The genome of *Lyso bacter capsici AZ78*: a biocontrol agent of *Plasmopara viticola*

**Introduction**

The genus *Lyso bacter* (Family Xanthomonadaceae) encompasses bacterial strains that share physiological features, such as the release of lytic enzymes and antibiotics, that make them capable to control plant diseases (Hayward et al., 2010). Recently, we showed that the application of *L. capsici AZ78* cells on grapevine plants drastically reduces the infections of *Plasmopara viticola* (Puopolo et al., 2014). Additionally, we provided the evidence that *L. capsici AZ78* can be combined with copper fungicides, thus increasing the efficacy against this pathogen (Puopolo et al., 2014).

**Objective and future prospective**

The aim of my PhD project was to analyze the genome of *L. capsici AZ78* in order to have information useful for its possible employment as a new active ingredient in biofungicides.

**The genome**

The *L. capsici AZ78* genome (JAJA00000000) consists of 6,315,650 bases assembled into three contigs, and the G+C content is 66.4%. The genome contains 5,292 coding sequences, 93 predicted RNAs of which 1 is a tRNA, 7 rRNAs and 85 tRNAs.

**Production of antibiotics**

*L. capsici AZ78* genome has genes involved in the production of secondary metabolites toxic to Gram-positive bacteria, phytopathogenic fungi and oomycetes. Specifically, the *AZ78_1098* gene has homology with the gene of *L. enzymogenes* C3 involved in the synthesis of a macrocyclic lactam antibiotic (Fig. 1) (Puopolo et al., 2016).

**Lytic enzyme and siderophore production**

The direct biocontrol activity of *L. capsici AZ78* is based on the presence of several lytic enzymes. Specifically, the genome has genes coding for chitinases, glucanases, lipases, proteases, and xylanases (Tab. 1). The in vitro experiments confirmed the outcome of the genome analysis (Fig. 2). Moreover, *L. capsici AZ78* compete with other microorganisms for the iron resources in the environment by the production of siderophores.

**Resistance to copper and toxic compounds**

The genome of *L. capsici AZ78* contains genes responsible for the transport, homeostasis, uptake and resistance to copper ions (Tab. 2). All these data are in agreement with the *in vitro* experiments, which showed that the combination of this bacterial strain with copper based fungicides is possible (Fig. 3) (Puopolo et al., 2014; 2016). Moreover, the genome analysis revealed the presence of genes coding for efflux pumps involved in the resistance to antibiotics, heavy metals and toxic compounds (Tab. 2).

**Conclusion**

All the information provided by the genome of *L. capsici AZ78* will be helpful to determine the mechanisms involved in the biological control of phytopathogenic fungi and oomycetes. This knowledge is important for the future development of *L. capsici AZ78* as an active ingredient in new biofungicides.

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**References**


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