

***NosZ* gene cloning, reduction performance and structure of *Pseudomonas citronellolis* WXP-4
nitrous oxide reductase**

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S1.1 His tag protein purification

The Ni-Agarose Resin was added to the chromatographic column. After the gel was separated from the solution, ethanol slowly flowed out from the bottom outlet liquid (1 mL packing for purification of 20-30 mg protein). After adding 5 column volumes of deionized water to rinse the column, the column equilibrated by 10 column volumes of Binding Buffer.

Then, Binding Buffer was used to dilute the sonicated crude enzyme solution equally and load it on the column at an appropriate flow rate to collect the flow-through solution. Other proteins were washed away by adding 15 column volumes of Soluble Elution Buffer, and then appropriate amount of Soluble Elution Buffer were used to elute and collect N₂OR.

S1.2 SDS-PAGE

40 μ L of protein solution and 10 μ L of 5 \times SDS Loading buffer were mixed, and boiled in water bath for 10 mins. 4%-20% of the precast gel was putted into the protein electrophoresis tank correctly, and 1 L Tris-MOPS-SDS electrophoresis buffer was used for electrophoresis. After carefully pull out the comb in the gel, 7 μ L protein sample were added to the gel hole. The SDS-PAGE electrophoresis system (Basic Bio-rad Laboratories) ran at 140 V for 70 minutes until the sample reaches the bottom of the gel to complete the electrophoresis. Finally, the gel was placed in a protein staining and decolorizing instrument for 10 mins.

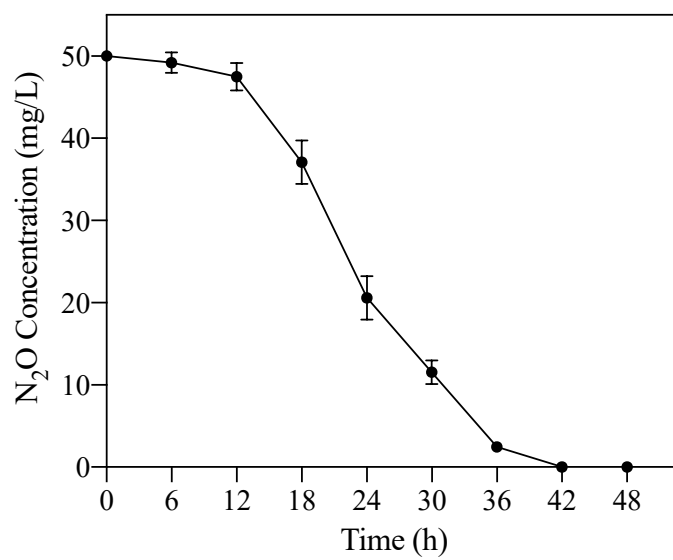


Fig. S1 N₂O reduction performance of *P. citronellolis* WXP-4.

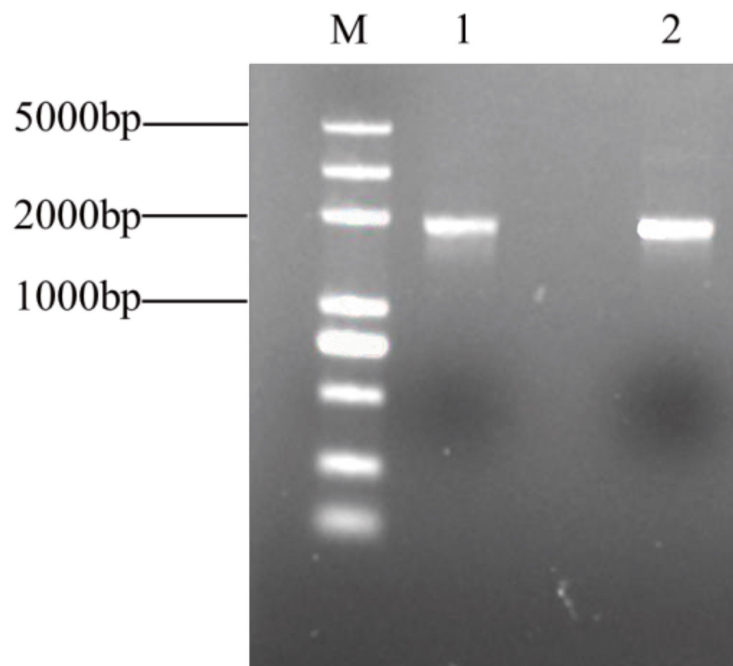


Fig. S2 Agarose gel electrophoresis of the *nosZ* gene PCR products. M: marker; 1 and 2: PCR products of *nosZ* gene.

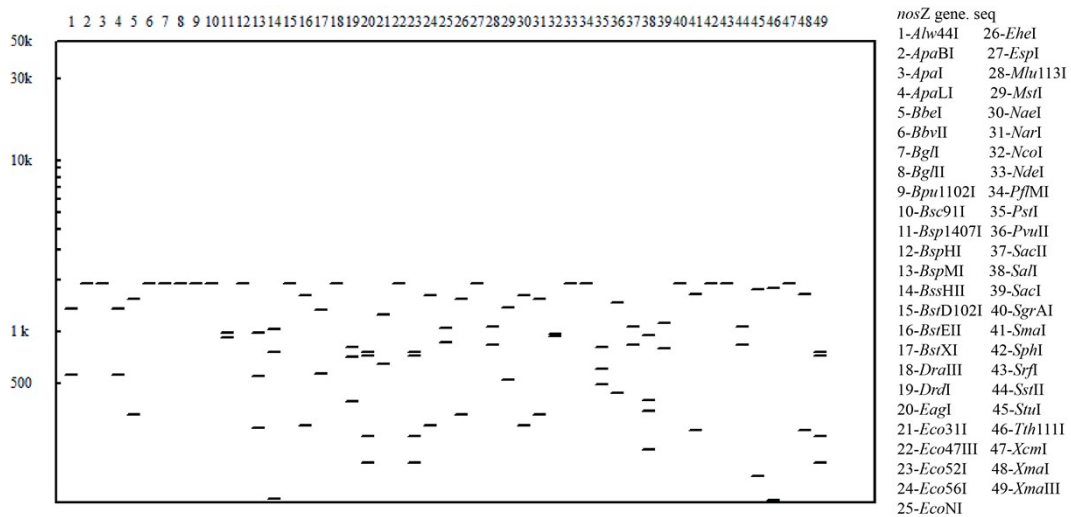
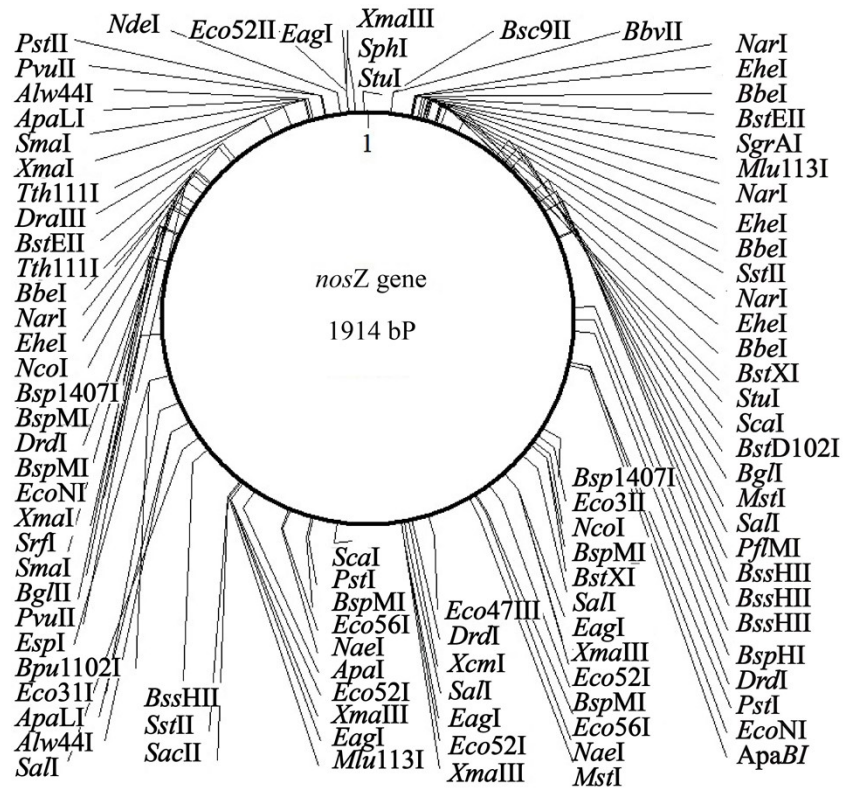


Fig. S3 Restriction map of *nosZ* gene. Electrophoretic simulation of single enzyme digestion of *nosZ* gene.

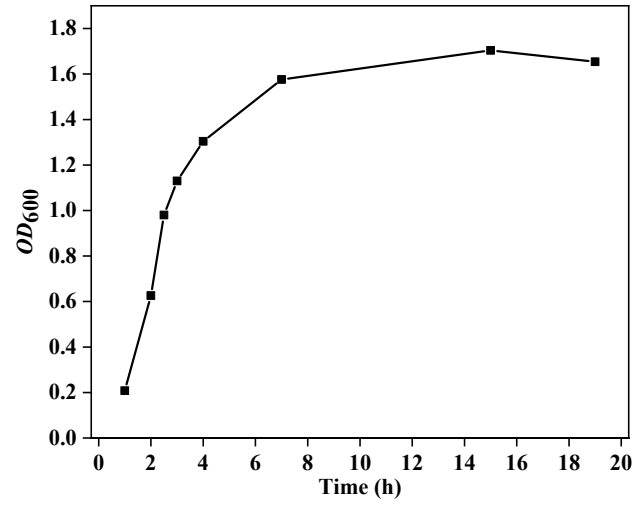


Fig. S4 Growth curve of *E. coli* BL21(DE3)-pET28a-nosZ.