

GENETIC AND MORPHOLOGICAL DIFFERENTIATION BETWEEN TWO PECTINID POPULATIONS OF *ARGOPECTEN PURPURATUS* FROM THE NORTHERN CHILEAN COAST  
 DIFERENCIACIÓN GENÉTICA Y MORFOLÓGICA ENTRE DOS POBLACIONES DEL PECTÍNIDO *ARGOPECTEN PURPURATUS* DE LA COSTA NORTE DE CHILE

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ABSTRACT

Genetic variation among individuals from two populations of the scallop *Argopecten purpuratus* (Lamarck, 1819) occurring along the Northern Chilean coast were examined at a geographical scale using allozyme electrophoresis and morphological features. Significant differences in the shell length and weight of the adductor muscle were observed in young individuals between these two geographically-close populations, although those differences decreased and were no longer significant as size increased. The genetic variability of *A. purpuratus* is high and comparable to that of most pectinid species. Private alleles and heterozygote deficiency at the loci Aat-1, Aat-2, Cap, Mdh-2 and Pgm were observed in both populations. These populations display considerable genetic differentiation and morphological differences. Our results support the hypothesis of a limited genetic flow between the two sites. In particular, marine currents may not allow the exchange of larvae between the two populations and thus could be partly responsible for the observed differentiation.

*Keywords:* Allozymes, *Argopecten*, Genetic diversity, Morphologic differentiation.

RESUMEN

La diversidad genética entre ejemplares de dos poblaciones del pectínido *Argopecten purpuratus* (Lamarck, 1819) presentes a lo largo de la costa Norte de Chile fueron estudiadas a una escala geográfica, utilizando marcadores electroforéticos de aloenzimas y las características morfológicas. Diferencias significativas en el largo de la concha y el peso del músculo aductor fueron observadas en individuos juveniles entre estas dos poblaciones geográficamente cercanas, sin embargo estas diferencias disminuyen y dejan de ser significativas en tallas mayores. La variabilidad genética de *A. purpuratus* es alta comparable a la mayoría de las especies de pectínidos. Alelos específicos y una deficiencia en heterocigotos fueron observados en ambas poblaciones para los locus Aat-1, Aat-2, Cap, Mdh-2 y Pgm. Estas poblaciones presentan una diferenciación genética y morfológica considerable. Nuestros resultados sugieren la hipótesis de un flujo genético limitado entre estos dos sitios. En particular, las corrientes marinas pueden influenciar al intercambio de larvas limitado entre estas dos poblaciones, y podrían ser por una parte responsables de las diferencias observadas.

*Palabras claves:* Aloenzimas, *Argopecten*, Diversidad genética, Diferenciación morfológica.

INTRODUCTION

The pectinid bivalve *Argopecten purpuratus* (Lamarck, 1819) is distributed along the Pacific coast between 100 and 33°S. It occurs between Arica (18°25'S) and Valparaiso (BORE & MARTINEZ, 1980) along the Chilean coast. This species lives on sedimentary grounds in sheltered areas. Populations are discontinuously distributed at 5 - 40 m depth where sea-water temperature annually varies between 12 and 20°C.

The highest density of *A. purpuratus* in Chile is found in Mejillones and La Rinconada bay, near Antofagasta (23°25'S) with a range of 1 to 37 ind/m<sup>2</sup> (NAVARRO *et al.*, 1991; AVENDAÑO & CANTILLANEZ, 1992) in contrast to 0.2 to 5 ind/m<sup>2</sup> for the Tongoy pectinid-bed (ILLANES, 1987). The world-wide market for pectinid-muscle in 1984 was in the order of 24.550 tons of which 456.4 tons of *A. purpuratus* frozen muscle. (ACHURRA & VIDAL, 1987). However, the increase in international demand has caused an over-fishing of the stocks

since the 1990. Production of *A. purpuratus* is decreasing, as reflected in the annual landed tonnage that has dropped dramatically from 4997 tons in 1985 to 492 tons in 1987 despite an identical fishing effort (AVENDANO, 1993). This decrease is also due to illegal fishing activities and has called the attention on the need to protect this resource.

Studies on the morphological and genetic structures of these populations are part of these global measures. In pectinids, the intraspecific genetic variations in the different species has been established, *i.e.* heterozygosity and polymorphism rates (*Argopecten gibbus* (KRAUSE *et al.*, 1994), *Patinopecten yessoensis* (NIKIFOROV & DOLGANOV, 1982), *Argopecten ventricosus* (CRUZ & IBARRA, 1997), *Chlamys opercularis* (BEAUMONT, 1982), *Chlamys varia* (MATHERS, 1975), *Placopecten magellanicus* (FOLTZ & ZOUROS, 1984), *Pecten maximus* (WILKINS, 1978; BEAUMONT *et al.*, 1993) and *Pecten jacobaeus* (PENA *et al.*, 1995). GALLEGUILLOS & TRONCOSO (1989) and VON BRAND & KIJIMA (1990) have already established allozymic data on the genetic variability in other Chilean populations. The aim of the present study was to expand these preexisting data through an analysis of the genetic structure of other Chilean pectinid populations. Also, this study will suggest a proposal whereby a zone of the Bay of Antofagasta be set up as a reserve, zone where the environmental conditions are such that the species *Argopecten purpuratus* can be maintained. Preliminary studies have revealed (AVENDAÑO, 1993) the occurrence of a particular morphologie in these individuals with respect to the size of their adductor muscles. An attempt will be made to determine if this economically valuable characteristic is of genetic origin.

## MATERIAL AND METHODS

Samples were collected from two wild populations located in the Mejillones and La Rinconada Bays (Fig. 1). 1500 pectinids were randomly collected from each site at a 20-30 m depth of by divers and shell-height, -length and width, as well as adductor muscle weight, were measured. The two following linear relations were established: (1) Width =  $a + b$  (height) and (2) thickness =  $a + b$  (height) where  $a$  is a constant and  $b$  is the slope and their residual variances were compared. The polynomial regression graphs, *i.e.* thickness =  $f$  (height) and muscle weight =  $f$  (height) were also analysed in individuals from ranged in 5 mm-size class to compare the morphological and weight characteristics in the two populations.

Allozymic analyses were performed on a 132 adults (70 to 85 mm in size). Scallops were dissected in laboratory and the adductor muscle and digestive gland were homogenized in grinding buffer (PASTEUR *et al.*, 1987), centrifuged at 10.000 g for 10 minutes at 4°C, and the resulting supernatant

was stored at -80°C. Electrophoresis was carried out on SIGMA starch gel (11%) either in a continuous system (buffer 1: Tris-citrate buffer: Tris 0.62 M, citric acid 0.14 M, pH = 8) or in a discontinuous system (Poulik gel: Tris 0.07 M, citric acid 0.005 M, pH = 8.7; Poulik electrodes: boric acid 0.3 M, NaOH 0.06 M, pH = 8.2, *i.e.* buffer 2) according to the studied loci.

Seven enzymatic systems were studied. Two isozymes, Aspartate aminotransferase (AAT, EC 2.6.1.1 in buffers 1 and 2) and Cytosol aminopeptidase (CAP, EC 3.4.11.1 in buffers 1 and 2), are implicated in osmoregulation processes. The five others, Phosphoglucose Isomerase (GPI, EC 5.3.1.9 in buffer 1), Phosphoglucomutase (PGM, EC 2.7.5.1 in buffer 1 and 2), Malate Dehydrogenase (MDH, EC 1.1.1.37 in buffer 1), Octopine Dehydrogenase (ODH, EC 1.5.1.11 in buffer 1) and Superoxide dismutase (SOD, EC 1.15.1.1 in buffer 1) are involved in energetic metabolism reactions. Isozymes were revealed and stained according to the classical techniques (PASTEUR *et al.*, 1987). The loci were ranked according to their migration distance from the cathode to the anode. The alleles were designated as a function of relative mobility from the origin, the most common allele present being given an arbitrary score of 100.

A locus was considered to be polymorphic when the frequency of the most common allele was less than 95%. Estimates of allele frequencies, the proportion of polymorphic loci, (P), the average number of alleles per locus (Na), the observed number of alleles (No), the average observed (Ho) and expected (unbiased H of Nei, 1978) and heterozygosity per locus were calculated for each population using BIOSYS-1 (SWOFFORD & SELANDER, 1981, 1989).

Genetic differentiation between *A. purpuratus* populations and Hardy-Weinberg equilibrium were estimated using the Fst and Fis fixation indices of WRIGHT (1965). These indices were obtained by using the "GENETIX 3.0" (BELKIR *et al.*, 1996) and BIOSYS-1 software (SWOFFORD & SELANDER, 1981, 1989). Fst and Fis departures from zero were tested according to LI & HORVITZ (1953) and WORKMAN & NISWANDER (1970) by using the commonly applied  $\chi^2$  tests 2NFst (k-1) and NFis<sup>2</sup> (k-1) respectively. To adjust the significance levels of multiple tests, the standard Bonferroni technique (MILLER, 1980; LESSIOS, 1992) in which a predetermined significance level,  $\alpha$ , is divided by the number of tests per locus, k, to obtain a corrected significance level  $\alpha' = \alpha/k$  ( $\alpha = 0.05$ ) was used.

Gene flow was estimated from the Nm value calculated using the following equation  $F = 1 / (4Nm + 1)$  where N is the effective population number, m is the migration rate and F is the equilibrium value of Fst (fixation indice) whose calculation is correct for this model on the condition that none of the alleles undergo mutation when passing from one generation to the next one. F values correspond to the Fst value obtained in a multi-locus analysis. The equation,  $F = 1 / (4Nm + 1)$  is based on the infinite-alleles model of mutation where m replaces the mutation rate  $\mu$  (WRIGHT, 1951, 1965; SLATKIN, 1985).

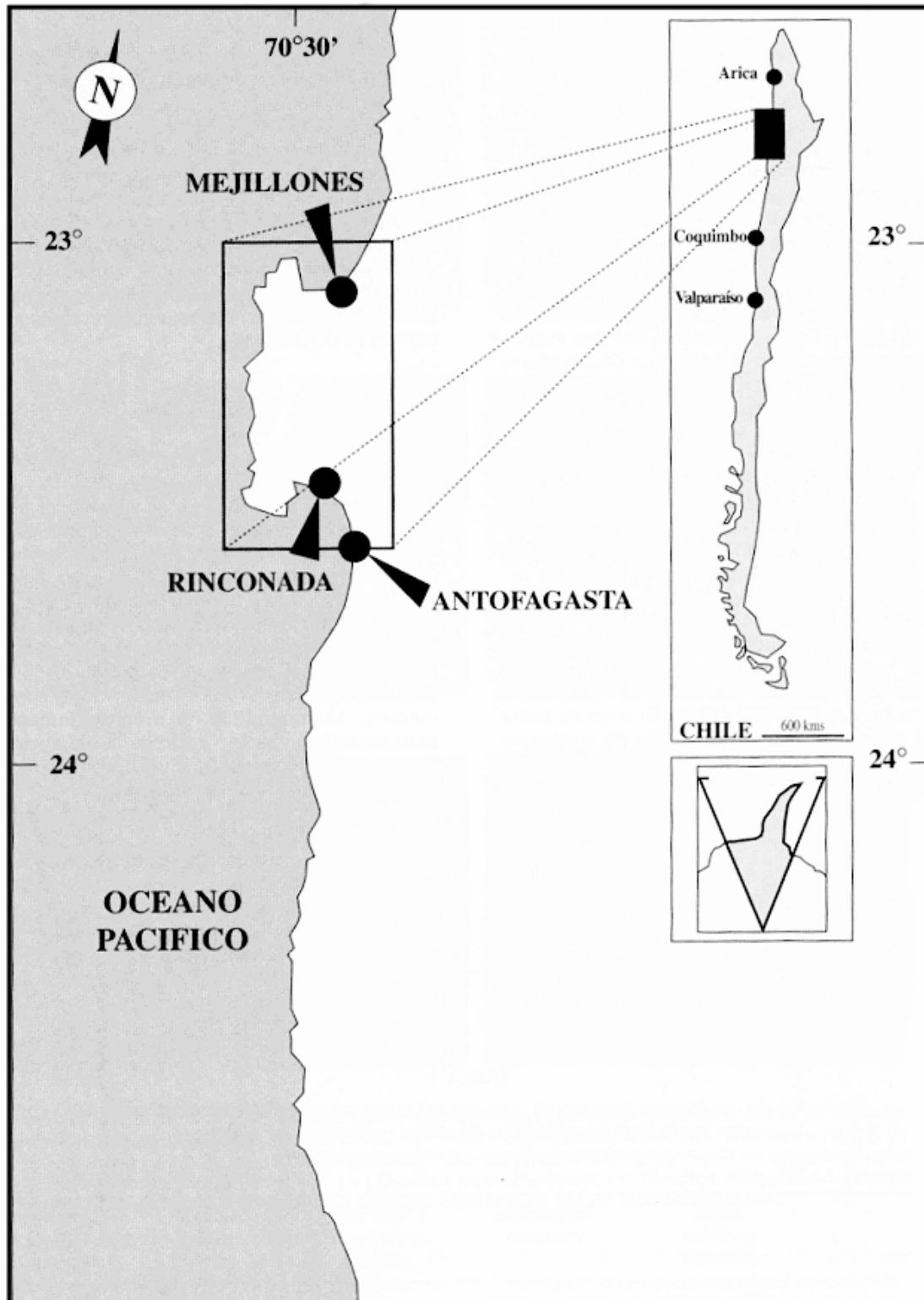


Figure 1: Sampling sites of *Argopecten purpuratus* on the Northern Chilean Pacific coast.  
 Ubicación geográfica de las áreas de muestreo de *Argopecten purpuratus* de la costa Norte del Pacífico chileno.

The effective number of alleles ( $N_e$ ) is calculated using the following equation  $N_e = 4N\mu + 1 = 1/\sum p_i^2$  where  $\sum p_i^2$  is the homozygosity in terms of allelic frequency.  $N_e$  is defined as the number of equally frequent alleles within an ideal population that would produce the same homozygosity as the studied population. This index is used to compare the various distributions of allele frequencies (SLATKIN, 1985).

## RESULTS

### Genetic analysis

The allele frequencies of ten loci and the sample sizes for electrophoretic analyses are given in Table 1. Six of these loci, Aat-1, Aat-2, Gpi, Cap, Pgm and Odh, were polymorphic within the two populations. The loci, Mdh-1, Mdh-2, Sod-1 and Sod-2 were monomorphic in Mejillones as were Sod-1 and Sod-2 in La Rinconada.

Fst analysis performed on the entire set of studied loci exhibited significant differences in the allelic frequency distribution seven alleles from four of the loci: Aat-1<sup>100</sup>  $\chi^2_{(4)} = 177.56$  ( $p \leq 0.01$ ), Aat-1<sup>103</sup>  $\chi^2_{(4)} = 160.72$  ( $p \leq 0.01$ ), Gpi<sup>95</sup>  $\chi^2_{(6)} = 31.99$  ( $p \leq 0.01$ ), Gpi<sup>105</sup>  $\chi^2_{(8)} = 24.07$  ( $p \leq 0.01$ ), Pgm<sup>100</sup>  $\chi^2_{(6)} = 98.92$  ( $p \leq 0.01$ ), Pgm<sup>105</sup>  $\chi^2_{(6)} = 117.37$  ( $p \leq 0.01$ ) and Odh<sup>100</sup>  $\chi^2_{(6)} = 17.03$  ( $p \leq 0.01$ ). Private alleles in each population were detected, six in La Rinconada bay (Aat-1<sup>103</sup>, Aat-2<sup>94</sup>, Mdh-1<sup>110</sup>, Mdh-2<sup>110</sup>, Pgm<sup>90</sup> and Odh<sup>93</sup>) and two (Aat-2<sup>106</sup> and Cap<sup>95</sup>) in the Mejillones population. (Table 1). Among these private alleles, only the Aat-1<sup>103</sup> allele showed a high frequency ( $> 0.1$ ). The Nm value calculated with the multi-locus Fst represents an exchange of 2.84 migrants per generation between the two populations of *Argopecten purpuratus*.

The parameters of genetic variability highlighted differences between the two populations (Table 2). The percentage of polymorphic loci (P) and the Na value were higher in the La Rinconada population than in Mejillones. Except for the locus Pgi ( $N_e = 2.291$ ) and to a lesser extent Odh ( $N_e = 1.371$ ),  $N_e$  values in Mejillones were close to 1 whereas they but were higher than 1 regardless of the loci, with the exception of Aat-2 in the La Rinconada population. Four loci, (Aat-1, Gpi, Odh and Pgm) had an  $N_e$  value greater than 1.45, suggesting that the number of alleles contributing to the genetic structure of the La Rinconada population is higher than that in the Mejillones population.

A divergence from Hardy-Weinberg expectations was observed in the Mejillones population for the loci

Aat-1  $\chi^2_{(1)} = 60.413$ ,  $p \leq 0.01$ , Aat-2  $\chi^2_{(3)} = 60.524$ ,  $p \leq 0.01$ , Cap  $\chi^2_{(3)} = 22.501$ ,  $p \leq 0.01$  and Pgm  $\chi^2_{(3)} = 47.00$ ,  $p \leq 0.01$ ) and in the La Rinconada population for the loci Aat-1  $\chi^2_{(3)} = 111.54$ ,  $p \leq 0.01$ , Aat-2  $\chi^2_{(3)} = 39.102$ ,  $p \leq 0.01$ , Cap  $\chi^2_{(1)} = 6.605$ ,  $p \leq 0.05$ , Gpi  $\chi^2_{(10)} = 37.533$ ,  $p \leq 0.01$ ) and Pgm  $\chi^2_{(1)} = 46.79$ ,  $p \leq 0.01$ ). Departures from the Hardy-Weinberg equilibrium are due to heterozygote deficiencies (Table 2).

### Biometrical study

Analysis revealed that the slope obtained Regression (1) for the La Rinconada Bay population (R) was significantly higher than for the Mejillones Bay population (M) ( $t = 2.42$ ,  $p = 0.008$ ) (Table 3), although the difference in curve shape was negligible (Fig. 2). The comparison of residual variances ( $F = 1.49$ ,  $p = 0.000$ ) also indicated that Mejillones individuals had a much higher shape variability than that of La Rinconada.

For relation (2) results, Mejillones presented higher "shell thickness" values ( $t = 6.67$ ,  $p = 0.000$ ) and shape variability ( $F = 1.137$ ,  $p = 0.016$ ) than did La Rinconada (Fig. 2).

The comparison of mean weight of the adductor muscle in individuals from the two populations showed that, up to 75 mm, muscles in Mejillones population were significantly heavier. Above this size, the differences were no longer significant and this trend seemed to be reversed in large sized individuals (Table 4 and Fig. 3).

## DISCUSSION

Levels of genetic variability observed within the two *Argopecten purpuratus* populations of the north Chilean coast are within the range found in other bivalve species, especially in pectinid species. This group of bivalves is usually characterised by high genetic variability in terms of polymorphism and observed-heterozygosity for several autosomal loci (BEAUMONT & BEVERIDGE, 1984; HUELVAN, 1985; PENA *et al.*, 1995). Nevertheless, studies in other pectinid species have shown that this high variability is not typical since low polymorphism and heterozygosity rates have been observed in pectinid species such as *Patinopecten yessoensis* (NIKIFOROV & DOLGANOV, 1982) and *Placopecten magellanicus* (FOLTZ & ZOUROS, 1984). The comparison of these genetic parameters described by several authors in different marine species has shown variations in relation to a given locus and within a same locus. This variation depends on the demographic structure, habitat and fitness of individuals (DENIS *et al.*, 1993; MORAGA *et al.*, 1994; JOLLIVET *et al.*, 1995). Previous studies have shown significant differences in the allelic frequencies of the Pgi locus within populations of black scallop, *Chlamys varia*, and queen scallop, *Chlamys opercularis*, living on the West and East coasts of Ireland (MATHERS, 1975). The population from the Irish Sea and English Channel on the one hand, and that from the West coast of France and Ireland on the other hand, were thus characterised. Other allozymic markers, i.e. Odh, Pgm and one anonymous locus, Pt-A, have enabled differentiation of populations of *C. opercularis* at an allelic frequency level for the locus Pt-A in particular (BEAUMONT, 1982). The inter-site differences in allelic frequencies of the loci Aat-1, Aat-2, Odh, Pgi

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TABLE 1

Allelic frequencies within the two populations of *Argopecten purpuratus*. (n): number of individuals. Fst: test for heterogeneity of gene frequencies among populations. \*: significant value at the  $\alpha$  threshold (Bonferroni's correction).

Frecuencias alélicas dentro de dos poblaciones de *Argopecten purpuratus*. (n): número de individuos. Fst: test de heterogeneidad de frecuencias de genes inter poblaciones \*: valor significativo del umbral  $\alpha$  (Corrección de Bonferroni).

| Locus                | allele | MEJILLONES | LA RINCONADA | Fst             |
|----------------------|--------|------------|--------------|-----------------|
| Aat-1                | (n)    | (72)       | (60)         |                 |
|                      | 100    | 0.951      | 0.600        | <b>0.3363*</b>  |
|                      | 103    | -          | 0.325        | <b>0.3044</b>   |
| Aat-2                | 106    | -0.049     | 0.075        | -0.0083         |
|                      | (n)    | (72)       | (60)         |                 |
|                      | 94     | -          | 0.017        | 0.0108          |
|                      | 100    | 0.923      | 0.958        | 0.0003          |
| Gpi                  | 103    | 0.042      | 0.025        | -0.005          |
|                      | 106    | 0.035      | -            | 0.0184          |
|                      | (n)    | (72)       | (58)         |                 |
|                      | 90     | 0.007      | 0.017        | -0.0031         |
| Cap                  | 95     | 0.007      | 0.052        | <b>0.0303 *</b> |
|                      | 100    | 0.548      | 0.569        | -0.0092         |
|                      | 105    | 0.361      | 0.241        | <b>0.0228 *</b> |
|                      | 110    | 0.076      | 0.121        | 0.0008          |
|                      | (n)    | (71)       | (60)         |                 |
| Mdh-1                | 95     | 0.014      | -            | 0.0054          |
|                      | 100    | 0.958      | 0.950        | -0.0108         |
|                      | 110    | 0.028      | 0.050        | -0.0042         |
|                      | (n)    | (72)       | (60)         |                 |
| Mdh-2                | 100    | 1          | 0.992        | 0.0015          |
|                      | 110    | -          | 0.008        | 0.0015          |
|                      | (n)    | (72)       | (60)         |                 |
| Pgm                  | 100    | 1          | 0.975        | 0.0149          |
|                      | 110    | -          | 0.025        | 0.0149          |
|                      | (n)    | (72)       | (60)         |                 |
|                      | 90     | -          | 0.008        | 0.0015          |
| Odh                  | 95     | 0.021      | 0.017        | -0.0071         |
|                      | 100    | 0.972      | 0.808        | <b>0.1249</b>   |
|                      | 105    | 0.007      | 0.167        | <b>0.1482</b>   |
|                      | (n)    | (72)       | (60)         |                 |
|                      | 93     | -          | 0.008        | 0.0015          |
| Sod-1                | 100    | 0.840      | 0.742        | <b>0.0215</b>   |
|                      | 105    | 0.153      | 0.217        | 0.0054          |
|                      | 110    | 0.007      | 0.033        | 0.0112          |
|                      | (n)    | (72)       | (60)         |                 |
| Sod-2                | 100    | 1          | 1            | -               |
|                      | (n)    | (72)       | (60)         |                 |
|                      | 100    | 1          | 1            | -               |
| Multi-locus analysis |        |            |              | 0.08069         |

and Pgm in populations from Mejillones and La Rinconada Bays also suggest genetic differentiation. In fact, the marine currents restricts larval exchange and could therefore partly explain the apparent very limited genetic flow between these two populations. Fst analysis seems to confirm this hypothesis by highlighting the existence of private alleles (Aat-1<sup>103</sup>)

or indicator-allele (Gpi<sup>105</sup> Pgm<sup>105</sup>) in each population. Our results are in agreement with those obtained by FEVOLDEN (1989), dealing with the genetic variability of North Atlantic *Chlamys islandica* populations and which demonstrates a restricted gene flow due to surface marine current circulation (gyres and particular currents).

TABLE 2

Genetic variability parameters within the two populations of *Argopecten purpuratus*.

**Ne**: effective number of allele per locus. **Ho**: observed heterozygosity.

**Fis**: deviation from Hardy-Weinberg expectations, (\*: 5% significance level).

*Parámetros de la variabilidad genética dentro de las dos poblaciones de Argopecten purpuratus.*

**Ne**: número efectivo de alelos por locus. **Ho**: heterozigosidad observada.

**Fis**: desviación de las condiciones de Hardy-Weinberg esperada, (\*nivel significativo al 5%).

|  | Mejillones (72)   |       |               | La Rinconada (60) |       |               |
|--|-------------------|-------|---------------|-------------------|-------|---------------|
|  | Ne                | Ho    | Fis           | Ne                | Ho    | Fis           |
| Aat-1  | 1.102             | 0.014 | <b>0.850*</b> | 2.122             | 0.017 | <b>0.968*</b> |
| Aat-2  | 1.172             | 0.097 | <b>0.325*</b> | 1.089             | 0.050 | <b>0.380*</b> |
| Gpi  | 2.291             | 0.458 | 0.185         | 2.503             | 0.362 | <b>0.397*</b> |
| Cap  | 1.088             | 0.042 | <b>0.382*</b> | 1.105             | 0.067 | <b>0.298*</b> |
| Mdh-1  | 1                 | -     | -             | 1.016             | 0.017 | -0.008        |
| Mdh-2  | 1                 | -     | -             | 1.051             | 0.017 | <b>0.791*</b> |
| Pgm  | 1.057             | 0.041 | <b>0.233*</b> | 1.468             | 0.083 | 0.179         |
| Odh  | 1.371             | 0.292 | -0.078        | 1.669             | 0.333 | 0.152         |
| Sod-1  | 1                 | -     | -             | 1                 | -     | -             |
| Sod-2  | 1                 | -     | -             | 1                 | -     | -             |
| Mean heterozygosity                                | 0.095 (S.E 0.049) |       |               | 0.098 (S.E 0.043) |       |               |
| Mean number of alleles per locus (Na)              | 2.20 (S.E 0.36)   |       |               | 2.70 (S.E 0.42)   |       |               |
| Percentage of polymorphic loci (P: 0.95 criterion) | 0.3               |       |               | 0.5               |       |               |

TABLE 3

Morphological study: test on the slopes of relation (1) (width = a + (b x height)) and relation (2) (thickness = a + (b x height)). (M): Mejillones. (R): La Rinconada.

*Estudio morfológico: test de pendientes de la relación (1) (largo = a + (b x alto)) y de la relación (2) (espesor = a + (b x alto)). (M): Mejillones. (R): La Rinconada.*

|                  | Intercept (mm) | Slope | Correlation coefficient | F     | Prob level   | residuals | df   |
|------------------|----------------|-------|-------------------------|-------|--------------|-----------|------|
| Mejillones (1)   | -3.48          | 1.139 | 0.984                   | 45219 | <b>0.000</b> | 8732      | 1461 |
| La Rinconada (1) | -4.89          | 1.157 | 0.987                   | 54128 | <b>0.000</b> | 5648      | 1404 |
| Mejillones (2)   | 4.15           | 0.363 | 0.917                   | 7783  | <b>0.000</b> | 5201      | 1464 |
| La Rinconada (2) | -1.624         | 0.404 | 0.926                   | 8486  | <b>0.000</b> | 4386      | 1404 |

TABLE 4

Morphological study: polynomial regressions analysis. Pm: mean muscle weight for Mejillones individuals.

Pr: mean muscle weight for La Rinconada individuals. Nm: total number of individuals in Mejillones population., Nr: total number of individuals in La Rinconada population.

*Estudio morfológico: análisis de regresiones polinomiales. Pm: peso medio del músculo para los ejemplares de Mejillones. Pr: peso medio del músculo para los ejemplares de La Rinconada. Nm: número total de individuos de la población de Mejillones Nr: número total de individuos de la población de La Rinconada.*

| Height (mm) | Pm   | Pr   | t   | p (means)    | Nm  | Nr  | Residual variances |
|-------------|------|------|-----|--------------|-----|-----|--------------------|
| 55          | 2.45 | 1.96 | 4.3 | <b>0.000</b> | 146 | 139 | <b>0.000</b>       |
| 55 - 60     | 3.26 | 2.92 | 3.1 | <b>0.002</b> | 120 | 150 | <b>0.000</b>       |
| 60 - 65     | 4.32 | 3.94 | 3.0 | <b>0.003</b> | 137 | 206 | <b>0.000</b>       |
| 65 - 70     | 5.46 | 5.04 | 3.4 | <b>0.001</b> | 204 | 251 | <b>0.000</b>       |
| 70 - 75     | 6.34 | 6.04 | 2.1 | <b>0.034</b> | 219 | 225 | <b>0.000</b>       |
| 75          | 9.18 | 9.11 | 0.4 | <b>0.707</b> | 607 | 399 | <b>0.000</b>       |

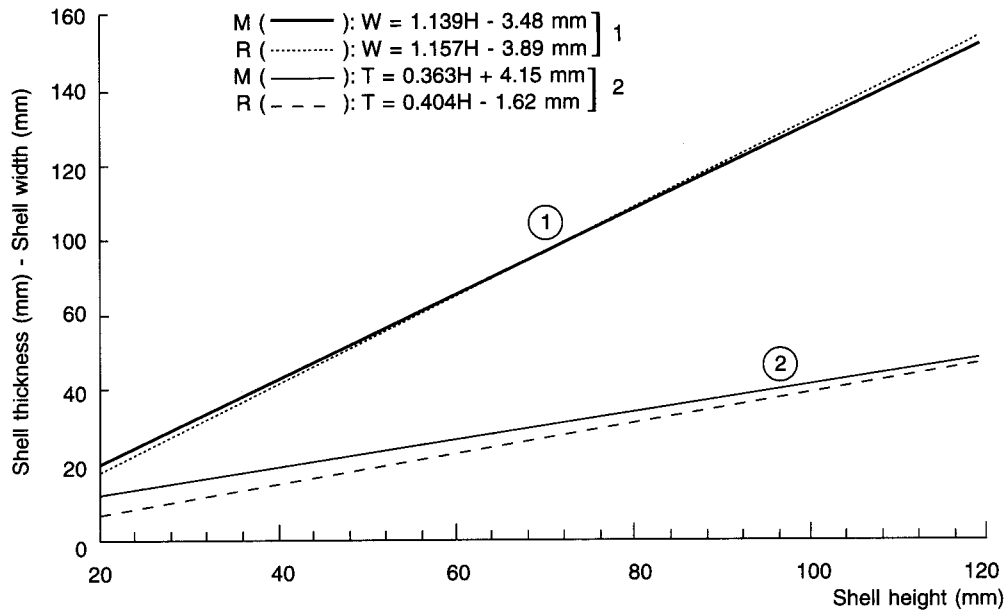


Figure 2: Morphological study: plots of relation (1) (width = a + (b x height)) and relation (2) (thickness = a + (b x height)). (M): Mejillones. (R): La Rinconada.  
 Estudio morfológico: curva de la relación (1) (largo = a + (b x altura) y de la relación 2 (espesor = a + (b x altura). (M): Mejillones. (R): La Rinconada.

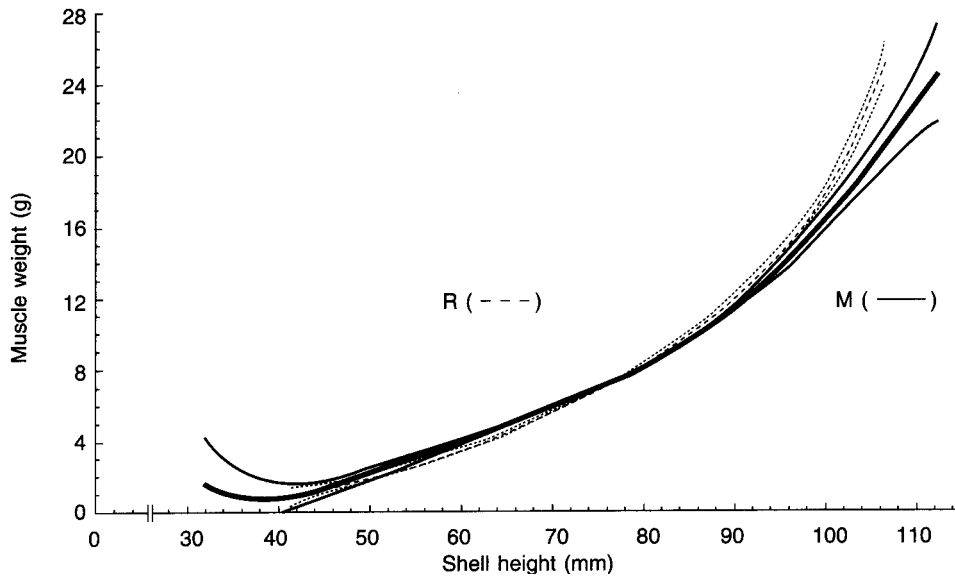


Figure 3: Morphological study: plots of polynomial regressions: thickness = f (height) and muscle weight = f (height). (M): Mejillones. (R): La Rinconada.  
 Estudio morfológico: curva de regresión polinomial: espesor = f (altura) y peso del músculo = f (altura). (M): Mejillones. (R): La Rinconada.

Genetic studies in molluscs have correlated the degree of heterozygosity to the organism's basal metabolism. If heterozygote superiority can be attributed to reduced maintenance costs, then highly heterozygous individuals may be able to divert a

greater proportion of energy towards either somatic or gonadal growth depending on their age (KOEHN & SHUMWAY, 1982; HAWKINS *et al.*, 1986). For example, RODHOUSE *et al.* (1986) found a positive correlation between multiple-locus heterozygosity

and fecundity in older individual of the mussel *Mytilus edulis*, although the same was not true of younger individuals. This restriction in energy requirements results from a better efficiency of allozymes encoded by heterozygote genotypes, which reduces the protein production rate necessary for basal metabolism and thus spares ATP molecules. This energy may then be allocated to somatic growth, to resisting starvation (SINGH & ZOUROS, 1978; HAWKINS et al., 1985) or to gamete production (DIEHL et al., 1986; RODHOUSE et al., 1986, RIOS et al., 1996). The accumulation of energy in muscles increases the mobility of individuals, favors food catch in *Thais haemastoma* (GARTON, 1984), and increases the ability to escape predators in *Placopecten magellanicus* (ZOUROS & FOLTZ, 1984). For a same shell height, individuals from Mejillones had a greater shell thickness and adductor muscle weight than those of La Rinconada. However, this difference decreased and an opposite trend appeared with increasing size. These results in association with a higher heterozygosity rate for the La Rinconada population are in agreement with those previously obtained.

The high deficiency of heterozygotes observed here corroborates the general rule prevailing in marine bivalves (ZOUROS & FOLTZ, 1984; GAFFNEY et al., 1990). On the other hand, *A. irradians irradians* is exceptional in showing little or no deficiency in heterozygotes (BRICELJ & KRAUSE, 1992). The heterozygote deficiency observed in the two Chilean populations may stem from a weak Wahlund effect, which could be the reason behind a higher differentiation of some enzymatic systems at a sub-population level. However, the Nm value (Nm = 2.84) indicates that less than 3 migrants are exchanged per generation; this is in agreement with the hypothesis of a limitation of the Wahlund effect. It could also be argued that the recruited spat did not come from a panmictic population, but from several disequibrated and non cross-fertilised sub-populations. This would increase the deficiency in heterozygotes for loci whose allelic frequencies are already strongly differentiated in the original sub-population. The observed deficiency in heterozygotes may also be explained by a selection pressure, which would act on specific loci, resulting in a differential mortality at the larvae stage, and induce heterozygosity deficiency in adult populations for these selected loci (ZOUROS & FOLTZ, 1984). In addition, the marine currents between these two bays may limit larval exchange, thus contributing to the genetic differentiation. The detection of private alleles in the two populations corroborates this hypothesis. Heterozygote deficiency could also be explained by self-fertilization, which is common in marine hermaphrodite species (BEAUMONT & BUDD, 1983).

As a target aquaculture-species in the Northern regions of Chile, all information on the biology of *A. purpuratus* is essential in the choice of genitors in hatcheries. The reproductive cycles of the Mejillones and La Rinconada scallop banks from 1989 to 1993

described by AVENDAÑO & LE PENNEC (1997) as well as the number of emitted gametes between the two populations, suggest that Mejillones individuals are more appropriate as genitors for hatcheries than those from La Rinconada. On the other hand, our data concerning the dimensions of the adductor muscle, in addition to enzyme polymorphism, as indicated by higher values of P, Na and Ne, suggest that the La Rinconada population would be a more suitable source of genitors for future aquaculture attempts and genetic diversity conservation.

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