

ABSTRACT

EVOLUTION OF REGULATORY ELEMENTS IN THE 2,4-DICHLOROPHENOXYACETIC ACID PATHWAY

The broadleaf herbicide 2,4-dichlorophenoxyacetic acid (2,4-D) has been used worldwide on cereal and grain crops since its introduction in the late 1940s. Bacteria have acquired the ability to use 2,4-D as a primary carbon and energy source. The enzymatic genes exist in subtypes and have been studied thoroughly. The regulation of the 2,4-D pathway isn't completely understood. A regulatory gene *tfdR* has been identified. This regulator has been classified as a *LysR*-type regulator, because of sequence identity and a specific motif at the N-terminus. This research sought to determine if *tfdR* also existed in subtypes, and if the regulatory gene was recruited into the pathway independently of the structural genes. DNA alignments show 75-90% sequence identity, while amino-acid alignments show 82-91% sequence identity. Phylogenetic analysis revealed three subtypes of *tfdR* and indicated independent recruitment of the regulator. One organism was regulating the pathway using *tcbR*, a related *LysR*-type regulator.

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