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AhlD, an N-acylhomoserine Lactonase in *Arthrobacter* sp. and its Homologues in Diverse Bacteria

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N-acylhomoserine lactones (AHLs) are widely conserved quorum-sensing signals in many Gram-negative bacteria, which play an important role in the regulation of the virulence factors in pathogenic bacteria. With the aim of isolating strains and enzymes capable of interrupting quorum sensing by AHL inactivation, bacteria were screened for AHL degradation by their ability to utilize *N*-3-oxo-hexanoyl homoserine lactone (OHHL) as the sole carbon source. Representative isolates degrading OHHL were identified as members of the genera *Arthrobacter*, *Ralstonia* and *Rhodococcus*. One of these isolates, *Arthrobacter* sp. IBN110 was found to grow rapidly on OHHL, and degrade various AHLs with different lengths and acyl side chain substitutions. The gene encoding the enzyme catalyzing AHL degradation, designated *ahlD*, was cloned from *Arthrobacter* sp. IBN110 and found to encode a protein of 273 amino acids. A mass spectrometry analysis indicated that AhlD probably hydrolyzes *N*-hexanoyl-homoserine lactone via AHL-lactonase, and releases the *N*-hexanoyl-homoserine. A comparison of AhlD with other known AHL-degrading enzymes, *Bacillus* sp. 240B1 AiiA, a *Bacillus thuringiensis* subsp. *kyushuensis* AiiA homologue, and *Agrobacterium tumefaciens* AttM, revealed 25, 26, and 21% overall identities in the deduced amino acid sequences, respectively. These identities were relatively low, but, the HXDH≈H≈D motif was conserved in all the AHL-lactonases, suggesting that this motif is essential for AHL-lactonase activity. From a database search based on the conserved motif, putative AhlD-like lactonase genes were found in several other bacteria, including *Klebsiella pneumoniae*, *Bacillus stearothermophilus*, *Sulfolobus solfataricus* and *Thermoplasma volcanium*. In practical, it was observed that AhlD homologues, AhlK, AhlS and AhlT from *K. pneumoniae*, *S. solfataricus* and *T. volcanium* have AHL-degrading activity, indicating AhlD-like lactonases were distributed in diverse bacteria. Expression of *ahlD* gene in plant pathogen *Erwinia carotovora* reduced significantly both the AHL amount and pectate lyase activity. In addition, the *Arthrobacter* sp. IBN110 attenuated soft rot disease in potatos caused by *E. carotovora*. The results implicate the possibility of applying the AHL-degrading bacteria and AhlD homologues in the control of the AHL-producing pathogenic bacteria.