

MCB PLANT BIOLOGY SEMINAR SERIES F2009

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“Exploring non-coding RNAs in the multicellular bacterium *Streptomyces coelicolor*”

Monday, November 23, 2009

3:30 p.m.

SCI2315

ABSTRACT:

Streptomyces are soil dwelling bacteria that are renowned for their developmental complexity, and their metabolic capabilities. Their life cycle encompasses several differentiated states and culminates in the formation of long spore chains, much like that of the filamentous fungi. The streptomycetes also produce large numbers of metabolites having significant medical and agricultural value, including herbicides and most known antibiotics. *Streptomyces coelicolor* is the model organism for studying the regulation of development and metabolite production in the streptomycetes (Bentley et al., 2002), and while great strides have been made in piecing together regulatory networks governing these processes, there is still much that is not understood.

We are exploring the role of non-coding RNAs in the gene regulation of *S. coelicolor*. Taking a comparative genomics approach to non-coding RNA identification in *S. coelicolor*, and coupling this with the cloning of small RNAs (as cDNAs), we have amassed a small library of validated non-coding RNAs for further investigation (Swiercz et al., 2008). These include an unusual population of ‘tRNA halves’ (Haiser et al., 2008), as well a number of antisense and *trans*-acting RNAs. Subsequent genetic and biochemical investigations have demonstrated a role in antibiotic regulation for one antisense-regulated gene cluster, and defined a role in sporulation and spore germination for the gene products associated with a conserved functional RNA region (Haiser et al., 2009). We are currently working to expand our understanding of RNA-regulation in the streptomycetes by investigating additional non-coding RNAs, and by working to elucidate the mechanisms underlying RNA-mediated gene regulation in these bacteria.

Contact Annette Nassuth (anassuth@uoguelph.ca) should you wish to meet with the seminar speaker