

Supplementary Tables

1. CHAPTER ONE

Table S1.1. Putative relationships produced by ML Relate with observed heterozygosity of each sample. The sample removed from the data set for likely contamination (if any) is listed in the final column.

| Relationship | Sample 1 ID | Sample 2 ID | Ln Likelihood of Relationship | Sample 1 H_o | Sample 2 H_o | Sample Removed |
|---------------------|--------------------|--------------------|--------------------------------------|-------------------------------|-------------------------------|-----------------------|
| Full Sib. | Geoje012315_06 | Geoje012315_05 | -4439.78 | 0.214 | 0.192 | Geoje012315_05 |
| Full Sib. | Geoje012315_09 | Geoje012315_11 | -7084.81 | 0.435 | 0.372 | both |
| Full Sib. | Namhae021015_0 | Namhae021015_06 | -6920.88 | 0.306 | 0.277 | both |
| Full Sib. | YSBlock121315_14 | YSBlock121315 | -4464.73 | 0.311 | 0.148 | YSBlock121315_14 |
| Full Sib. | Boryeong07_13 | Boryeong07 | -5672.15 | 0.203 | 0.335 | Boryeong07_10 |
| Full Sib. | YSBlock121315_19 | YSBlock121315 | -4049.89 | 0.148 | 0.307 | YSBlock121315_14 |
| Half Sib. | YSBlock121315_21 | Pohang010715 | -6061.02 | 0.234 | 0.284 | Pohang010715_26 |
| Half Sib. | YSBlock121315_21 | Pohang010715 | -6082.91 | 0.227 | 0.284 | Pohang010715_26 |
| Half Sib. | JinBay121807_21 | Jukbyeon07_31 | -5095.94 | 0.171 | 0.181 | - |
| Half Sib. | Geoje012315_09 | Geoje012315_11 | -6856.83 | 0.358 | 0.372 | both |
| Half Sib. | Namhae021015_06 | Geoje012315_04 | -6751.17 | 0.277 | 0.255 | both |
| Half Sib. | Namhae021015_10 | Geoje012315_04 | -6731.77 | 0.275 | 0.255 | both |
| Half Sib. | Namhae021015_13 | Geoje012315_05 | -6493.12 | 0.265 | 0.192 | Namhae021015_13 |
| Half Sib. | Namhae021015_06 | Geoje012315_04 | -7186.79 | 0.277 | 0.255 | both |
| Half Sib. | Namhae021015_09 | Geoje012315_11 | -7470.77 | 0.306 | 0.372 | both |
| Half Sib. | Namhae021015_09 | Geoje012315_09 | -7827.96 | 0.306 | 0.435 | both |
| Half Sib. | Namhae021015_10 | Geoje012315_04 | -6727.46 | 0.272 | 0.255 | both |
| Half Sib. | JinBay121807_25 | Geoje011215_29 | -4389.64 | 0.170 | 0.217 | - |
| Half Sib. | JinBay121807_37 | Geoje011215_29 | -5239.29 | 0.169 | 0.217 | - |
| Half Sib. | JinBay121807_39 | Geoje011215_19 | -5274.12 | 0.186 | 0.170 | - |
| Half Sib. | JinBay021108_22 | Geoje011215_18 | -5231.58 | 0.172 | 0.200 | - |

Table S1.2. Information for individuals which were sampled in one region and genetically assigned to a different region. Table (a) includes genetic analysis and lab data that was explored to check for contamination. Table (b) includes metadata collected during sampling, as well as individual age determined by otolith aging techniques. Percent missing data was calculated as proportion of loci not genotyped in the individual. DNA and RAD plate proximity describe whether individuals from the population to which the sample was assigned was close to the sample during DNA extraction or RAD library preparation.

| (a) | Sampling Site | Collection Date | Individual ID | H_o | % Missing Data | Related Samples (ML relate) | DNA Plate Proximity | RAD Plate Proximity | DNA Quality |
|-----|---------------|-----------------|---------------|-------|----------------|---------------------------------|---------------------|--------------------------|-------------------|
| | Pohang | 1/7/2015 | 11 | 0.176 | 1.0 | None | None | None | Good |
| | Pohang | 2/5/2015 | 06 | 0.210 | 0.9 | None | None | None | Good |
| | Geoje | 1/23/2015 | 06 | 0.215 | 1.2 | None | None | None | Good |
| | Geoje | 2/4/2014 | 06 | 0.150 | 6.7 | None | None | None | Good |
| | Namhae | 2/10/2015 | 22 | 0.177 | 0.8 | None | None | None | Good |
| | Namhae | 2/10/2015 | 30 | 0.185 | 0.3 | None | None | Yes | Good |
| | Jukbyeon | 12/10/2007 | 01 | 0.153 | 3.7 | None | Yes | None | Good |
| | Jukbyeon | 12/10/2007 | 13 | 0.179 | 3.8 | None | None | None | Good |
| | Jukbyeon | 12/10/2007 | 31 | 0.181 | 0.8 | Half-sib with Jinhae Bay sample | None | Yes (not related sample) | Slightly Degraded |
| | Jukbyeon | 12/10/2007 | 33 | 0.179 | 0.9 | None | None | Yes | Good |

| (b) | Sampling Site | Collection Date | Individual ID | Population Assigned | Age | TL (cm) | BL (cm) | BW (g) | GW (g) | GSI |
|-----|---------------|-----------------|---------------|---------------------|-----|---------|---------|--------|--------|------|
| | Pohang | 1/7/2015 | 11 | West | 3 | 41.0 | 37.0 | 1740.2 | 193.5 | 11.1 |
| | Pohang | 2/5/2015 | 06 | West | 5 | 51.0 | 46.7 | 1800 | 362 | 20.1 |
| | Geoje | 1/23/2015 | 06 | West | n/a | 55.5 | 51.9 | 2100 | n/a | n/a |
| | Geoje | 2/4/2014 | 06 | West | 3 | 68.2 | 63.6 | 3481.2 | n/a | n/a |
| | Namhae | 2/10/2015 | 22 | West | 4 | 61.5 | 57.4 | 1800 | 90.5 | 5.0 |
| | Namhae | 2/10/2015 | 30 | West | 4 | 55.5 | 50.9 | 1500 | 63.5 | 4.2 |
| | Jukbyeon | 12/10/2007 | 01 | West | n/a | 39 | n/a | 36 | n/a | n/a |
| | Jukbyeon | 12/10/2007 | 13 | West | n/a | 41 | n/a | 35 | n/a | n/a |
| | Jukbyeon | 12/10/2007 | 31 | South | n/a | 50 | n/a | 42.5 | n/a | n/a |
| | Jukbyeon | 12/10/2007 | 33 | West | n/a | 43 | n/a | 37.5 | n/a | n/a |

Table S1.3. Results from the Wilcoxon rank sum test for statistically significant differences in F_{is} and observed heterozygosity (H_o) between (a) the 2007-2008 and 2015-2016 spawning seasons in the western population, and (b) the 2007-2008 and 2013-2014 spawning seasons in the southern population, and (c) the 2013-2014 and 2014-2015 spawning seasons in the southern population.

| | Population | Season 1 | Season 2 | Variable | W | p-value |
|-----|------------|-----------|-----------|----------|----------|--------------------------|
| (a) | West | 2007-2008 | 2015-2016 | F_{is} | 10682000 | 1.24×10^{-6} |
| | | | | H_o | 11733000 | 0.003 |
| (b) | South | 2007-2008 | 2013-2014 | F_{is} | 9735100 | 5.57×10^{-12} |
| | | | | H_o | 10183000 | 6.91×10^{-4} |
| (c) | South | 2013-2014 | 2014-2015 | F_{is} | 11950000 | $< 2.20 \times 10^{-16}$ |
| | | | | H_o | 9687500 | 1.12×10^{-11} |

2. CHAPTER TWO

Table S2.1. Results from linear regressions run to test assumptions for the sliding window analyses. We conducted a linear regression between the weighted average F_{st} in the full data set, and the corresponding weighted average H_o in the eastern and western populations (a). Linear models also tested whether the number of markers used to generate the weighted average F_{st} on each linkage group was correlated with (b) the number of outlier regions identified on that linkage group, or (c) the width of those outlier regions.

| (a) | d.f. | F-statistic | p-value | Adjusted R² |
|---------------------------|-------------|--------------------|-------------------------|-------------------------------|
| Eastern population | 1,3403 | 28.1 | 1.22×10^{-7} | 0.008 |
| Western population | 1,3403 | 187 | $< 2.2 \times 10^{-16}$ | 0.052 |

| (b) | d.f. | F-statistic | p-value | Adjusted R² |
|---------------------------|-------------|--------------------|----------------|-------------------------------|
| Eastern population | 1,16 | 5.12 | 0.488 | -0.023 |
| Western population | 1,21 | 1.26 | 0.284 | 0.009 |
| Full data set | 1,21 | 5.24 | 0.053 | 0.127 |

| (c) | d.f. | F-statistic | p-value | Adjusted R² |
|---------------------------|-------------|--------------------|----------------|-------------------------------|
| Eastern population | 1,21 | 0.391 | 0.541 | -0.037 |
| Western population | 1,21 | 14.8 | 0.001 | 0.449 |
| Full data set | 1,21 | 0.021 | 0.886 | -0.058 |