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Physiological role of the mycobacterial Pup-proteasome degradation pathway and its relation to virulence

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Pupylation, the conjugation of a prokaryotic ubiquitin-like protein (Pup) to polypeptide targets, marks proteins for proteasomal degradation. The Pup-proteasome system (PPS) was initially identified in *Mycobacterium tuberculosis*, where it was shown to be essential for full virulence of this pathogen. Later, the strict conservation of PPS genes in actinobacterial and nitrospiral species, most of which are non-pathogenic, suggested a fundamental role for this proteolytic pathway in bacterial physiology. To better understand the physiological roles of PPS components in *M. tuberculosis* and related species, we focused our efforts on *Mycobacterium smegmatis*, a model mycobacterial organism. We report that the PPS is essential for prolonged survival of *M. smegmatis* at stationary phase. Accordingly, analysis of pupylation dynamics during growth revealed increased levels of pupylated proteins and increased expression of pupylation-associated genes during stationary phase. Integration of our results with previously published data suggests that the demonstrated importance of the Pup-proteasome system for *M. smegmatis* persistence at stationary phase is also relevant for *M. tuberculosis*, as well as for other actinobacterial species.

Biography

Eyal Gur has completed his Ph.D. at the age of 31 years from Tel Aviv University and postdoctoral studies from Massachusetts Institute of Technology. He is now a principal investigator at Ben-Gurion University of the Negev, working on intracellular protein degradation in bacteria.

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