**Data file descriptions for PCR genetic screening for presence of sea urchin DNA in rock lobster faecal samples**

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(full description of methods available in Draft Final Report of the *Fisheries Research & Development Corporation* research project #FRDC2007\_045)

1St File is: “1.FRDC2007\_045\_genetic\_tests\_on\_lobster\_faeces.xlsx”

This file contains data describing characteristics of lobsters (*Jasus edwardsii*) caught by research traps at 2 research sites (Elephant Rock & North Bay) in north eastern and south eastern Tasmania respectively, over 4 sampling occasions spanning years 2009 to 2011.

Data column headers include “Lobster no.” identifying unique individuals and capture dates, “Date”, “Session” & “Site” when/ where caught, “Tag no.” such that recaptured lobsters could be identified, “Sex”, “Carapace length” in mm, “Size category” whereby size 1 = carapace lengths less than legal size (<110 mm Carapace Length (CL)); size 2 = >110 & <140 mm CL; and size 3 => 140 mm CL), “Resident/ Translocated” indicates if the lobster was a local resident or a lobster experimentally translocated to the site, “Location” indicates if the lobster was caught inside or outside the experimental research areas protected from fishing, “Habitat” describes the type of reef where lobster caught and is split into categories of kelp beds, patchy kelp, urchin barrens, & sessile invertebrates (i.e. sponges gardens etc).

Where faecal material was retrievable from the anal pore of live lobster specimens, this material was placed in a uniquely labeled vial “Vial name”, after which the “Putative feeding” sample - if deemed to be truly faecal material i.e.” True feeding” as opposed to lobster somatic material or blood - was subject to the DNA extraction protocol described in #FRDC2007\_045. In a small number of circumstances multiple lobster faecal samples were combined if the amount of material per individual was small, hence “Individual feeding” versus “pooled” was assigned. For all feeding categories 1=presence and 0 = absence.

PCR amplification was run on faecal DNA using primers for the sea urchins *Centrostephanus rodgersii* and *Heliocidaris erythrogramma.* Amplification of primer regions coding for each urchin species was then scored by “*Ct* value” which is the number of PCR cycles taken for the reaction in each sample to reach a critical amplification threshold value. For samples where amplification was not observed, *Ct* value is logically absent. Note that critical amplification thresholds were unique for each urchin species (see #FRDC2007\_045). Furthermore, *Ct* values themselves were subject to screening, with very low or very high values indicative of erroneous PCR amplification (e.g. primer dimer processes), thus the range of tolerance for *Ct* values for which a sample was scored as a positive test to a particular sea urchin primer was set. Thus samples testing positive to each sea urchin species is shown as a binary response (1’s vs. 0’s) under the headers “Centro positive (*Ct* >8 <=40)” and “Helio positive (Ct >8 <=40)”.

2nd file is: “2.FRDC2007\_045\_genetic\_tests\_on\_environmental\_samples.xlsx”

This file contains data describing results of PCR amplification of environmental samples, i.e. sediment material extracted from crevices on the reef surface, to sea urchin primers. “Site” & “vial name” as per previous descriptions, “Depth” is reef depth in metres, columns containing *Ct* values as per previous descriptions.

3rd file is: “3.FRDC2007\_045\_genetic\_tests\_on\_urchin\_faeces.xlsx”

This file contains data describing results of PCR amplification of sea urchin faecal samples, i.e. as urchin faeces are also common on the benthos this test was designed to examine if urchin DNA could be absorbed by lobsters by eating not only the urchins directly, but also by consuming urchin faecal material possibly containing urchin DNA. “Faecal type” indicates either *Centrostephanus rodgersii* or *Heliocidaris erythrogramma* faecal material, “no. faecal pellets” is the quantity of pellets per sample, *Ct* value columns as described above.

4th file is: “4.FRDC2007\_045\_genetic\_tests\_on\_lobster\_faeces\_fed\_env\_samples.xlsx”

This file contains data describing results of PCR amplification of lobster faecal material after being fed either sea urchin faecal material, sediments containing urchin material, or sea urchin gonad material. “Treatment” indicates the type of material that was packaged up as food items fed to lobsters in the laboratory, either *Centrostephanus rodgersii* or *Heliocidaris erythrogramma* faecal material, “Quantity” is the quantity of pellets per sample, “Hrs post feeding” is the time from consumption of the food item by lobsters to when lobster faecal material was extracted for PCR analysis, *Ct* value columns as described above.

5th file is: “5.FRDC2007\_045\_Urchin\_delta\_within\_Research\_Reserves.xlsx”

This file contains data describing the change in abundance of sea urchins within the Elephant Rock Research Reserve (ERRR) and the North Bay Research Reserve (NBRR) in north eastern and south eastern Tasmania respectively, observed during initial sampling in 2008 and at the conclusion of the study in 2011.

Data column headers include “Site” identifying the Research Reserves at Elephant Rock (ERRR) and North Bay (NBRR), “centro\_decline\_in\_density” which is the decline of *Centrostephanus rodgersii* density observed from start to finish of the experiment, “helio\_decline\_in\_density” which is the decline of *Heliocidaris erythrogramma* density observed from start to finish of the experiment (note that negative numbers indicate increase in urchin density), “reef\_area\_defining\_urchin\_population (m2)” is the area over which urchin density estimates were obtained and apply to, “centro\_decline\_in\_abundance” is the decline in abundance of *Centrostephanus rodgersii* observed from start to finish of the experiment, “helio\_decline\_in\_abundance” is the decline in abundance of *Heliocidaris erythrogramma* observed from start to finish of the experiment (note that negative numbers indicate increase in urchin abundance).

6th file is: “6. FRDC2007\_045\_Urchin\_delta\_relative\_to\_controls.xlsx”

This file contains data describing the change in abundance of sea urchins within the Elephant Rock Research Reserve (ERRR) and the North Bay Research Reserve (NBRR) in north eastern and south eastern Tasmania relative to two respective control sites for each Research Reserve, as observed during initial sampling in 2008 and at the conclusion of the study in 2011.

Data column headers include “Site” identifying the Research Reserves at Elephant Rock (ERRR) and North Bay (NBRR) and respective controls, “Decline\_in\_Centro\_density” which is the decline of *Centrostephanus rodgersii* density observed from start to finish of the experiment, “Decline\_in\_Helio\_density” which is the decline of *Heliocidaris erythrogramma* density observed from start to finish of the experiment (note that negative numbers indicate increase in urchin density).