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| File names |
| OERA Data Sheet 1  OERA Data Sheet 2  OERA Data Sheet 3  OERA Data Sheet 4  ***1Other****: Trap vs Trawl Summer 2012*  ***1Other****: Sediment Spring 2013* |

* Every file (except ***Other:****“Trap vs Trawl Summer 2012*” and ***Other***: *“Sediment Spring 2013”*)
* Columns A to BZ in all 4 sheets for each file are identical
* BlankcCells = no data/ missing information
* ***1 Other:*** *“Trap vs Trawl Summer 2012*” and *“Sediment Spring 2013”*  are unique files and not related or organised in the same manner as all other files (ad hoc trawling and trapping for hemolymph sampling and sediment sampling and analysis from each station, respectively)

Sheets 1-4; columns A to BU;

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Column | Field | | Description | | Possible Entries/Units |
| A | YrSeLoTr | | Sampling year, season, location and treatment | | 2012 Spring Cheticamp Trap  2012 Spring Margaree Trap  2012 Spring Louisbourg Trap  2012 Spring GrandeRiviere Trap  2012 Fall Cheticamp Trap  2012 Fall Margaree Trap  2012 Fall Cheticamp Cage  2012 Fall Margaree Cage  2012 Fall Louisbourg Trap  2012 Fall GrandeRiviere Trap  2013 Spring Cheticamp Trap  2013 Spring Margaree Trap  2013 Spring Cheticamp Cage  2013 Spring Margaree Cage  2013 Spring Louisbourg Trap  2013 Spring GrandeRiviere Trap  2013 Fall Cheticamp Trap  2013 Fall Margaree Trap  2013 Fall Cheticamp Cage  2013 Fall Margaree Cage |
| B | Year | Sampling year | | 2012; 2013 | |
| C | Season | | Sampling Season | | Spring; Fall |
| D | Location | | Crab trapping or caging site | | Margaree, Cheticamp, GrandeRiviere, Louisbourg |
| E | Treatment | | Treatment on crab | | Cage (enclosed crab, experimental); Trap (wild caught crab/control) |
| F | Uni\_Id | | Serial crab number | | 1 to 1177 |
| G | Depart\_Id | | Crab number | | 1 to 345 (some files restart at 1) |
| H | Sex | | Sex of crab | | 1 = male  2= female  3 = pigmy male |
| I | CC\_F | | Carapace Condition | | 1 = new soft  2 = new clean  3 = hard clean  3M = hard clean and little moss  4= hard light moss  5 = old heavy moss |
| J | Mat\_F | | Maturity | | 1 = Mature  2 =Immature  3 = Unknown |
| K | L\_Miss\_F | | Missing legs | | 1 = M/X; missing  2 = regenerated  3 = H (missing; human manipulation/no scar yet)  4 = ½ regenerated  5 = 1/2  6 = CL (cracked leg)  7 = D (digit missing)  8 = B ( bud only) |
| L | R\_Miss\_F | |
| M | Duro\_F | | Durometer measurement (shell hardness) | | 0-100 |
| N | CW\_F | | Carapace width | | Units: mm |
| O | ChH\_F | | Male Chela/claw height | | Units: mm |
| P | Abd\_F | | Female abdomen width | | Units: mm |
| Q | Wt | | Total weight  Total crab weight – 1.4 (weight of tag) | | Units: grams |
| R | Egg\_C\_01 | | Egg color (visual observation) | | 1. light orange 2. dark orange 3. black 4. cocoon (post-hatching) |
| S | Egg\_PC\_F | | Percentage of remaining eggs | | 1. Absent (no eggs) 2. 1-49% 3. 50-74% 4. 75-99% 5. 100% |
| T | Egg\_Dev | | Egg developmental stage | | Stage 1-14 according to Moriyasu and Lanteigne (1998) |
| U | Gon\_C\_01 | | Gonad/ovary color (visual observation) | | 1. White 2. Beige 3. Orange |
| V | Gon\_Wt | | Gonad/ovary weight | | Units: grams |
| W | Hep\_Wt | | Hepatopancreas weight | | Units: grams |
| X | EC\_a | | Egg color (determined by colorimeter L\*A\*B\*) | | Hue |
| Y | EC\_b | | Egg color (determined by colorimeter L\*A\*B\*) | | Lightness |
| Z | EC\_L | | Egg color (determined by colorimeter L\*A\*B\*) | | Saturation |
| AA | Egg\_C\_02 | | Egg color (visual observation by colorimeter operator) | | 1. light orange 2. dark orange 3. black 4. cocoon |
| AB | Gon\_a | | Gonad color (determined by colorimeter L\*A\*B\*) | | Hue |
| AC | Gon\_b | | Gonad color (determined by colorimeter L\*A\*B\*) | | Lightness |
| AD | Gon\_L | | Gonad color (determined by colorimeter L\*A\*B\*) | | Saturation |
| AE | Gon\_C\_02 | | Gonad color (visual observation by colorimeter operator) | | 1. White 2. Beige/beige orange/partially orange/orange pico/light orange 3. Orange 4. Dark orange |
| AF | Hep\_a | | Hepatopancreas color (determined by colorimeter L\*A\*B\*) | | Hue |
| AG | Hep\_b | | Hepatopancreas color (determined by colorimeter L\*A\*B\*) | | Lightness |
| AH | Hep\_L | | Hepatopancreas color (determined by colorimeter L\*A\*B\*) | | Saturation |
| AI | Hep\_C | | Hepator color (visual observation by colorimeter operator) | | 1. Brown 2. Watery brown 3. Dark brown-black 4. Brown blackish greenish 5. Light brown 6. Watery light brown 7. Brown-pinkish 8. Dark brown 9. Watery dark brown 10. Brown-reddish 11. Dark green/greenish 12. Watery green/greenish 13. Reddish 14. Yellowish |
| AJ | Hem\_T | | Hemolymph sampling time | | Time that hemolymph was sampled |
| AK | Tag\_Nbr | | Tag number | | ID number from dissections |
| AL | Sp\_Tag\_Nbr | | Spaghetti tag number | | Original caged crab tag number (prior to caging); |
| AM | Dissection | | Dissection date | | Day month year (DDMMYYYY) |
| AN | St\_Nbr | | Fishing zone | | 12  19  23 |
| AO | Station | | Station name | | Cheticamp/Louisbourg/Grande-Riviere/Margaree |
| AP | Gear | | Gear | | Trap or Cage |
| AQ | PT\_F | | Position Type | | LL (Latitude/Longitude) |
| AR | Lat\_F | | Latitude | |  |
| AS | Lon\_F | | Longitude | |  |
| AT | Start\_T | | Start of Sampling (time) | | Time at beginning of dissections |
| AU | End\_T | | End of Sampling (time) | | Time at end of dissections |
| AV | Depth | | Water depth | | In fathoms |
| AW | Vessel | | Name of vessel | | CGC Opilio/Fishfull Thinking/ Britanny Madison/CGC M. Perley |
| AX | TC | | Water temperature | | In Celcius |
| AY | Sampler\_01 | | Sampling team | | R. Allain/R. Cormier/P.Degrace/J.F. Landry/K.Landry/C. Laplante/M.  Moriasu/S.Curry/P. Tramunt |
| AZ | Sampler\_02 | |
| BA | Sampler\_03 | |
| BB | Sampler\_04 | |
| BC | Sampler\_05 | |
| BD | Sampler\_06 | |
| BE | Biol\_Comm | | Unusual or special observations during sample dissections | | Notes; |
| BF | Immersion | | Cage immersion date | | For caged crab samples only |
| BG | PT\_I | | Position type | | Latitude/longitude (LL) |
| BH | Lat\_IB | | Latitude (start of cage line) | |  |
| BI | Lon\_IB | | Longitude (start of cage line) | |  |
| BJ | Lat\_IE | | Latitude (end of cage line) | |  |
| BK | Lon\_IE | | Longitude (end of cage line) | |  |
| BL | Time\_S | | Time at beginning of caging | |  |
| BM | Time\_E | | Time once line of cage complete | |  |
| BN | Temp\_Prb\_Nbr | | Temperature probe number | |  |
| BO | Cage\_Nbr | | Cage number | |  |
| BP | CC\_I | | Initial evaluation (pre-caging): Carapace condition | | 1 = new soft  2 = new clean  3 = hard clean  3M = hard clean and little moss  4= hard and light moss  5 = old and heavy moss according to Hébert et al. (2014) |
| BQ | Mat\_I | | Initial evaluation (pre-caging): Maturity | | 1 = Mature  2 =Immature  3 = Unknown |
| BR | L\_Miss\_I | | Initial evaluation (pre-caging): Missing legs (Left) | | 1 = M/X; missing  2 = regenerated  3 = H (missing; human manipulation/no scar yet)  4 = ½ regenerated  5 = 1/2  6 = CL (cracked leg)  7 = D (digit missing)  8 = B ( bud only) |
| BS | R\_Miss\_I | | Initial evaluation (pre-caging): Missing legs (Right) | |
| BT | Duro\_I | | Initial evaluation (pre-caging):Shell Hardness | | 0-100 |
| BU | CW\_I | | Initial evaluation (pre-caging): Carapace width | | Units: mm |
| BV | ChH\_I | | Initial evaluation (pre-caging): Chela height (Males) | | Units: mm |
| BW | Abd\_I | | Initial evaluation (pre-caging): Abdomen width (Females) | | Units: mm |
| BX | Egg\_C\_03 | | Initial evaluation (pre-caging): Egg color | | 1. light orange 2. dark orange 3. black 4. cocoon |
| BY | Egg\_PC\_I | | Initial evaluation (pre-caging): Percentage of remaining eggs | | 1. Absent (no eggs) 2. 1-49% 3. 50-74% 4. 75-99%   100% |
| BZ | In\_cooler | | Time that caged crab was collected and placed in cooler | | \*For Cheticamp and Margaree Caged Spring 2013, the time was averaged (not exact time) |

OERA Data Sheet 1; Columns CA to DZ (Fecundity, Commensal organisms in gills, condition of gill, antennule and hepatopancreas)

|  |  |  |  |
| --- | --- | --- | --- |
| CA | Embryo\_Stg | Embryonic stage according to Moriyasu and Lanteigne (1998) | 1-14 |
| CB | Nbr\_Egg\_Count | Number of eggs counted in sub-sample |  |
| CC | Wt\_Sub | Weight of sub-sample | Units: grams |
| CD | Tot\_Egg\_Wt | Total weight of egg sample | Units: grams |
| CE | Tot\_Nbr\_Egg | Total number of eggs |  |
| CF | GF\_Type\_01 | Estimated number of copepod genus *Coullia*  (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CG | GF\_Type\_02 | Estimated number of copepod, *Tisbe celata* (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CH | GF\_Type\_03 | Estimated number of bryozoa (order Ctenostomadida) (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CI | GF\_Type\_04 | Estimated number of turbellariaflatworms, *Ectocotyla hirudo* and *E. multitesticulata* (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CJ | GF\_Type\_05 | Estimated number of nematoda, unknown genus and species (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CK | GF\_Type\_06 | Estimated number of Harpacticoida, copepoda nauplii (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CL | GF\_Type\_07 | Estimated number of Kinorhyncha, *Echinoderes elongates* (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CM | GF\_Type\_08 | Estimated number of polychaeta larvae, *Ophryotrocha geryonicola* (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CN | GF\_Type\_09 | Estimated number of mites (halacaridae). *Copidognathus sp.* (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CO | GF\_Type\_10 | Estimated number of Turbellaria, egg capsules (Total abundance of a given pre-grouped gill fouling organisms was estimated based on a count of subsample in a gridded petri dish and the number of gill lamellaeused) |  |
| CP | GF\_Total\_Nbr | Addition of counts of all types of commensal organisms observed (type I to X) |  |
| CQ | Tube\_Cap\_Wt | Weight of tube and cap | Units: grams |
| CR | Tube\_Homog\_Wt | Weight of tube and homogenate | Units: grams |
| CS | Net\_Wet\_Wt | Weight of tube and homogenate minus tube and cap | Units: grams |
| CT | Tube\_Frz\_Dry\_Wt | Weight of tube and freeze dried sample | Units: grams |
| CU | Net\_Dry\_Wt | Weight of tube and freeze dried sample minus tube and cap | Units: grams |
| CV | Moist | Weight of net wet minus weight of net dry | Units: grams |
| CW | Moist\_PC | Value of moisture X 100 |  |
| CX | HP\_Wt\_g\_01 | Hepatopancreas sample 1 weight | Units: grams |
| CY | HP\_Wt\_g\_02 | Hepatopancreas sample 2 weight | Units: grams |
| CZ | HP\_Wt\_g\_03 | Hepatopancreas sample 3 weight | Units: grams |
| DA | Vess\_Wt\_g\_01 | Vessel sample 1 weight | Units: grams |
| DB | Vess\_Wt\_g\_02 | Vessel sample 2 weight | Units: grams |
| DC | Vess\_Wt\_g\_03 | Vessel sample 3 weight | Units: grams |
| DD | Final\_Wt\_g\_01 | Final weight of sample 1 | Units: grams |
| DE | Final\_Wt\_g\_02 | Final weight of sample 2 | Units: grams |
| DF | Final\_Wt\_g\_03 | Final weight of sample 3 | Units: grams |
| DG | PC\_Lip\_01 | Sample 1 final mass minus vessel mass 1 divided by hepatopancreas sample 1 mass X 100 | Units: grams |
| DH | PC\_Lip\_02 | Sample 2 final mass minus vessel mass 2 divided by hepatopancreas sample 2 mass X 100 | Units: grams |
| DI | PC\_Lip\_03 | Sample 3 final mass minus vessel mass 3 divided by hepatopancreas sample 3 mass X 100 | Units: grams |
| DJ | PC\_Ave\_Lip | Average of % lipid 1, 2 and 3 |  |
| DK | PC\_St\_Dev\_01 | Standard deviation of average lipid percentage (%) |  |
| DL | HP\_Wt\_mg\_01 | Hepatopancreas sample 1 weight | Units: mg |
| DM | HP\_Wt\_mg\_02 | Hepatopancreas sample 2 weight | Units: mg |
| DN | HP\_Wt\_mg\_03 | Hepatopancreas sample 3 weight | Units: mg |
| DO | Glyco\_Wt\_mg\_01 | Glycogen sample 1 weight | Units: mg |
| DP | Glyco\_Wt\_mg\_02 | Glycogen sample 2 weight | Units: mg |
| DQ | Glyco\_Wt\_mg\_03 | Glycogen sample 3 weight | Units: mg |
| DR | Glyco\_Tiss\_01 | Glycogen sample 1 weight divided by hepatopancreas sample 1 weight X 1000 |  |
| DS | Glyco\_Tiss\_02 | Glycogen sample 2 weight divided by hepatopancreas sample 2 weight X 1000 |  |
| DT | Glyco\_Tiss\_03 | Glycogen sample 3 weight divided by hepatopancreas sample 3 weight X 1000 |  |
| DU | Ave\_Glyco\_Tiss | Average milligram of glycogen per gram of dry tissue of sample 1, 2 and 3 |  |
| DV | St\_Dev\_02 | Standard deviation of average milligram of glycogen per gram of dry tissue |  |
| DW | Hp\_Cond | Hepatopancreas condition | 1. Smooth 2. Relatively convoluted 3. Convoluted 4. Highly Convoluted |
| DX | Gill\_Cond | Gill condition | 1. Clean 2. Relatively clean (clean with some organic/inorganic substances 3. Medium (abundant organic and/or inorganic substances) 4. Very dirty (Filled with compacted sediment-like substances) |
| DY | Gr\_Hair\_Cond | Group hair condition | 1. Clean 2. Relatively clean 3. Intermediate 4. Dirty |
| DZ | Ant\_Cond | Antennule condition (morphological observations) | 1. Clean 2. Relatively clean (some dirtiness on the aesthetasc hairs) 3. Intermediate 4. Dirty 5. Damaged outer flagellum and/or aesthetasc hairs |

OERA Data Sheet 2; Columns CA to FZ (Stomach Content Analysis and Stable Isotope Analysis)

|  |  |  |  |
| --- | --- | --- | --- |
| CA | Stom\_Cont | Wet weight of stomach and its content | Units: grams |
| CB | Stom\_W | Wet weight of emptied stomach | Units: grams |
| CC | Stom\_D | Dry weight of emptied stomach | Units: grams |
| CD | Fullness | Visual estimation of stomach fullness | 1. 25% full 2. 50% full 3. 75% full 4. 100% full   0 - empty |
| CE | Prey\_ID | Identification of prey items to the lowest taxon possible |  |
| CF | Filter\_D | Dry weight of filter paper | Units: grams |
| CG | Filter\_W | Wet weight of filter paper | Units: grams |
| CH | Filter\_Cont\_W | Wet weight of filter paper and stomach content | Units: grams |
| CI | Cont\_W | Weight of wet filter plus content minus weight of wet filter | Units: grams |
| CJ | Filter\_Cont\_D | Dry weight of filter paper and stomach content | Units: grams |
| CK | Cont\_D | Weight of dry filter plus content minus weight of dry filter | Units: grams |
| CL | Polych\_PC | Estimated percentage of preys identified as polychaete in stomach | 5-100% |
| CM | Polych\_W | Total wet stomach content weight X percentage of polychaete | Units: grams |
| CN | Polych\_D | Total dry stomach content weight X percentage of polychaete | Units: grams |
| CO | Det\_PC | Estimated percentage of preys identified as detritus in stomach | 5-100% |
| CP | Det\_W | Total wet stomach content weight X percentage of detritus | Units: grams |
| CQ | Det\_D | Total dry stomach content weight X percentage of detritus | Units: grams |
| CR | Rock\_PC | Estimated percentage of preys identified as rocks in stomach | 5-100% |
| CS | Rock\_W | Total wet stomach content weight CUX percentage of rocks | Units: grams |
| CT | Rock\_D | Total dryCV stomach content weight X peCWrcentage of rocks | Units: grams |
| CU | Mollusk\_PC | Estimated percentage of preys identified as mollusks in stomach | 5-100% |
| CV | Mollusk\_W | Total wet stomach content weight X percentage of mollusks | Units: grams |
| CW | Mollusk\_D | Total dry stomach content weight X percentage of mollusks | Units: grams |
| CX | Gastrop\_PC | Estimated percentage of preys identified as gastropod in stomach | 5-100% |
| CY | Gastrop\_W | Total wet stomach content weight X percentage of gastropod | Units: grams |
| CZ | Gastrop\_D | Total dry stomach content weight X percentage of gastropod | Units: grams |
| DA | Biv\_PC | Estimated percentage of preys identified as bivalve in stomach | 5-100% |
| DB | Biv\_W | Total wet stomach content weight X percentage of bivalve | Units: grams |
| DC | Biv\_D | Total dry stomach content weight X percentage of bivalve | Units: grams |
| DD | Fish\_PC | Estimated percentage of preys identified as fish in stomach | 5-100% |
| DE | Fish\_W | Total wet stomach content weight X percentage of fish | Units: grams |
| DF | Fish\_D | Total dry stomach content weight X percentage of fish | Units: grams |
| DG | Crust\_PC | Estimated percentage of preys identified as crustacean in stomach | 5-100% |
| DH | Crust\_W | Total wet stomach content weight X percentage of crustacean | Units: grams |
| DI | Crust\_D | Total dry stomach content weight X percentage of crustacean | Units: grams |
| DJ | Amphi\_PC | Estimated percentage of preys identified as amphipods in stomach | 5-100% |
| DK | Amphi\_W | Total wet stomach content weight X percentage of amphipods | Units: grams |
| DL | Amphi\_D | Total dry stomach content weight X percentage of amphipods | Units: grams |
| DM | Shrimp\_PC | Estimated percentage of preys identified as shrimp in stomach | 5-100% |
| DN | Shrimp\_W | Total wet stomach content weight X percentage of shrimp | Units: grams |
| DO | Shrimp\_D | Total dry stomach content weight X percentage of shrimp | Units: grams |
| DP | Crab\_PC | Estimated percentage of preys identified as crab in stomach | 5-100% |
| DQ | Crab\_W | Total wet stomach content weight X percentage of crab | Units: grams |
| DR | Crab\_D | Total dry stomach content weight X percentage of crab | Units: grams |
| DS | Cop\_PC | Estimated percentage of preys identified as copepod in stomach | 5-100% |
| DT | Cop\_W | Total wet stomach content weight X percentage of copepod | Units: grams |
| DU | Cop\_D | Total dry stomach content weight X percentage of copepod | Units: grams |
| DV | Plant\_PC | Estimated percentage of preys identified as plant in stomach | 5-100% |
| DW | Plant\_W | Total wet stomach content weight X percentage of plant | Units: grams |
| DX | Plant\_D | Total dry stomach content weight X percentage of plant | Units: grams |
| DY | Hydr\_PC | Estimated percentage of preys identified as hydroid in stomach | 5-100% |
| DZ | Hydr\_W | Total wet stomach content weight X percentage of hydroid | Units: grams |
| EA | Hydr\_D | Total dry stomach content weight X percentage of hydroid | Units: grams |
| EB | Plast\_PC | Estimated percentage of preys identified as plastic in stomach | 5-100% |
| EC | Plast\_W | Total wet stomach content weight X percentage of plastic | Units: grams |
| ED | Plast\_D | Total dry stomach content weight X percentage of plastic | Units: grams |
| EE | Rope\_PC | Estimated percentage of preys identified as rope in stomach | 5-100% |
| EF | Rope\_W | Total wet stomach content weight X percentage of rope | Units: grams |
| EG | Rope\_D | Total dry stomach content weight X percentage of rope | Units: grams |
| EH | Insect\_PC | Estimated percentage of preys identified as insect in stomach | 5-100% |
| EI | Insect\_W | Total wet stomach content weight X percentage of insect | Units: grams |
| EJ | Insect\_D | Total dry stomach content weight X percentage of insect | Units: grams |
| EK | Starf\_PC | Estimated percentage of preys identified as starfish in stomach | 5-100% |
| EL | Starf\_W | Total wet stomach content weight X percentage of starfish | Units: grams |
| EM | Starf\_D | Total dry stomach content weight X percentage of starfish | Units: grams |
| EN | Egg\_PC | Estimated percentage of preys identified as eggs in stomach | 5-100% |
| EO | Egg\_W | Total wet stomach content weight X percentage of eggs | Units: grams |
| EP | Egg\_D | Total dry stomach content weight X percentage of eggs | Units: grams |
| EQ | Plankt\_PC | Estimated percentage of preys identified as plankton in stomach | 5-100% |
| ER | Plankt\_W | Total wet stomach content weight X percentage of plankton | Units: grams |
| ES | Plankt\_D | Total dry stomach content weight X percentage of plankton | Units: grams |
| ET | Feath\_PC | Estimated percentage of preys identified as feather in stomach | 5-100% |
| EU | Feath\_W | Total wet stomach content weight X percentage of feather | Units: grams |
| EV | Feath\_D | Total dry stomach content weight X percentage of feather | Units: grams |
| EW | Bryoz\_PC | Estimated percentage of preys identified as bryozoan in stomach | 5-100% |
| EX | Bryoz\_W | Total wet stomach content weight X percentage of bryozoan | Units: grams |
| EY | Bryoz\_D | Total dry stomach content weight X percentage of bryozoan | Units: grams |
| EZ | Polych\_T\_PC | Estimated percentage of preys identified as polychaete tube in stomach | 5-100% |
| FA | Polych\_T\_W | Total wet stomach content weight X percentage of polychaete tube | Units: grams |
| FB | Polych\_T\_D | Total dry stomach content weight X percentage of polychaete tube | Units: grams |
| FC | Foram\_PC | Estimated percentage of preys identified as foraminifera in stomach | 5-100% |
| FD | Foram\_W | Total wet stomach content weight X percentage of foraminifera | Units: grams |
| FE | Foram\_D | Total dry stomach content weight X percentage of foraminifera | Units: grams |
| FF | Echino\_PC | Estimated percentage of preys identified as echinoderms in stomach | 5-100% |
| FG | Echino\_W | Total wet stomach content weight X percentage of echinoderms | Units: grams |
| FH | Echino\_D | Total dry stomach content weight X percentage of echinoderms | Units: grams |
| FI | Barn\_PC | Estimated percentage of preys identified as barnacles in stomach | 5-100% |
| FJ | Barn\_W | Total wet stomach content weight X percentage of barnacles | Units: grams |
| FK | Barn\_D | Total dry stomach content weight X percentage of barnacles | Units: grams |
| FL | Brt\_St\_PC | Estimated percentage of preys identified as brittle stars in stomach | 5-100% |
| FM | Brt\_St\_W | Total wet stomach content weight X percentage of brittle stars | Units: grams |
| FN | Brt\_St\_D | Total dry stomach content weight X percentage of brittle stars | Units: grams |
| FO | Paras\_PC | Estimated percentage of preys identified as parasite in stomach | 5-100% |
| FP | Paras\_W | Total wet stomach content weight X percentage of parasite | Units: grams |
| FQ | Paras\_D | Total dry stomach content weight percentage of parasite | Units: grams |
| FR | Totals | Total percentage of all preys identified in stomach | 100% |
| FS | SIA\_Amt | Weight of tissue analysed | Units: mg |
| FT | SIA\_CO2 | the amount of CO2 gas measured by the mass spectrometer, a function of the weight of  tissue used and the total amount of carbon (%C) it contains |  |
| FU | SIA\_N2 | the amount of N2 gas measured by the mass spectrometer, a function of the weight of tissue  used and the total amount of nitrogen (%N) it contains |  |
| FV | D\_13\_C | ratio of heavy (13C) to light (12C) carbon in the sample according to the formula: δ13C =  [(Rsample/Rstandard)-1]\*1000 where R is 13C/12C and the standard is VPDB (Vienna Peedee Belemnite) |  |
| FW | D\_15\_N | ratio of heavy (15N) to light (14N) in the sample according to the formula: δ15N =  [(Rsample/Rstandard)-1]\*1000 where R is 15N/14N and the standard is AIR (atmospheric nitrogen) |  |
| FX | C\_PC | percent of the sample that is carbon by weight; e.g. 200 µg sample with 40% carbon has 80 µg  carbon by weight | % |
| FY | N\_PC | percent of the sample that is nitrogen by weight; e.g. 200 µg sample with 10% nitrogen has 20µg  nitrogen by weight | % |
| FZ | C\_N\_Ratio | Ratio of carbon to nitrogen in the sample; simple division of %C by %N |  |

OERA Data Sheet 3; Columns CA to ES (Gill, Ovary and Hepatopancreas Histology)

|  |  |  |  |
| --- | --- | --- | --- |
| CA | PPT | Amount of eosinophilic (proteinaceous) precipitate in vessels | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| CB | Auto | Degree of autolysis (% of tissue area affected) | 0; < 10%  1; 10 to 25%  2; 25 to 50%  3; 50 to 75%  4; >75% |
| CC | Apopwall | Apoptotic cells observed in the tubule wall | 0 = absent  1= present |
| CD | Apoplumen | Apoptotic cells observed in the tubule lumen | 0 = absent  1= present |
| CE | Secpkt | Sloughed cells in the tubule lumen as indicators of recent feeding cycle (secretory packets) | 0 = absent  1= present |
| CF | Bvac | Degree of B-cell cytoplasmic vacuole filling subjectively averaged over all cells, as a suggested indicator of recent feeding | 0 = none seen  1; < 50% filled  2; > 50% filled |
| CG | Rlip | Degree of R-cell lipid vacuoles filling the cytoplasm. R-cells containing only vacuoles with goldern-brown, granular contents were graded as “none”. Celle where lipid vacuoles were so abundant that the cell shape was distorted were classed as >100% | 0; none seen  1; <10%  2; 10 to ≤ 50%  3; 50 to ≤ 75%  4; 75 to 100%  5; > 100% |
| CH | Tubhem | Migrating single cells (basal cells of Johnson) | 0 = none seen  1 = few  2 = moderate  3 = many  4 = very many |
| CI | TubInfil | Hemocyte infiltrates in tubular epithelium | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CJ | TubNod | Hemocyte nodules/aggregates in tubular epithelium | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CK | Tubpig | Pigment (melanin) deposits in lumen associated with inflammatory infiltrates | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CL | TubFib | Evidence of fibroplasia and/or collagen deposits | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CM | TubNec | Tubule cell necrosis not related to autolysis | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CN | TubOrgs | Organisms in tubule lumen (number/type) | 0 = none seen  1 = bacteria  2 = yeast/fungi  3 = protozoan  4 = other |
| CO | THCCirc | Estimation of circulating hemocyte numbers based on subjective assessment of hemocyte numbers in vessels | 0 = normal (low numbers in smaller vessles)  1 = moderate number in smaller vessels  2 = small vessels filled with hemocytes  3 = large and small vessels filled with hemocytes |
| CP | RI | Reserve inclusion (RI) cell fullness | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| CQ | CTInfil | Number of hemocytes in connective tissue | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CR | CTHfoci | Presence of hemocyte foci in connective tissue (non-organised) | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CS | CTNod | Presence of organised hemocyte nodules in connective tissue | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CT | CTFib | Presence of fibroplasia in connective tissue | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CU | CTPig | Presence of pigment (melanin) deposits in connective tissue | 0 = none seen  1 = mild  2 = moderate  3 = marked  4 = severe |
| CV | CTOrg | Presence/absence of organisms in connective tissue | 0 = none seen  1 = bacteria  2 = yeast/fungi  3 = protozoan  4 = other |
| CW | FPHyper | Degree of activation of the fixed phagocyte cells located around small vessels (none, mild, moderate, marked). Degree of cytoplasmic vacuolation, presence of phagocytosed material was used to determine an overall tissue score | 0 = normal  1 = mildly increased  2 = moderately increased  3 = markedly increased |
| CX | FPActvn | Degree of fixed phagocytes hyperplasia based on a subjective assessment of phagocyte density/numbers | 0 = no vacuolation  1 = slight vacuolation  2 = lots of vacuolation with or without cytoplasmic debris  3 = phagocytosed infectious agent present |
| CY | Bryo | Presence of byrozoans | 0 = absent  1= present |
| CZ | Cope | Presence of copepods | 0 = absent  1= present |
| DA | Flat | Presence of flatworms | 0 = absent  1= present |
| DB | Egg | Presence of eggs (varied types 1-3 were observed but not identified) | 0 = none seen  1= type 1  2 = type 2  3 = type 3 |
| DC | Nem | Presence of nematodes | 0 = absent  1= present |
| DD | Poly | Presence of polychaetes | 0 = absent  1= present |
| DE | Amphi | Presence of amphipods | 0 = absent  1= present |
| DF | Other | Presence of other unidentified flora (numbered 1-7) | 1-7 |
| DG | Other2 | Presence of other unidentified flora (by wet mounts) | 0 = absent  1 = present |
| DH | BT | Degree of bacterial fouling on gill surface | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DI | Sed | Degree of sediment accumulation on gill surface | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DJ | ViralIncl | Presence and location of intracytoplasmic inclusions | 0 = none seen  1 = epithelium  2 = endothelium  3 = both |
| DK | VirusLoadEpi | Abundance of intracytoplasmic inclusions - epithelium | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DL | VirusLoadEndo | Abundance of intracytoplasmic inclusions - endothelium | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DM | RIcell | Reserve inclusion (RI) cell fullness | 0 = none seen  1 = mild  2 = moderate  3 = many |
| DN | Neph | Nephrocyte vacuolation | 0 = none seen  1 = small vacuoles  2 = large vacuoles |
| DO | HemInfil | Diffuse hemocyte infiltrates in loose connective tissue | 0 = none seen  1 = few  2 = moderate  3 = many |
| DP | HemAgg | Hemocyte aggregates in loose connective tissue | 0 = none seen  1 = few  2 = moderate  3 = many |
| DQ | HemNod | Hemocyte nodules in loose connective tissue | 0 = none seen  1 = few  2 = moderate  3 = many |
| DR | MelPig | Brown-gold pigment (melanin) deposition | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DS | RedPig | Reddish hyaline pigment deposition | 0 = none seen  1 = mild  2 = moderate  3 = marked |
| DT | PN | Pyknotic nuclei in epithelial cells | 0 = absent  1 = present |
| DU | FN | Faded nuclei of epithelial cells | 0 = absent  1 = present |
| DV | Uabscess | Presence of microabsess | 0 = absent  1 = present |
| DW | Spent | Overall stage (preliminary progression) | 0= no  1 = recent  2 = recovering  3 = resorbing  4 = mixed |
| DX | Newspent | Overall stage (renumbered for hypothesised progression) | 0 = not spawned  1 = recently spawned  2 = mixed pattern  3 = recovering from spawn  4 = resorbing |
| DY | Hem\_infil | Hemocyte infiltrates in connective tissue | 0 = normal  1 = mildly increased  2 = moderately increased  3 = markedly increased |
| DZ | Ov\_Stg | Ovary stage (wrt vitellogenesis) | 0 = previtellogenic  1 = vitellogenic, early (oocytes contain < 50% of secondary yolk droplets)  2 = vitellogenic, late (>50% of oocytes are filled with secondary yolk droplets |
| EA | Basopct | Percentage of basophilic oocytes (cytoplasm is mainly basophilic; can have a few eosinophilic granules but background is blue) | % |
| EB | Prim\_pct | Percentage of primary oocytes (cytoplasm is eosinophilic and less than 50% fill by secondary yolk droplets) | % |
| EC | Secon\_pct | Secondary oocytes (cytoplasm eosinophilic and contains > 50% secondary yolk droplets) | % |
| ED | Chor\_sep | Degree of chorion separation | 0 = none  1 = mild  2 = moderate  3 = marked |
| EE | MC | Abundance of mitotic centres | 0 = none seen  1 = present but small with minimal mitoses  2 = readily observed due to larger size and frequent mitotic figures |
| EF | Resorb | Abundance of resorbing oocytes – basophilic, primary, or secondary (based on # observed/50 normal apprearing oocytes (primary and secondary combined) | # / 50 |
| EG | Pink\_rem | Abundance of ovulated/spawned follicles with small amount of paler eosinophilic material remaining | 0 = absent  1 = present |
| EH | Blue\_mat | Presence of smooth, basophilic material | 0 = absent  1 = present |
| EI | Ovnrem5050 | Count of ovulation remnants (follicular epithelial cells) | # (1-49) counted/50  Resorbing oocytes  50 = too many to count |
| EJ | Degen | Presence of degenerative nodules | 0 = absent  1 = present |
| EK | Hem\_foci | Hemocyte foci/aggregates (not organised) | 0 = none seen  1 = few  2 = moderate  3 = many |
| EL | Fib\_gen | Fibroplasia or fibrosis | 0 = none  1 = mild  2 = moderate  3 = marked |
| EM | Orgnod | Organising hemocyte nodules | 0 = none seen  1 = few  2 = moderate  3 = many |
| EN | Mel\_nod | Pigmented (melanin) hemocyte nodules | 0 = none seen  1 = few  2 = moderate  3 = many |
| EO | Fib\_nod | Fibrosis associated with hemocyte nodules | 0 = none  1 = mild  2 = moderate  3 = marked |
| EP | Nec | Necrosis, generalised | 0 = none  1 = mild  2 = moderate  3 = marked |
| EQ | Agent | Observations of infectious agents | 0 = none seen  1 = bacteria  2 = yeast/fungi  3 = protozoan  4 = other |
| ER | Karyo | Observation of karyolitic nuclei in follicular epithelial cells (not analysed) | 0 = absent  1 = present |
| ES | Sperm | Observation of spermatid in sections | 0 = absent  1 = present |

OERA Data Sheet 4: Columns CA to CZ: Hemolymph Biochemistry Analysis

|  |  |  |  |
| --- | --- | --- | --- |
| CA | Na | Biochemistry profile for plasma and serum samples: Sodium | Units: mmol/L |
| CB | K | Biochemistry profile for plasma and serum samples: potassium | Units: mmol/L |
| CC | NaK | sodium: potassium ratio |  |
| CD | Cl | Biochemistry profile for plasma and serum samples: chloride | Units: mmol/L |
| CE | Ca | Biochemistry profile for plasma and serum samples: calcium | Units: mmol/L |
| CF | Phos | Biochemistry profile for plasma and serum samples: phosphorus | Units: mmol/L |
| CG | Mg | Biochemistry profile for plasma and serum samples: magnesium | Units: mmol/L |
| CH | Urea | Biochemistry profile for plasma and serum samples | Units: mmol/L |
| CI | Creat | Biochemistry profile for plasma and serum samples: creatinine | Units: mmol/L |
| CJ | Gluc | Biochemistry profile for plasma and serum samples: glucose | Units: mmol/L |
| CK | Chol | Biochemistry profile for plasma and serum samples: cholesterol | Units: mmol/L |
| CL | Trig | Biochemistry profile for plasma and serum samples: triglyceride | Units: mmol/L |
| CM | AMY | Biochemistry profile for plasma and serum samples: amylase | Units: U/L |
| CN | LIP | Biochemistry profile for plasma and serum samples: lipase | Units: U/L |
| CO | ALP | Biochemistry profile for plasma and serum samples: alkaline phosphatase | Units: U/L |
| CP | AST | Biochemistry profile for plasma and serum samples: aspartate aminotransferase | Units: U/L |
| CQ | ALT | Biochemistry profile for plasma and serum samples: alanine aminotransferase | Units: U/L |
| CR | GGT | Biochemistry profile for plasma and serum samples: gamma glutamyl transferase | Units: U/L |
| CS | GD | Biochemistry profile for plasma and serum samples: glutamate dehydrogenase | Units: U/L |
| CT | SDH | Biochemistry profile for plasma and serum samples: sorbitol dehydrogenase | Units: U/L |
| CU | TPb | Total protein (using the **b**iuret method) | Units: g/L |
| CV | Alb | Biochemistry profile for plasma and serum samples: albumin | Units: g/L |
| CW | Glob | Biochemistry profile for plasma and serum samples: globulin | Units: g/L |
| CX | AG | albumin: globulin ratio |  |
| CY | Lactate | Biochemistry profile for plasma and serum samples | Units: mmol/L |
| CZ | Uric | Biochemistry profile for plasma and serum samples: uric acid | Units: µmol/L |

File “Trap vs Trawl Summer 2012”

|  |  |  |  |
| --- | --- | --- | --- |
| Column | Field | Description | Possible Entries/Units |
| A | Zone | Fishing area | 19 |
| B | Dissection | Sampling date | ddmmyyyy |
| C | Vessel | Name of vessel | CGC Opilio; Marco Michel |
| D | Depart\_Id | Crab number | 1 to 150 (trap); 1 to 120 (trawl) |
| E | Sex | Sex of crab | 1 = male  2 = female  3 = pigmy male |
| F | CC | Carapace Condition | 1 = new soft  2 = new clean  3 = hard clean  3M = hard clean and little moss  4= hard light moss  5 = old heavy moss |
| G | L\_Miss | Missing legs (healed/ scar); left side | 1= M/X; Missing; scarring  2 = Regenerated  3 = Missing, no scar tissue  4 = ½ regenerated  5 = ½  6 = CL (cracked leg)  7 = D (digit missing)  8 = B (bud only) |
| H | R\_Miss | Missing legs (healed/scar); right side | 1= M/X; Missing; scarring  2 = Regenerated  3 = Missing, no scar tissue  4 = ½ regenerated  5 = ½  6 = CL (cracked leg)  7 = D (digit missing)  8 = B (bud only) |
| I | CW | Carapace width | Units: mm |
| J | ChH | Chela Height | Units: mm |
| K | Abd | Abdomen Width | Units: mm |
| L | Egg\_C | Visual observation of egg color | 1 = light orange  2 = dark orange  3 = black  4 = cocoon |
| M | Hem\_T\_01 | Time of first hemolymph sample | Time of hemolymph sample (in decimals) |
| N | Hem\_T\_02 | Time of second hemolymph sample | Time of 2nd hemolymph sample (Only for crabs caught by trapping and initially placed in vivier tanks); in decimals |
| O | Trawl\_Nbr | Trawl tow number | 1 to 8 |
| P | Biol\_Comm | Relevant biological comments |  |

File “Sediment Spring 2013”

Each of the five samples was processed in the following manner:

Two sub-samples (designated A and B, respectively) were extracted from each vial, and placed in conical filters.  These 10 samples were then well rinsed with distilled water to remove salt.  The samples were then air-dried, and a portion of each sample was placed on a 12 mm aluminum stub.  The material was affixed to each stub with double-sided carbon tape.

The ten stubs were then carbon-coated by high-vacuum thermal evaporation, and examined in the scanning electron microscope (SEM).

For each sample, three secondary electron images were collected, at a screen magnification of 50x (image 0001) and 150x (images 0002 and 0003).  These images were collected using an accelerating voltage of 15 kV, and a beam current of 0.1 nA.

For each sample, approximately 150 mineral grains were identified as to mineral species.  Additionally, each sample was examined with backscattered electron imaging, and high atomic number minerals in trace quantities were identified.

For each sample, 2 x-ray spectra were collected from agglomerated fine-grained sheet silicates (sheet 2). The spectra were processed for semi-quantitative compositional results, expressed as oxides, and tabulated. These oxide weight% results are only semi-quantitative, and the analyzed agglomerates have irregular surface topography, and are variably porous.

The mineral identification and x-ray spectra collection were completed using an accelerating voltage of 15 kV and a beam current of 1.5 nA.  Spectra collection times were 50 s.