

**Diversity of gene clusters for polyketide and nonribosomal peptide
biosynthesis revealed by metagenomic analysis of the Yellow Sea
sediment**

Running title: Natural product gene diversity of marine sediment

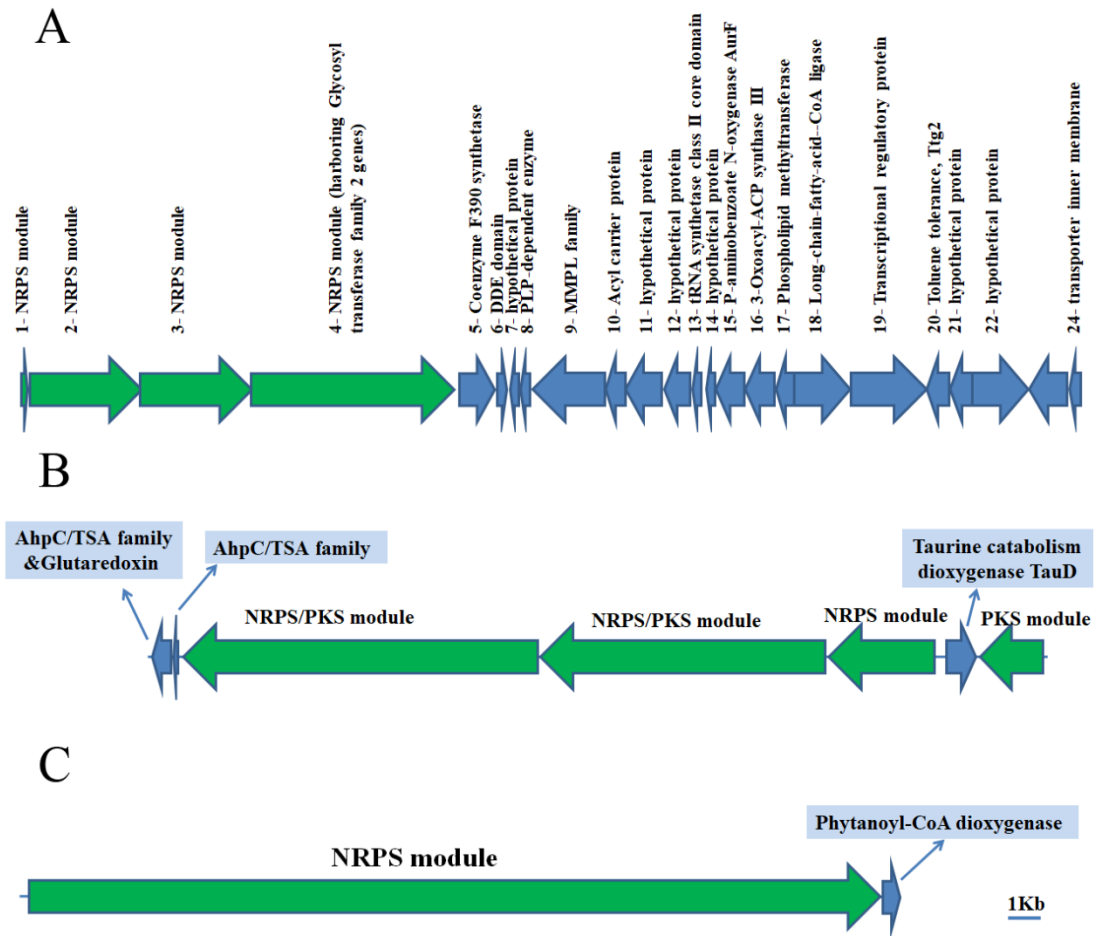
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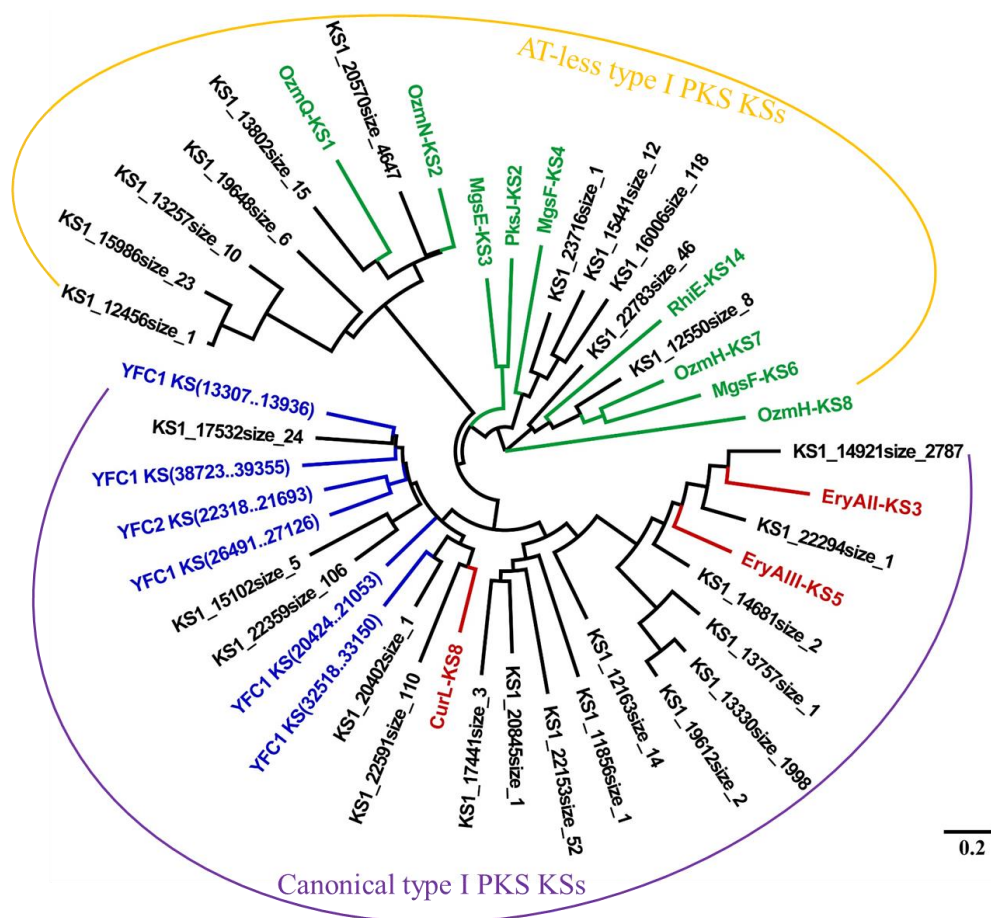
Correspondence

Dr. Xing Yan

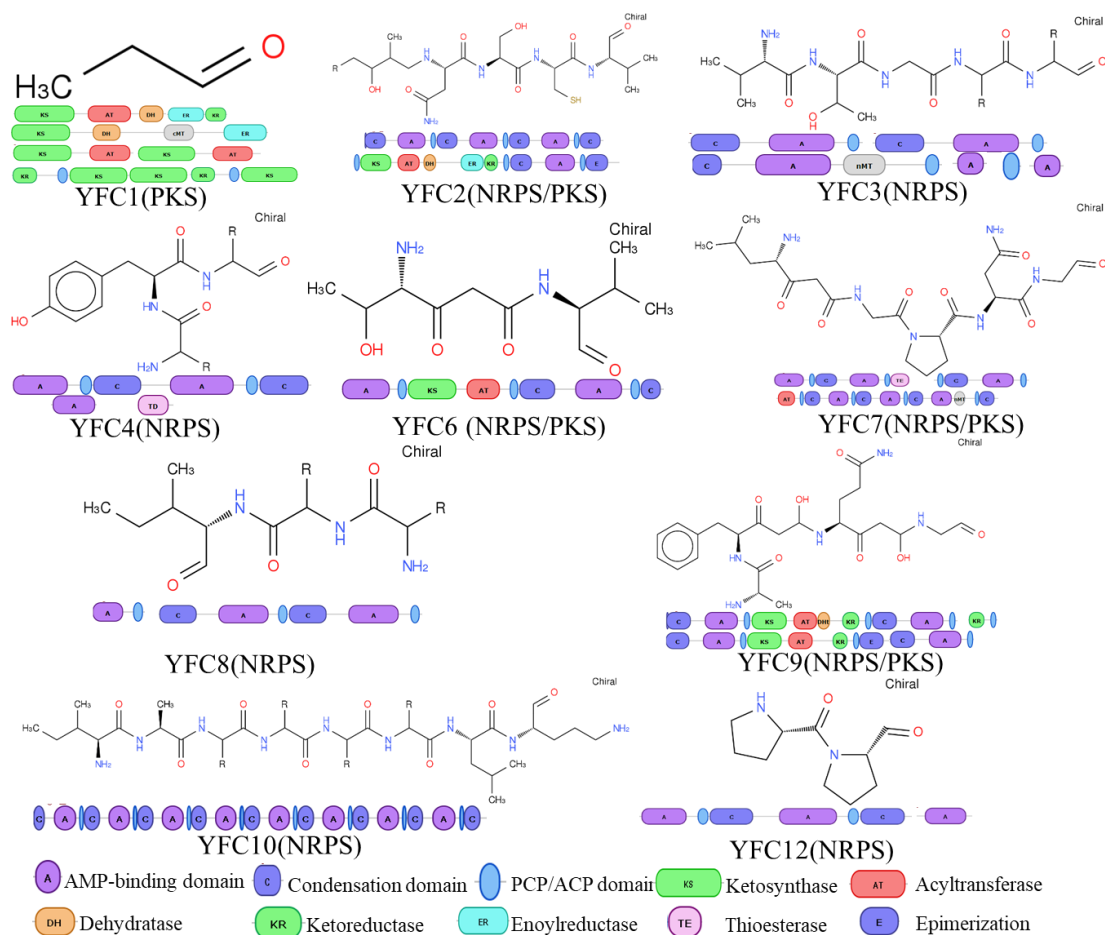
E-mail: yanxing@sibs.ac.cn



Supplementary Fig. S1 Gene organizations of 3 contigs YFC3 (A), YFC10 (B) and YFC5 (C) recovered from Yellow Sea sediment. The fosmid contigs were annotated with FGENESB (<http://linux1.softberry.com/berry.phtml>) and BLASTX.



Supplementary Fig. S2 Phylogenetic trees of KS representative sequences of each OTU obtained from Yellow Sea sediment and the reference functional characterized sequences. The representative KS sequences of each OTU were marked with black; The sequences identified in fosmid contigs were marked with blue; The reference AT-less type I PKS KSs were marked with green; The reference Canonical type I PKS KSs were marked with green.



Supplementary Fig. S3 Potential PKS or NRPS substructure biosynthesized by the fosmid contigs predicted with antiSMASH were shown. All the NRPS/PKS domains of each contig used to predict the structure were shown underneath the structure. Rough prediction of core scaffold based on assumed PKS/NRPS colinearity; tailoring reactions not taken into account.