Proteomic Analysis of 17β-Estradiol Degradation by *Stenotrophomonas maltophilia*

Zhongtian Li[1], Renu Nandakumar[2], Nandakumar Madayiputhiya[2], and Xu Li[1,*]

[1]Department of Civil Engineering, [2]Proteomic and Metabolomic Core Facility, Redox Biology Center, Department of Biochemistry, University of Nebraska-Lincoln

** Corresponding author:*
844 N. 16th St., N117 SEC Link
Lincoln, NE 68588-6105
Tel.: +01-402-472-6042; Fax: +1-402-472-8934
E-mail address: xli4@.unl.edu

Supporting Information.

6 Pages

3 Figures

1 Table

Preliminary Degradation Experiment

Each E2 degrading bacterial strain isolated from the enrichment reactors was added to 250-mL R2A medium saturated with E2 or E1. After 28 hours of growth at 30℃, 50-mL of each cell culture was collected and centrifuged (8,000 × g, 15 min at 4℃). The cell pellets were washed using phosphate buffer saline (pH=7.2) twice and transferred to a flask containing 100-mL sterile E2-saturated NMS medium or 100-mL sterile E1-saturated NMS medium. The flasks were placed on the shaking table (120 rpm) in a 30℃ water bath for 26 hours. At the end of the experiment, 70 mL of reactor content was filtered through a sterile 0.2 μm Teflon® filter and the filtrate was stored in an amber glass bottle at -20℃ for estrogen measurements. Sterile E2-saturated NMS and E1-saturated NMS media with no bacterial cells were used as controls in the experiment.

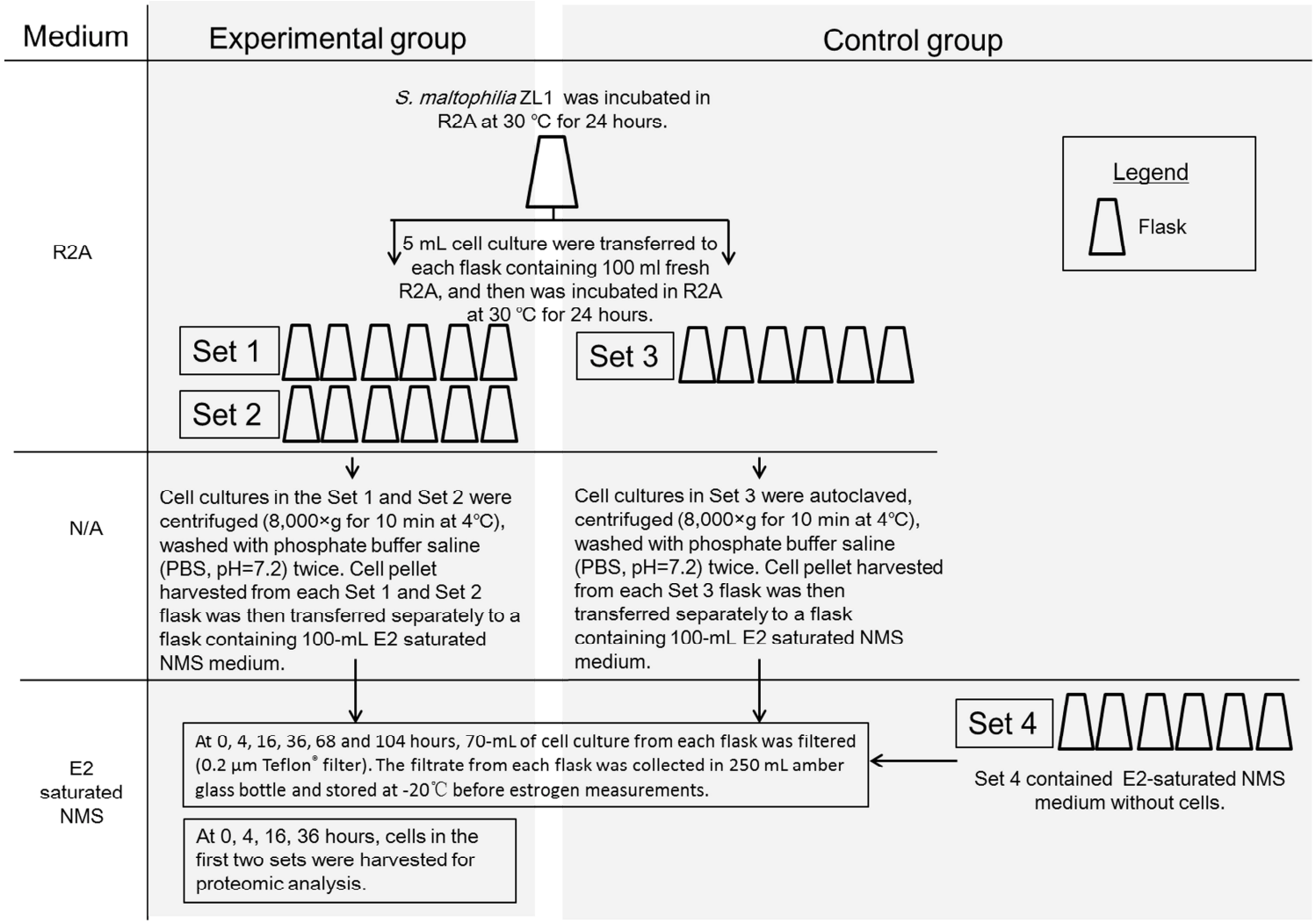

Figure S1. Flow chart describing the E2 degradation experiment.

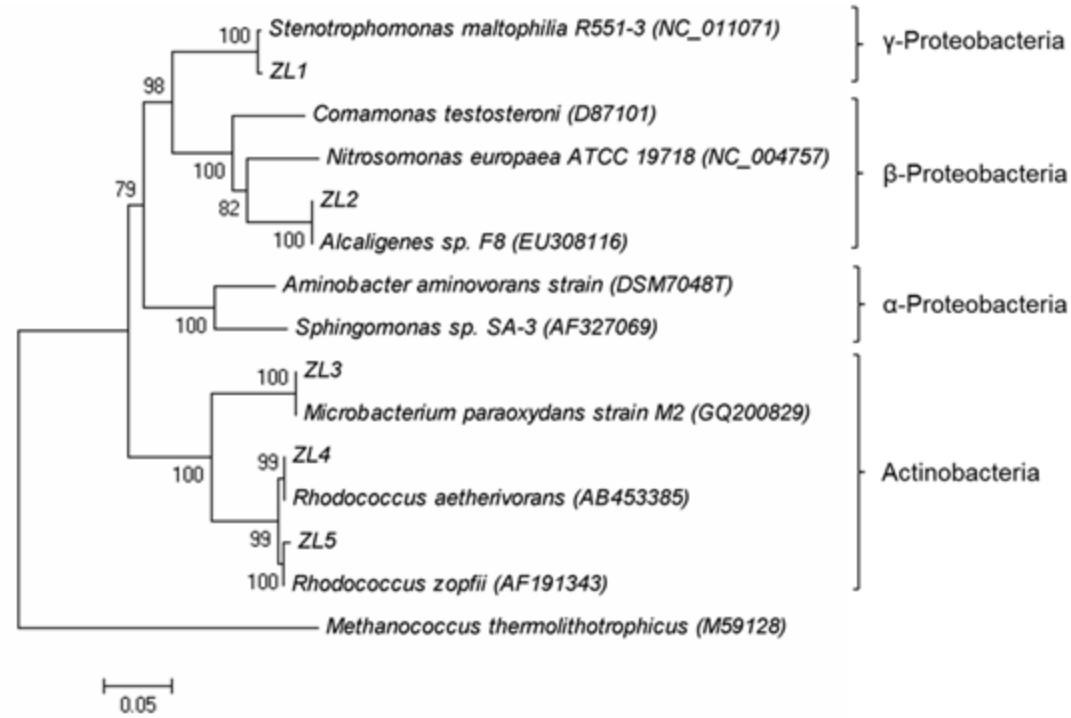

Figure S2. Phylogenetic tree of the estrogen degrading bacteria isolated from the enrichment experiment. Construction of the phylogenetic tree was based on the neighbor-joining method with 1000 bootstrap replications. An archaeal strain *Methanococcus thermolithotrophicus* was used as an out-group.

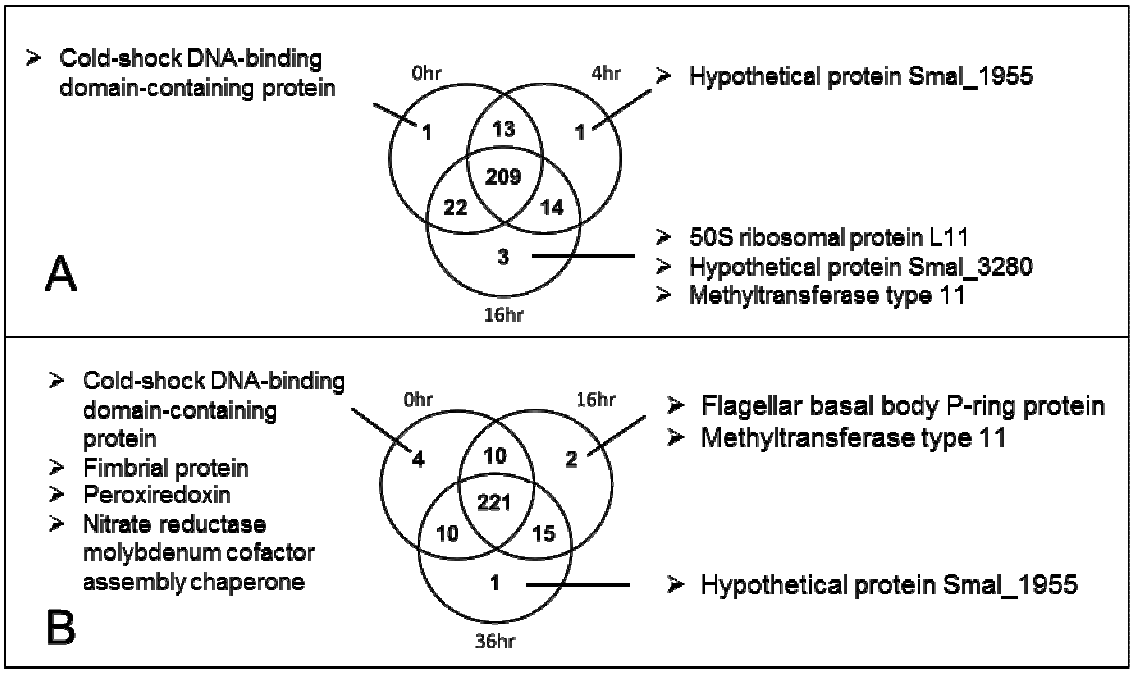

Figure S3. Venn diagram comparing expressed protein profiles among the three time points in Phase 1 (0, 4 and 16 hr) (A) and those among the two times points in Phase 2 (16 and 36 hr) and time zero. Unique proteins were listed for each sampling event.

Table S1. Extracted protein concentrations in mg/mL at 0, 4, 16, and 36 hours.

	0	4	16	36
Rep 1	5.60	5.54	6.17	5.46
Rep 2	5.70	5.60	6.45	5.34
Average	5.65	5.57	6.31	5.40
Std. Deviation	0.07	0.04	0.20	0.08