

Supplementary figures

Figure S1. Genomic content of genes encoding the Moco biosynthetic pathway, MOSC-containing protein and AOR in *D. fastidiosa* JC13. The genes encoding the Moco biosynthetic pathway, MOSC-containing protein and AOR are shown in blue, red and yellow, respectively. Coding direction is also indicated.

Figure S2. Relationship between Mo/W transport systems, molybdoproteins and environmental factors in bacteria. (A) Habitat; (B) Oxygen requirement.

Figure S3. Distribution of predicted tungstoprotein families. The W-containing DMSOR family includes W-containing FDH and ACH.

Figure S4. Phylogenetic analysis of ACH proteins in *Gordonibacter pamelaee* 7-10-1-b. Sequences of ACH proteins were selected from *G. pamelaee* 7-10-1-b (grey) and some other representative organisms belonging to different phyla (black). Other protein branches of the DMSOR family are compressed and represented by family names, such as DMSOR (blue and bold), FDH (red and bold) and nitrate reductase (green and bold). Both bootstrap values and the measurement of distance for the branch lengths (shown by a bar) are indicated.

Figure S1

***Dielma fastidiosa* JC13**

NZ_HE578931:



NZ_HE578932:

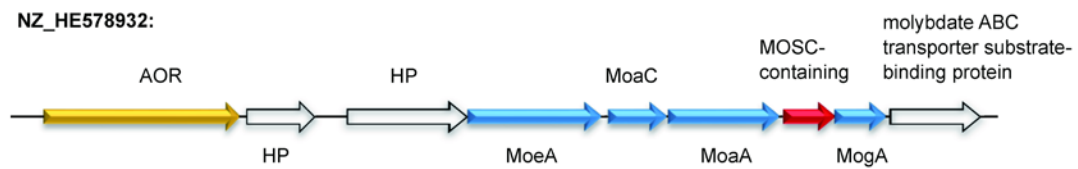
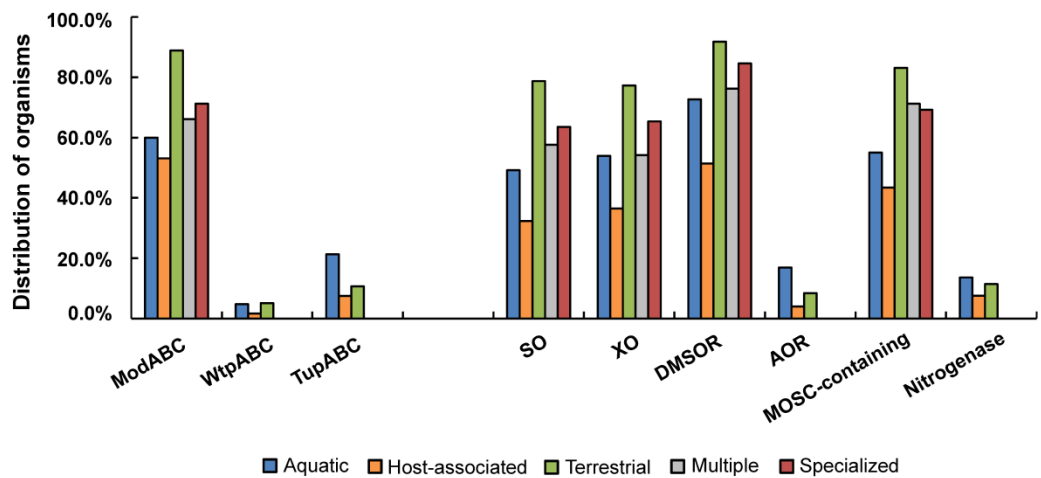


Figure S2

A.



B.

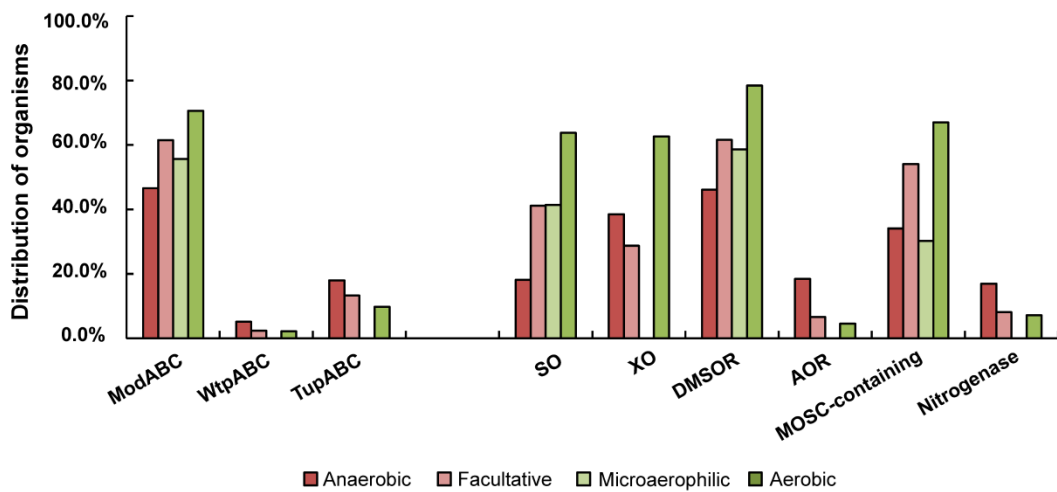


Figure S3

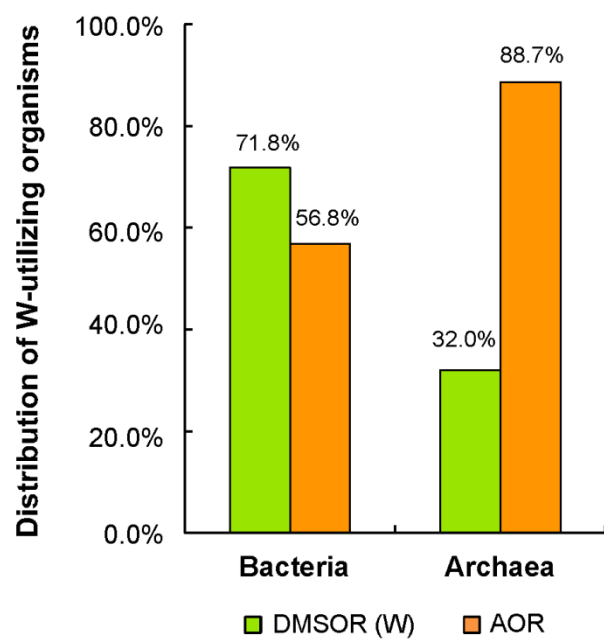


Figure S4

