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TESTING THE HYPOTHESIS OF ACQUIRED AMINOGLYCOSIDE RESISTANCE IN RALSTONIA SPP.

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Backgrounds

Ralstonia spp. are ubiquitous in water environments, including drinking water. The species *R. pickettii* and *R. mannitolilytica* have been associated to nosocomial outbreaks and to a wide array of antibiotic resistance phenotypes. Aminoglycoside resistance (AGR) is a variable phenotype in those *Ralstonia* species, suggesting that it can be acquired and not intrinsic as, for example, colistin resistance.

Objectives

Investigate the AGR mechanisms in *Ralstonia* spp. isolated from aquatic environments and assess a possible relationship with the type of water (mineral, tap, wastewater) from which they were isolated. Search hints for a possible AGR acquisition.

Methods

A collection of >50 *Ralstonia* spp. (including some successively transferred in the presence of gentamicin) were characterized for their AGR phenotypes. From this collection two *R. pickettii*, with distinct AGR phenotype and isolated from the same habitat (hospital effluent), were selected for comparative genome sequencing analysis. In this analysis, genetic determinants such as ICEs (integrative conjugative elements), efflux pumps and 16S rRNA methylases that could be worthwhile to screen in the *Ralstonia* spp. were selected.

Conclusions

Beside AGR, resistance to beta-lactams and colistin was frequent in *Ralstonia* spp., regardless the type of water. The comparative whole genome analysis revealed that genes related with tolerance to arsenic and toxic compounds, ICEs, lysozyme inhibitors and with phages/prophages were only present in the AGR strain. Whilst it was not possible to identify AGR determinants associated with ICEs, components of these genes cassettes were detected in most of the AGR strains, leading to the hypothesis that ICEs may be associated with genome dynamics mechanisms. AGR mechanisms through efflux pumps and/or 16S rRNA methylases are being explored in these strains.