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Social trematodes increase standing army size in areas of greater invasion threat

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There are two provided data files and R script file underlying our analyses:

* Survey\_Total\_Prevalence.csv
* Survey\_Total\_Caste.csv
* Biology Letters – R Code- ALL - FINAL.R

Below, we provide column header information for data columns that are not completely self-explanatory.

**Column header information for both data files:**

* *Number* is the number of the snail used for the Survey\_Total\_Prevalence. Allows us to combined files later on.
* *Sites* are individual locations within a given *Estuary.*
* *Date* is the date the snail was dissected.
* *Species* is the snail species (*C. californica* or *C. pliculosa*). Only the Pacific *C. californica* was used for this manuscript.
* *Variant -* Our sampling of *C. californica* included what were traditionally considered to be three species (*C. californica, C. mazatlanica* and *C.valida*), which are currently considered to represent morphological variants of a single, widespread species(*C. californica*) based on phylogenetic analyses of mitochondrial and nuclear DNA sequences (Miura et al., 2010).

Miura, O., Torchin, M. E. & E. Bermingham. 2010. Molecular phylogenetics reveals differential divergence of coastal snails separated by the Isthmus of Panama. *Molecular Phylogenetics and Evolution* **56,** 40–48.

**Column header information for Survey\_Total\_Prevalence.csv:**

* *Size* of the snail in mm.
* *Infection\_no* allows us to separate co-infections into multiple rows for easy data processing.
* *Region* is a general geographic area where the Estuary occurred.
* *Trematode* is the trematode species infecting a given snail.
* *Photo\_ID* is the photo identification for any photos that were taken.

**Column header information for Survey\_Total\_Caste.csv:**

* *species* (lowercase) is the species of trematode that was infecting a given snail. The codes used for both files are old species codes (See Table 1 for a comparison of old and new species codes)
* *Total\_weight* is the wet weight of the entire visceral mass in g.
* *Sample\_weight* is the wet weight in g of the visceral mass sample used for counting all soldiers and reproductives.
* *Visc\_sold\_sample* is the number of soldiers in the visceral mass sample.
* *Visc\_repro\_sample* is the number of reproductives in the visceral mass sample.
* *Visc\_sold\_total* is the total number of soldiers estimated for the entire visceral mass. Equation used: *visc\_sold\_sample* \* *total\_weight/sample\_weight*.
* *Visc\_repro\_total* is the same as *visc\_sold\_total* except for with reproductives.
* *mid\_sold\_total* and *mid\_repro\_total* are the number of soldiers and reproductives, respectively, in the entire visceral middle section.
* *mantle\_sold\_total* and *mantle\_repro\_total* are the number of soldiers and reproductives, respectively, in the entire mantle section.
* *Total\_sold* is the sum of *visc\_sold\_total*, *mid\_sold\_total*, and *mantle\_sold\_total*.
* *Total\_repro* is the sum of *visc\_repro\_total*, *mid\_repro\_total*, and *mantle\_repro\_total*.
* *Ratio* is *Total\_sold/Total\_repro*

Table 1 – The new species code using in the paper, the old species code used for analyses, the scientific name, and notes

|  |  |  |  |
| --- | --- | --- | --- |
| **New Species Code (used for paper)** | **Old Species Code (used for code and analyses)** | **Species** | **Notes** |
| Acsp | ACAN | *Acanthoparyphium spinulosum* |   |
| Ausp | AUST | *Austrobilharzia* sp. |   |
| Cajo | CATA | *Catatropis johnstoni* |   |
| Clmi | CLOA | *Cloacitrema michiganensis* |   |
| Euca | EUHA | *Euhaplorchis californiensis* |   |
| Hirh | HIMA | *Himasthla rhigedana* |   |
| Hisb | HIMB | *Himasthla* sp. B |   |
| INF | INF | Undetermined infection |   |
| Lgxi | LGXI |   | LGXI subsumes two species, Rema and Repo, which were not distinguished in Panama.  |
| Meap | MESO | *Mesostephanus appendiculatus* |   |
| Pasp | PARO | *Parorchis* sp. |   |
| Phov | PHOC | *Phocitremoides ovale* |   |
| Pruc | PROB | *Probolocoryphe uca* |   |
| Pysp | PYGI | *Pygidiopsoides spindalis* |   |
| Rebu | REBU + RENB | *Renicola buchanani* | In data sheets (Survey\_Total\_caste and Survey\_Total\_Prevalence), we use both terms (REBU and RENB) but for the summary tables (S3 and S4) we combine them and call them Rebu |
| Rece | RECE + RENC + RENIC | *Renicola cerithidicola* | In data sheets (Survey\_Total\_caste and Survey\_Total\_Prevalence), we use three terms (RECE, RENC, RENIC) but for the summary tables (S3 and S4) we combine them and call them Rece |
| Rema | REMA | *Renicola* sp. “martini” |   |
| Repo | REPO | *Renicola* sp. “polychaetophila” |   |
| Smcy | SMCY | Small cyathocotylid |   |
| Smmi | SMMI | Small microphallid |   |
| Acha | STIC | *Acanthotrema hancocki* |   |