA cluster
trnD[b]	2 tRNA cluster
argT[b]	tRNA^{Arg}
leuT[b]	tRNA^{Leu}
glyT[b]	tRNA^{Gly}
trpT, U[b]	tRNA^{Trp} (UCA), tRNA^{Trp} (UCC)
hisT[b]	tRNA^{His}
serT[b]	tRNA^{Ser}
lysT[b]	tRNA^{Lys}
cysT[b]	tRNA^{Cys}
ileT[b]	tRNA^{Ile}
msr[b]	msRNA

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from *trn*D which is itself just upstream of *rrn*A (8). The loci for the tRNA genes are distributed throughout the genome although 18 of them are found, together with an operon for 13 ribosomal proteins (*rpn*), within a 168 kbp segment (*Bam*HI-E and -G) covering 16% of the genome. This widespread distribution of the tRNA loci on the *M. capricolum* genome suggests that their mapping will provide a sensitive test for differences in mycoplasma genome structure arising from major genomic rearrangements during phylogenetic divergence.

ACKNOWLEDGEMENT

This work was supported by funds from the Australian Research Council

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