

Divergence between sea urchins and their microbiota under speciation

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This PDF file includes:

Figs. S1 to S5

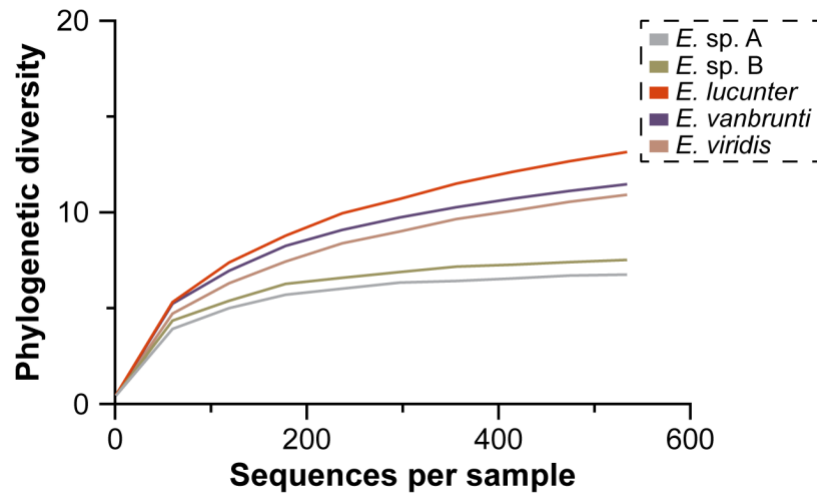


Figure S1. Alpha rarefaction curve for the bacterial community associated with the microbiota of eggs of *Echinometra*. The rarefaction depth was 534 sequences.

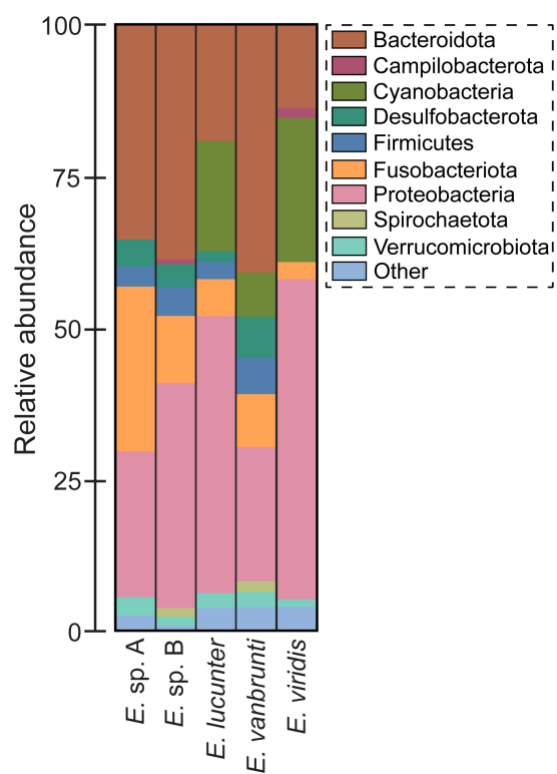


Figure S2. Phylum-level profiles of the bacterial communities associated with the eggs of the sea urchin *Echinometra* spp.

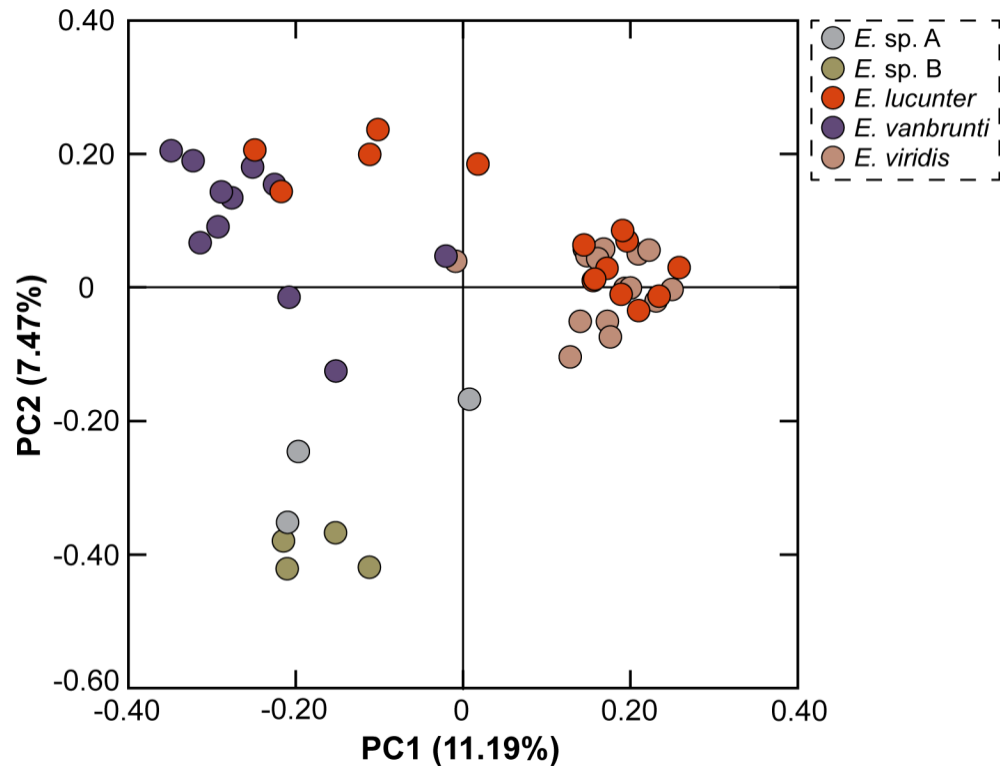


Figure S3. Species-specificity in the egg microbiota for *Echinometra*. Principal coordinate analysis depicting community relatedness of microbiome membership (unweighted UniFrac) for eggs from the sea urchin *Echinometra*.

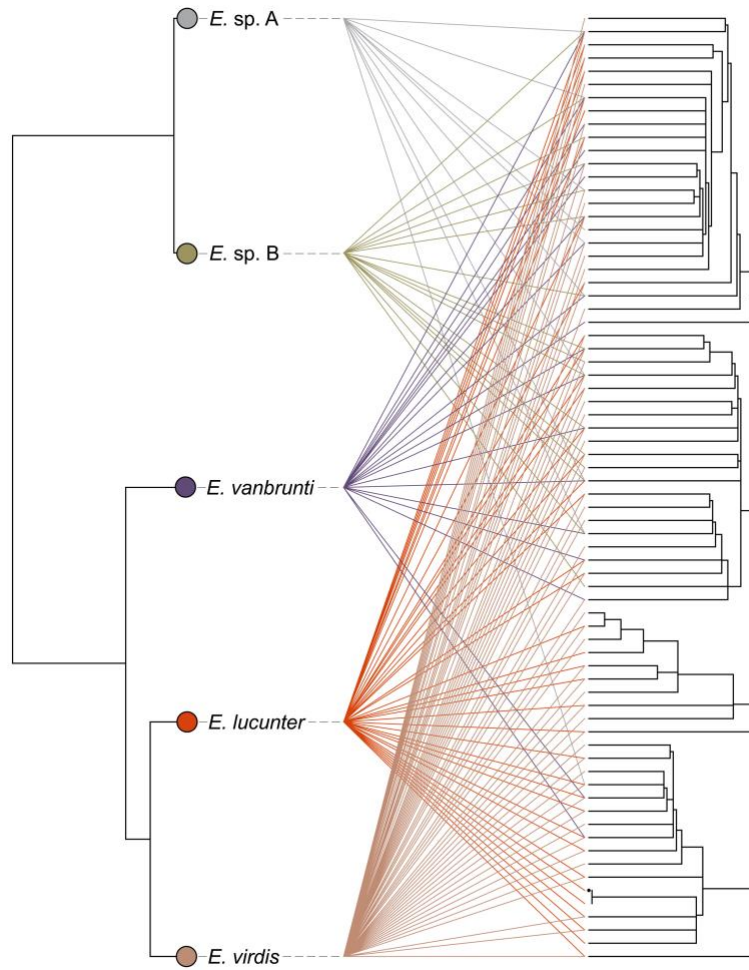


Figure S4. No co-phylogenetic signal between *Echinometra* and *Photobacterium*.

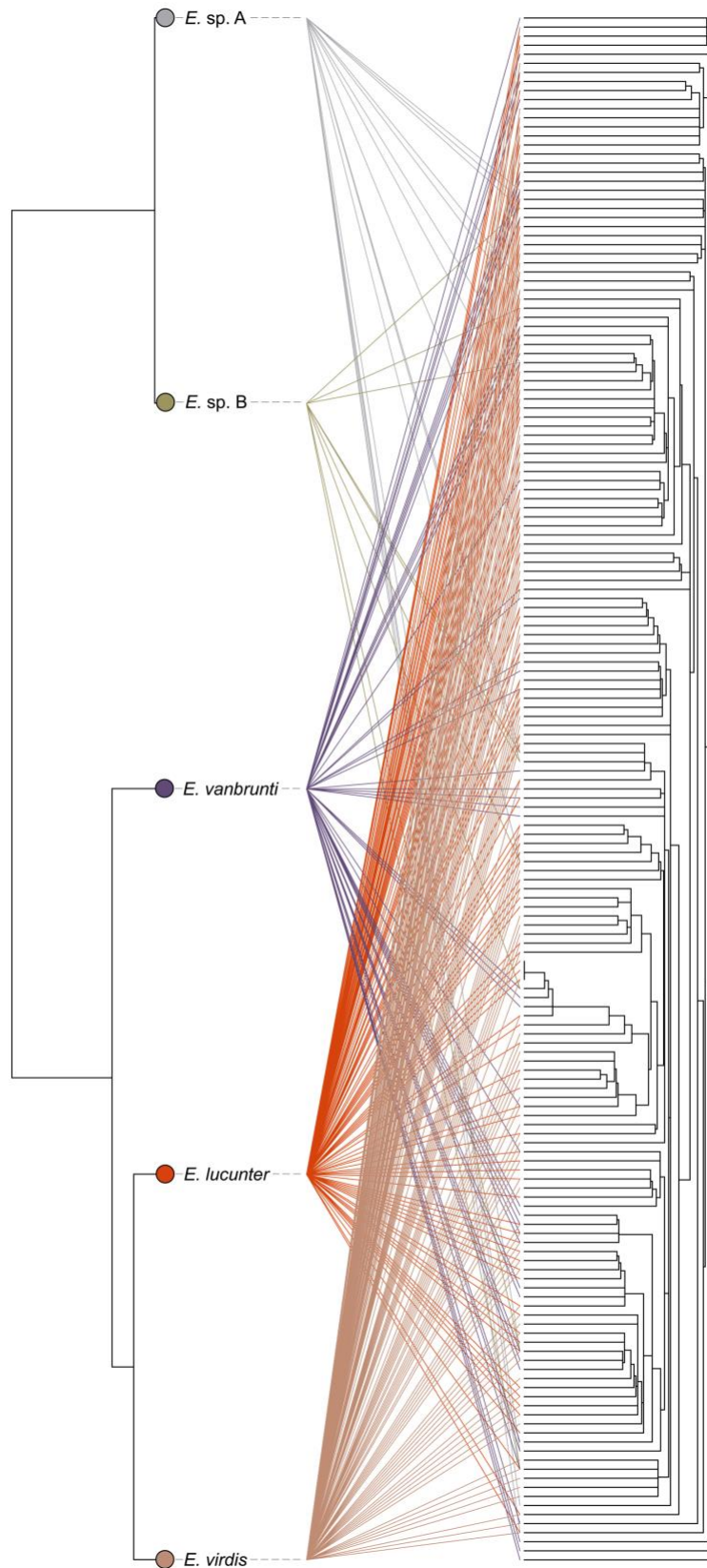


Figure S5. No co-phylogenetic signal between *Echinometra* and *Vibrio*.