INVESTIGATIONS OF EXPRESSION AND PROTEIN SEQUENCE OF THE AMINOACETYLTRANSFERASE GENE NAT1 FROM STREPTOMYCES NOURSEI

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INTRODUCTION

Nourseothricin (Nc) belongs to the group of streptothricin (St) antibiotics that includes grisin and racemomycin, which exhibit antibacterial, antifungal and antiviral activity (Bocker and Bergter, 1986). Although they are not used therapeutically they give remarkable effects as fodder additives in animal husbandry (Bocker and Bergter, 1986). Resistance against the streptothricins is mediated via acetylation (Keeratipibul, 1983, Tschaeppe et al., 1984, Haupt et al., 1986). From NMR studies Kobayashi et al. (1987) found that in Streptomyces lavendulae this involves a monoacytation of the beta-amino-group of the beta-lysine moiety of the streptothricin. The gene (stat) for this enzymatic activity was cloned and sequenced and its transcription start shown to be near the translational start (Horinouchi et al., 1987). In addition, a transposon-specified St-acetyltransferase (SAT) was identified in enterobacteria isolated from animals treated with Nc (Tschaeppe et al., 1984). The nucleotide sequence of this gene was determined by Hein et al. (1989). From Streptomyces noursei a gene (nat1) conferring resistance to Nc via acetylation was cloned as plasmid pNAT1 and analyzed (Krügel et al., 1988). Here we present the nucleotide sequence of nat1, its transcriptional start, a putative promoter and regulatory sequence, the deduced amino acid sequence and its comparative analysis via a protein data base. Transcriptional activity is detected by the expression of a promoterless
Fig. 1. Nucleotide sequence of natl. In the precoding region the open arrow shows the start of transcription; possible -10 and -35 regions are underlined, and small (sIR), medium (mIR) and large (lIR) inverted repeat sequences are indicated. A hypothetical ORF in the precoding region overlaps the start codon of natl (Krügel et al., in preparation).