I. ABSTRACT
in English

The presented work is focused on secondary metabolism and its regulation in *Streptomyces ambofaciens* and *Streptomyces lividans* with special interest in new biosynthetic pathways.

The sequencing of bacterial and fungal genomes revealed that the number of their secondary metabolite biosynthetic gene clusters greatly exceeds the number of produced secondary metabolites. Further studies showed that at least some of the newly discovered clusters, called cryptic since no product had been associated to them, were expressed in certain conditions and that they directed the biosynthesis of exploitable secondary metabolites (Gottelt *et al.*, 2010; Gross *et al.*, 2007; Pang *et al.*, 2004). Therefore, these cryptic clusters have been considered as one of the promising reservoirs of new bioactive molecules.

Using different approaches I studied the cryptic secondary metabolite biosynthetic gene clusters of *Streptomyces ambofaciens*, a strain exploited industrially for the production of the antibiotic spiramycin. In the second part of this work, I was interested in the regulation of secondary metabolite biosynthesis and in manipulating genes encoding regulatory proteins (Rep and DasR) in order to activate the expression of cryptic clusters. The third part of this work studied the effect of the inactivation of the *ppk* gene, encoding the enzyme polyphosphate kinase, on the production of secondary metabolites and on the whole protein expression pattern in *Streptomyces lividans*.