

Supplementary Materials

The *Pseudoalteromonas luteoviolacea* L-amino Acid Oxidase with Antimicrobial Activity is A Flavoenzyme

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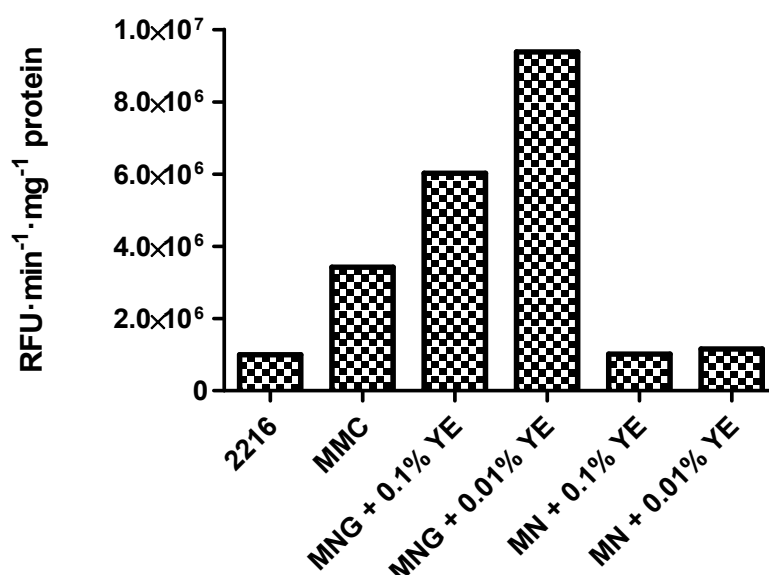


Figure S1. LAAO activity in the supernatants of strain CPMOR-2 cultivated in different media at the stationary phase. LAAO activity was assayed using casamino acids 2% as a substrate.

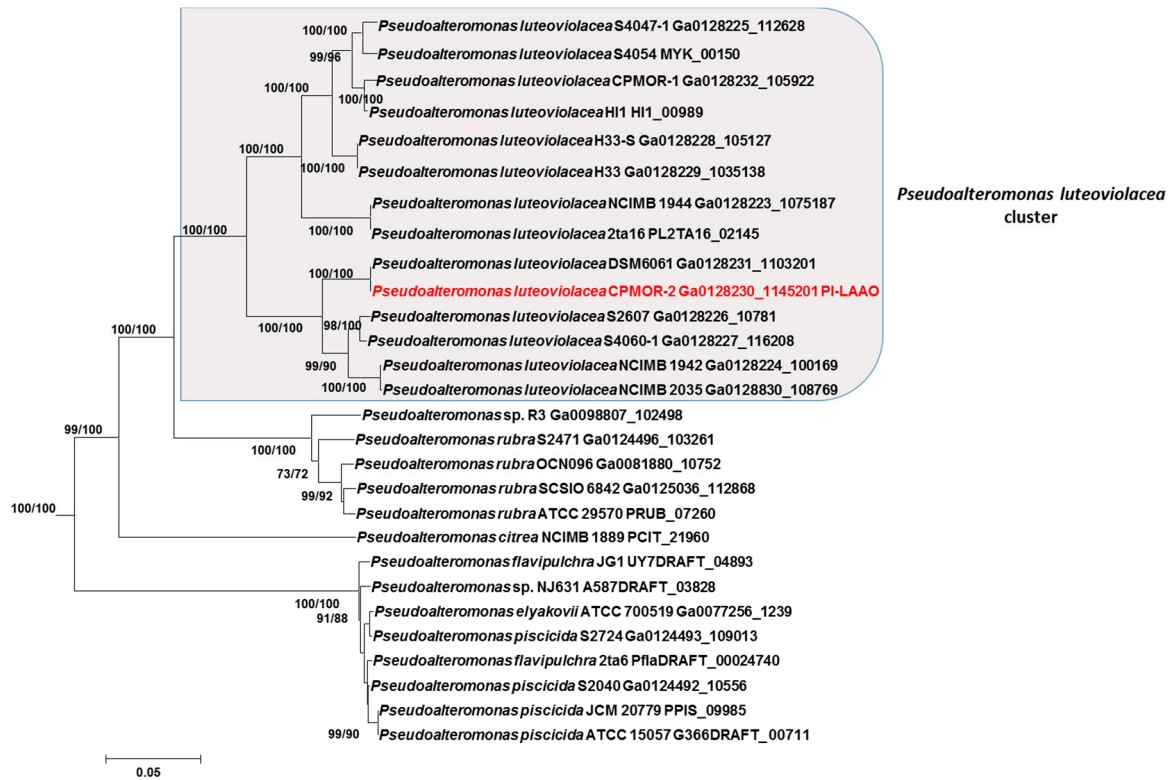


Figure S2. Phylogenetic relationships of Group 1, proteins similar to PI-LAAO in the genus *Pseudoalteromonas*. The tree was created by the NJ method integrated in the program MEGA6. Sequences were aligned using the program MUSCLE built in MEGA6. The evolutionary distances were computed using the p-distance method and are in the units of the number of amino acid differences per site. Numbers at branches indicate bootstrap values higher than 70% for both NJ and ML trees. PI-LAAO is indicated in red.

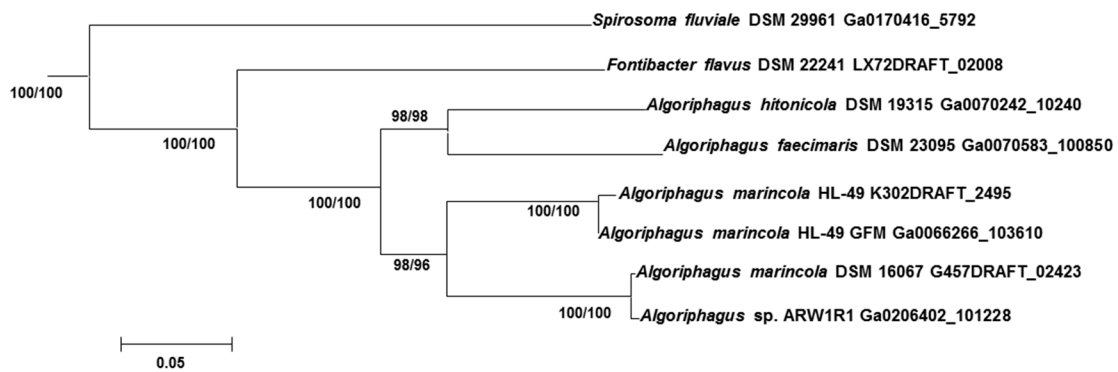


Figure S3. Phylogenetic relationships of Group 2 of proteins similar to PI-LAAO. The tree was created by the NJ method integrated in the program MEGA6. Sequences were aligned using the program MUSCLE built in MEGA6. The evolutionary distances were computed using the p-distance method and are in the units of the number of amino acid differences per site. Numbers at branches indicate bootstrap values higher than 70% for both NJ and ML trees.

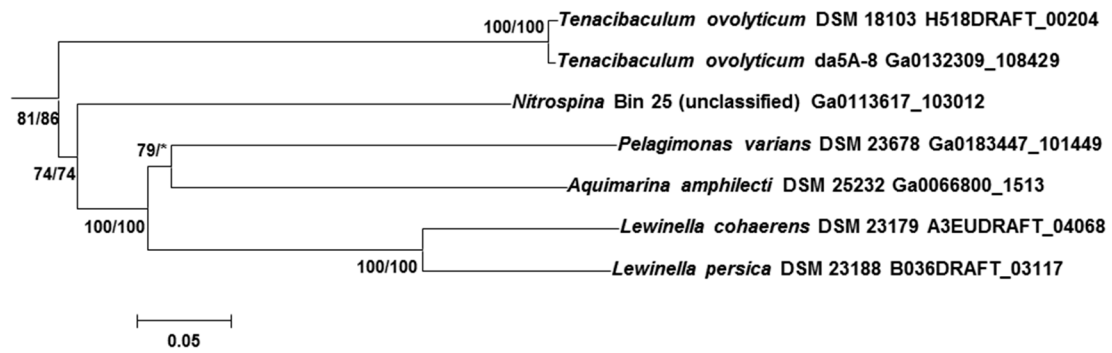


Figure S4. Phylogenetic relationships of Group 3 of proteins similar to Pl-LAAO. The tree was created by the NJ method integrated in the program MEGA6. Sequences were aligned using the program MUSCLE built in MEGA6. The evolutionary distances were computed using the p-distance method and are in the units of the number of amino acid differences per site. Numbers at branches indicate bootstrap values higher than 70% for both NJ and ML trees. An asterisk indicates that this branch was not detected, or it had a value lower than 70% in one of trees.