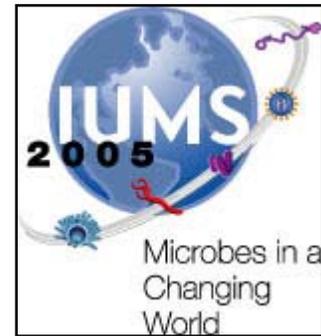


The XI International Congress of Bacteriology and Applied Microbiology
San Francisco, USA, BP-459, 23-28 July 2005.

Quorum Sensing in the Genus *Aeromonas*

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Background

The environmental distribution of the *N*-acylhomoserine lactone (AHL)-mediated gene expression systems amongst bacteria is very poorly understood with merely 2.2% (21 bacterial genera) of the total number of bacterial genera listed in the Bergey's Manual of Systematic Bacteriology, known to harbor the AHL producing species. At the species level, the percentage of AHL producers drops to a fraction of a percent. The genus *Aeromonas*, in which cell division is linked to quorum sensing, is a medically important genus, which expresses a range of high cell density associated virulence determinants. The purpose of this study was to investigate the genetic diversity of the quorum sensing system in the genus *Aeromonas*.

Materials

Spent culture supernatants from clinical, environmental or reference *Aeromonas* strains collected from diverse habitats were tested for the production of AHLs using three biosensor strains capable of detecting a diverse range of AHLs. Strains found negative for AHL production were checked for the presence of quorum sensing regulon genes using dot-blot hybridization against an *ahyRI* gene probe. The transcriptional regulator gene was PCR amplified from all the *Aeromonas* strains and sequenced. Phylogenetic analysis was performed using MEGA v2.1.

Results

All the strains used tested positive for the presence of the *LuxRI* gene homologs using the dot-blot analysis, whereas only three strains tested negative for production of the AHL using the three biosensors. Sequence analysis revealed insertion/deletion at two loci lying in the autoinducer-binding domain of the transcriptional regulator gene homologs. As compared to the other molecular chronometers for the genera, lack of agreement with the phylogenetic groupings based on this gene existed. No evidence for lateral gene transfer between aeromonads and other genera whose *luxR* gene homologues have thus far been sequenced was observed.

Conclusion

These findings indicate that the quorum sensing regulon is universally present with a very high percentage sequence similarity in the genus *Aeromonas*, irrespective of the nature of the isolates, whether clinical or environmental. Since, it is present universally in this genus, one can use this system as a potential target for treating the *Aeromonas* borne infections.