CONTROL OF THE SYNTHESIS OF RIBOSOMES IN *MYCOBACTERIUM FORTUITUM*

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The *purpose of this study* was to test the value of quantification using real-time PCR in the analysis of the kinetics and control of the synthesis of ribosomes, in rapidly growing mycobacteria carrying two (rrnA and rrnB) ribosomal RNA operons per genome. The analysis was undertaken to provide insights into the control of the bacterial growth rate.

Methods: *M. fortuitum* were recovered from cultures in liquid medium at five different points along the growth curve (from exponential to stationary phases). The mycobacterial total RNA was isolated, purified, and retro-transcribed using random-hexamers to obtain cDNA. Quantitative real-time PCR was applied using the Light-Cycler System (Roche) and SYBR green DNA intercalator. The species quantified included mature 16S rRNA, pre-*rrn* products (*rrn*A-P1; *rrn*A-PCL1; *rrn*B-P1), and mRNA coding for two ribosomal proteins S12 [*rps*L] and L7 [*rpl*L] corresponding to the small and large subunits of the ribosome respectively.

Results: Relative to 16S rRNA the amounts of the pre-*rrn* products were similar during exponential phase and decreased during stationary phase. The amounts of mRNA encoding S12 and L7 also diminished on entry into stationary phase.

Conclusion: The contributions of *rrn*A and *rrn*B operons to 16SrRNA synthesis were found to be different. The *rrn*A operon was found to make the major contribution to 16S rRNA synthesis during both exponential and stationary phases of growth; the PCL1 promoter was found to be more active than the P1 promoter. In contrast, the contribution of the *rrn*B promoter was less during stationary phase than in exponential phase.