Metabolic Pathways in *Microbispora sp.* ATCC-PTA 5024, Producer of NAI-107 Lantibiotic

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The actinomycete *Microbispora sp*. ATCC-PTA-5024 produces the lantibiotic NAI-107 (1) a promising drug to treat multidrug-resistant pathogen infections (2). *Microbispora* is a poorly characterized and this limited knowledge is detrimental to set-up NAI-107 production processes to efficiently deliver high-quality compound. High throughput techniques, like proteomics, may give insights on strain molecular physiology and biochemical capability and, above all, on metabolic pathways and regulatory mechanisms thereof associated with antibiotic production (3).
Thus *Microbispora* differential proteomic analyses were comparatively carried-out on wild type, null and super-producer strains by mean of 2-D-Differential Gel Electrophoresis and mass spectrometry procedures.
This study revealed differential regulation of pleiotropic regulators, stress response factors and proteins involved in many cell processes and metabolic pathways associated with NAI-107 production on-set and maintenance. In particular, proteins involved in molecular processes like amino sugar, nitrogen, phosphate and sulphur metabolism, oxidative stress and antibiotic biosynthesis and resistance are positively correlated while proteins involved in glycolysis, amino acid and nucleotide metabolism are negatively associated to NAI-107. Therefore, these data coupled to gene ontology, revealed a comprehensive set of differentially regulated proteins which may play roles as trigger or sustaining or response factors in NAI-107 production.
Altogether this information may be used as a knowledge background to rationally improve NAI-107 production by *Microbispora* fermentation optimization or for strain improvement by genetic engineering on targeted genes.

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Chromatin remodelers, nucleoplasm compartment and proteinopathies

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Recent advances in the field of transcriptome exploration have revealed novel sets of new ncRNAs like the long non-coding RNAs, which seem to be key components of epigenetic regulatory networks. Indeed, recent studies have shown that lncRNAs regulate the gene expression by chromatin remodelling, transcription, splicing and RNA decay control, enhancer function, and epigenetic regulation. An emerging theme from multiple model systems is that lncRNAs form extensive networks of ribonucleoprotein (RNP) complexes with numerous chromatin regulators and then target these enzymatic activities to appropriate locations in the genome. Using D. melanogaster as model system, I recently found a functional interaction between ISWI, the catalytic subunit of several ATP-dependent chromatin-remodeling complexes, and the lncRNA hsr-omega (hsrω). In Drosophila the nucleus-limited hsrω-n transcript is dynamically associated with several different