



Review of the literature on bivalve cytogenetics in the last ten years

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Abstract: This paper provides a review of the studies on bivalve chromosomes since 1992, in order to gather available data and to highlight the recent progress in different fields of cytogenetics: karyotype and chromosome markers, genome size, aneuploidy, natural and induced polyploidy, and hybridization.

Résumé: *Revue des travaux des dix dernières années sur l'étude cytogénétique des bivalves.* Cet article présente une revue sur l'étude des chromosomes des bivalves depuis 1992 afin de rassembler les données disponibles et de souligner les progrès récents dans les différents domaines de la cytogénétique : caryotype et marqueurs chromosomiques, taille du génome, aneuploïdie, polyploïdie naturelle et induite, et hybridisation.

Keywords: Bivalvia, Chromosomes, Cytogenetics

Introduction

Cytogenetic studies encompass different levels of biological organization ranging from the morphological to the molecular, depending on the applicable technology. Chromosomes can be studied as a morphological manifestation of the genome in terms of their microscopically visible size, shape, number and behaviour during meiosis and mitosis. At another level, banding studies reveal finer details of chromosomal morphology. Studies of natural or induced deviation from the diploid chromosome number also contribute significant cytogenetic data.

Among bivalves, the first investigations concerned the chromosome number (see Patterson review, 1969). Then, pre-treatment with colchicine and hypotonic treatment, combined with the air drying technique, permitted accurate assessments of chromosome morphology (see Nakamura

review, 1985). Later, the development of banding techniques which allowed chromosome identification in karyotypes began to be applied in bivalves (see Thiriot-Quiévreux review, 1994). Since these reviews, the study of bivalve chromosomes has greatly progressed in karyological as well as molecular information, as a result of routine application of several banding techniques and the development of techniques for in situ hybridization.

The aim of this paper is to provide a review of the studies on bivalve chromosomes since 1992, in order to gather available data and to highlight the recent progress in the different fields of bivalve cytogenetics.

Karyotypes and Chromosome markers

Data on standard karyotypes, banding techniques and FISH are given in Table 1, in which bivalve classification follows that of Boss (1982). Since 1992, new karyological data have been added for 65 bivalve species among which the first karyotype data are given for 49 species. Within the bivalve class, the most frequent chromosome number of $2n=38$,

Tableau 1 : Données récentes sur les chromosomes de bivalves : caryotype standard, techniques de marquages et FISH.

[illegible]

Table 1. Continued 2.
Tableau 1 : suite 2.

Family/Species	Origin	2n	Karyotype	NORs	C	Fluo	RE	G	N	RB	FISH	References
Anomidae												
<i>Anomia ephippium</i> ° *	W Mediterranean	12	1 m, 2 sm, 3 st									Thiriot-Quiévreux, unpublished
Unionidae												
<i>Hyriopsis cumingii</i> °	China	38	12 m, 5 sm, 2 st		+							Wang et al., 2000
<i>Unio conus</i> ° *	Ukraine	38	11 m, 7 sm, 1 st									Melnichenko, 2000
<i>Unio elongatus</i> ° *	Egypt	28	10 m, 4 sm									Ebied, 1998
<i>Unio pictorum</i> *	Ukraine	38	13 m, 6 sm									Melnichenko, 2000
Mutelidae												
<i>Mutela rostrata</i> ° *	Egypt	20	2 m, 2 sm, 6 t									Ebied, 1998
Laseidae												
<i>Lasaea australis</i> ° *	Australia	36	4 m, 6 sm, 3 st, 5 t									Thiriot-Quiévreux, 1992
<i>Lasaea colmani</i> ° *	Australia	40	5 m, 9 sm, 5 st, 1 t									O Foighil & Thiriot-Quiévreux, 1999
Cardiidae												
<i>Cerastoderma edule</i>	Galicja, Spain	38	12 sm, 4 st, 3 t									Insua & Thiriot-Quiévreux, 1992
	Galicja, Spain										rDNA	Insua et al., 1999
	Baltic Sea	38	3 m, 10 sm, 6 st	+								Thiriot-Quiévreux & Wolowicz, 1996 a
<i>Cerastoderma glaucum</i> °	Sète, Mediterranean		4 m, 9 sm, 6 st	+								Thiriot-Quiévreux & Wolowicz, 1996 a
Mactridae												
<i>Macra chinensis</i> °	Japan	38	9 sm, 9 st									Wada & Komaru, 1993
<i>Spisula solidissima</i> °	Magdalen Islands, Can.	38	4 m, 5 sm, 10 st/t									Xiang et al., 1993
<i>Tresus capax</i> °	Canadian Pacific	34	10 m, 7 sm								rDNA	Gonzalez-Tizon et al., 2000 b
Solenidae												
<i>Solen constrictus</i> ° *	Haiyang, China	38	15 m, 3 sm, 1 st									Wang et al., 1998 b
Tellinidae												
<i>Macoma balthica</i> *	Gdansk Bay, Baltic Sea	38	11 m, 2 sm, 6 st									Wolowicz & Thiriot-Quiévreux, 1997
<i>Macoma nasuta</i> ° *	Canadian Pacific	38	8 m, 6 sm, 5 st									Gonzalez-Tizon et al., 2000 b
Psammobiidae												
<i>Nuttallia nuttallii</i> ° *	Canadian Pacific	38	7 m, 12 sm									Gonzalez-Tizon et al., 2000 b
<i>Sinonovacula constricta</i> °	Qingdao, China	38	13 m, 4 sm, 1 st, 1 t	+			+				rDNA	Wang et al., 1998 c
Corbiculidae												
<i>Corbicula colorata</i> ° *	Korea	38	1 m, 18 st									Park et al., 2000
<i>Corbicula fluminalis</i> ° *	Egypt	26	6 m, 7 sm									Ebied, 1998
Veneridae												
<i>Ruditapes philippinarum</i>	Haiyang, China	38										Wang et al., 1998 b
<i>Venerupis pullastra</i> °	Galicja, Spain	38	3 m, 8 sm, 8 st									Insua & Thiriot-Quiévreux, 1992
<i>Venerupis rhomboides</i> °	Galicja, Spain	38	4 m, 8 sm, 4 st, 3 t									Insua & Thiriot-Quiévreux, 1992
Myidae												
<i>Mya arenaria</i> °	Gdansk Bay, Baltic Sea	34	10 m, 7 sm	+								Thiriot-Quiévreux et al., 1998

reported by Nakamura (1985) and Thiriôt-Quévieux (1994), is here confirmed.

Most bivalve karyotypes known before 1992 included a majority of metacentric and submetacentric chromosomes. However, since the majority of bivalve species studied were of commercial importance, this may have biased cytotaxonomical comparisons within the bivalve class. Looking at the 49 new species investigated, 21 are without known commercial importance of which 13 show karyotypes with a majority of subtelocentric-telocentric chromosomes. Thus, as more species are examined, the variety of karyotypes is increasing.

The families Mytilidae and Ostreidae have been intensively investigated, showing for some species, such as *Mytilus galloprovincialis* or *Crassostrea virginica*, distinct karyotypes according to different authors. This may be due either to their different geographical origin, leading to intraspecific polymorphism, or to differences in the techniques used. The recent use of statistical methods applied to computer-based measurements of chromosomes has allowed accurate cytotaxonomic comparisons (Insua et al., 1994; Ladron de Guevara et al., 1996; Leitão et al., 1999a; Zhang et al., 1999a).

Positive silver staining Ag-NORs have been observed in 21 bivalve species since 1992. The number of NOR bearing chromosome pairs varies from one to three among the studied species. The chromosomal location of Ag-NORs in most species was terminal on the short or long chromosome arm. Among the species, the overall tendency was for Ag-NORs to be found on metacentric-submetacentric chromosomes which are the dominant type of chromosomes in studied bivalves (Insua et al., 2001). Intraspecific heteromorphism involving the number of active Ag-NORs per cell was detected in all species. It has been suggested that chromosomal Ag-NORs can serve as characters for inferring phylogenetic relationship, such that a single pair of chromosomal NORs may represent a plesiomorphic character (Amemiya & Gold, 1990). For example, among the Ostreidae, *Crassostrea gigas* may be considered a more primitive species than the other studied species of Ostreidae (Thiriôt-Quévieux & Insua, 1992).

Techniques of chromosome banding have been successfully employed in eight species with C-banding and in five species with fluorochrome staining. N-banding and restriction enzyme treatment have only been successful in *Mytilus galloprovincialis*. Chromosomal markers, such as Ag-NOR staining, C-banding and fluorochrome staining, have allowed three species within *Mytilus* to be characterized at a cytogenetical level (Martínez-Lage et al., 1995, 1996). G-banding has been performed in *Mytilus galloprovincialis* and in three *Crassostrea* species, *C. gigas*, *C. angulata* and *C. virginica*, these latter showing specific G-banding patterns, allowing the individual identification of

all chromosome pairs (Leitão et al., 1999). Replication banding pattern has been obtained in *Mytilus galloprovincialis* (Martínez-Expósito et al., 1994b) and in *Brachidontes rodriguezi* (Torreiro et al., 1999).

The chromosomal location of specific DNA sequences has been determined in several bivalve species mainly by fluorescence in situ hybridization (FISH). Satellite DNA was first employed as a probe in *Crassostrea gigas*, showing two distinct heterochromatic regions on two chromosome pairs (Clabby et al., 1996). Vertebrate telomere probes yielded strong hybridization signals in telomeres of *Mytilus galloprovincialis* and *Crassostrea gigas*. The chromosomal location of ribosomal RNA genes (rDNA) was performed for 5S rDNA in *Aequipecten opercularis* and *Cerastoderma edule* (Insua et al., 1999), while 18S-28S have been reported in eleven bivalve species (see Table 1 for references). Therefore, the data presented here is restricted to physical mapping of genes or DNA fragments within bivalve species. These results are far behind the cytogenetic progress in other organisms. For example, in humans, the application of FISH using specific-chromosome probes or whole chromosome probes has opened the way for comprehensive studies on chromosome abnormalities, especially in tumors (e.g. Tsukamoto et al. 2001).

Recent molecular studies in bivalves have provided gene sequences in bivalves (e.g. Frisher et al. 2000) which are clarifying taxonomic relationships (e.g. O Foighil et al., 1995) and provide new insights into phylogenetic inferences (e.g. Josefowicz & O Foighil, 1998; Canapa et al., 2000).

Genome size

Nuclear DNA content has been determined in 32 bivalve species (Table 2). The DNA content per diploid nucleus ranged from 1.82 pg in *Crassostrea gigas* to 3.94 pg for the venerid *Tapes philippinarum* (Gonzalez-Tizon et al., 2000) and 4.24 pg for *Lithophaga curta* (Ieyama et al., 1994). In a previous exhaustive study on 53 bivalve species (Hinegardner, 1974), the range of diploid DNA content (2C) was 1.38 to 4.12 pg looking at the same bivalve families as in Table 2.

Intra and interspecific variation of genome size was observed by Rodríguez-Juiz et al. (1996) who studied 20 individuals per species. There is a low correlation between nuclear DNA content and chromosome number (Méndez et al., 2001). For example, the DNA content (2.33 pg) of *Ostrea edulis* (2n= 20) is almost identical to that of *Spisula solidissima* (2.32 pg) (2n=36). Hinegardner (1974) stated that the more generalized molluscs tend to have a higher amount of DNA than the specialized species. But, according to González-Tizón et al. (2000), this assumption cannot be considered universal. Further studies on an increasing

Table 2: DNA content of bivalve species analysed since 1992.**Tableau 2:** Contenu en ADN dans les espèces de bivalves étudiées depuis 1992.

Family/Species	Origin	2n	diploid DNA content pg	References
Mytilidae				
<i>Aulacomya ater maoriana</i>	New Zealand	unknown	2.24	Libertini et al., 1996
<i>Limnoperna fortunei</i>	Japan	30	2.96 *	Ieyama, 1996
<i>Mytilaster solidus</i>	North East Italy	28	3.08 *	Libertini et al., 1996
<i>Mytilus californianus</i>	Canadian Pacific	28	3.21	Gonzalez-Tizon et al., 2000 b
<i>Mytilus coruscus</i>	Japan	28	3.80 *	Ieyama et al., 1994
<i>Mytilus edulis</i>	Northern Europe	28	3.42	Rodriguez-Juiz et al., 1996
<i>Mytilus edulis eoteanus</i>	New Zealand	28	3.20 *	Libertini et al., 1996
<i>Mytilus galloprovincialis</i>	Japan	28	2.70 *	Ieyama et al., 1994
	Galicia, Spain		3.84	Rodriguez-Juiz et al., 1996
<i>Mytilus trossulus</i>	Canadian Pacific	28	3.02	Gonzalez-Tizon et al., 2000 b
<i>Perna canaliculus</i>	New Zealand	30	2.22 *	Libertini et al., 1996
<i>Septifer keenae</i>	Japan	28	2.12 *	Ieyama et al., 1994
<i>Septifer virgatus</i>	Japan	28	2.16 *	Ieyama et al., 1994
<i>Musculista senhousia</i>	Japan	30	2.32 *	Ieyama et al., 1994
<i>Lithophaga curta</i>	Japan	32	4.24 *	Ieyama et al., 1994
<i>Hormomya mutabilis</i>	Japan	30	3.58 *	Ieyama et al., 1994
<i>Modiolus auriculatus</i>	Japan	32	3.36 *	Ieyama et al., 1994
Ostreidae				
<i>Crassostrea gigas</i>	Canadian Pacific	20	1.82	Gonzalez-Tizon et al., 2000 b
<i>Ostrea edulis</i>	Galicia, Spain	20	2.33	Rodriguez-Juiz et al., 1996
Pectinidae				
<i>Chlamys hastata</i>	Canadian Pacific	38	3.28	Gonzalez-Tizon et al., 2000 b
<i>Chlamys opercularis</i>	Galicia, Spain	26	2.23	Rodriguez-Juiz et al., 1996
<i>Hinnites giganteus</i>	Canadian Pacific	unknown	2.57	Gonzalez-Tizon et al., 2000 b
<i>Pecten maximus</i>	Galicia, Spain	38	2.83	Rodriguez-Juiz et al., 1996
Cardiidae				
<i>Cerastoderma edule</i>	Galicia, Spain	38	2.73	Rodriguez-Juiz et al., 1996
Mactridae				
<i>Spisula solidissima</i>	Galicia, Spain	36	2.32	Rodriguez-Juiz et al., 1996
<i>Tresus capax</i>	Canadian Pacific	34	3.27	Gonzalez-Tizon et al., 2000 b
Tellinidae				
<i>Macoma nasuta</i>	Canadian Pacific	38	3.90	Gonzalez-Tizon et al., 2000 b
Psammobiidae				
<i>Nuttalia nuttallii</i>	Canadian Pacific	38	3.48	Gonzalez-Tizon et al., 2000 b
Veneridae				
<i>Protothaca staminea</i>	Canadian Pacific	38	3.50	Gonzalez-Tizon et al., 2000 b
<i>Ruditapes decussatus</i>	Galicia, Spain	38	3.62	Rodriguez-Juiz et al., 1996
<i>Tapes philipinarum</i>	Canadian Pacific	38	3.94	Gonzalez-Tizon et al., 2000 b
<i>Venerupis pullastra</i>	Galicia, Spain	38	3.56	Rodriguez-Juiz et al., 1996
<i>Venerupis rhomboides</i>	Galicia, Spain	38	3.23	Rodriguez-Juiz et al., 1996

* : original values are given in haploid DNA content

number of species studied with the same techniques could help to elucidate if a trend exists within bivalves.

Aneuploidy

Aneuploid cells have been observed in natural populations of *Ostrea angasi* (Li & Havenhand, 1997) and of *Mytilus* (Martínez-Expósito et al., 1992). The study of chromosome

loss in somatic cells of *Crassostrea gigas* has been extended to several populations (Thiriot-Quiévreux et al., 1992; Zouros et al., 1996). The consistency of the negative relationship between aneuploidy and growth rate has been observed over a ten year survey (Leitão et al., 2001b). Experimental evidence has suggested the existence of a genetic basis for the control of aneuploidy level (Leitão et al., 2001a). Evidence of differential chromosome loss has

been demonstrated in aneuploid karyotypes. Only four out of the ten chromosome pairs of *C. gigas* are affected by the loss of one homologous chromosome (Leitão et al., 2001c). This differential susceptibility opens a field for new investigations.

Polyploidy

Natural polyploidy has been observed in *Argopecten purpuratus* (Alvarez & Lozada, 1992), *Sphaerium striatinum* (Lee, 1999) and *Corbicula* spp. (Park et al., 2000). In the genus *Lasaea*, australian polyploid clonal lineages share an exclusive common ancestor despite differences in developmental modes, polyploidy and reproductive modes (Ó Foighil & Thiriot-Quévèreux, 1999).

High chromosome numbers have been reported and related to neoplastic disorders in *Macoma balthica* (Thiriot-Quévèreux & Wolowicz, 1996b; 2001) and in *Mya arenaria* (Reno et al., 1994), or to polyploidy in *Mytilus trossulus* (González-Tizón et al., 2000a). Cytogenetic disturbances due to ecotoxic factors have also been observed in other bivalve species (Barsiene & Lovejoy, 2000).

Polyploidy has been induced in several commercially important bivalve species (Beaumont & Fairbrother, 1991). The main methods of ploidy assessment are chromosome counts, polar body counts, image analysis, flow cytometry, microfluorometry, nuclear size and electrophoresis. Only papers dealing with chromosome counts will be included in the following paragraph.

Chromosome counts were scored in 6-8 h embryos (Guo et al., 1994) and in three-month-old viable tetraploids of *Crassostrea gigas* (Guo & Allen, 1994a), these latter showing 67% tetraploids, the remaining being aneuploid, diploid, triploid and mosaics.

The effect of blocking polar body I complicates subsequent chromosome segregation (Guo et al., 1992) and has been reported in triploids (Guo & Allen, 1994b; Que et al., 1997) and tetraploids (Guo & Allen, 1997b) of *C. gigas*. Tetraploids showed more aneuploids than normal diploids (Guo & Allen, 1997b). According to Wang et al. (1999), oysters tolerate a number of aneuploids without obvious growth retardation in triploid production of *C. gigas*. Chromosome counts of induced triploids in the Chilean blue mussel, *Mytilus chilensis*, were scored in 20-hour-old embryos and showed a high proportion of aneuploids (Toro & Sastre, 1995). In the scallop *Chlamys ferrerii*, patterns of chromosome segregation were observed in induced triploids and tetraploids, producing different ploidies in embryos (Yang et al., 2000a, b). Karyotype analyses of 6-hour-old embryos of *Pinctada fucata martensii* (3n x 2n cross) revealed high levels of aneuploidy, while ploidy examination of 4-month-old juveniles showed only diploid

and triploid chromosome numbers indicating that aneuploid larvae had died (Komaru & Wada, 1994). Chromosome counts in induced tetraploids (one-year-old) in *Pinctada martensii* showed different levels of ploidy (He et al., 2000).

These studies highlight that ploidy manipulation of bivalves results in different proportions of aneuploids, diploids and polyploids, but the question remains to assess the threshold of tolerance of aneuploid conditions. Research on the accurate assessment of karyological features of triploid and tetraploid bivalves provide a direct method for ploidy verification.

Interspecific hybridization

Numerous attempts at hybridization in the genus *Crassostrea* have been reported (Gaffney & Allen, 1993) as well as naturally occurring hybrids in the genus *Mytilus* (e.g. Gardner, 1994), in *Mercenaria* (e.g. Bert & Arnold, 1995) and in scallops (Beaumont, 2000). Genetic or biochemical controls yield confirmation of hybrid status. Cytogenetic studies of bivalve hybrids are very rare. In hybrids of *Crassostrea virginica* x *Crassostrea corteziensis* and of *Crassostrea virginica* x *Crassostrea rhizophorae*, the hybrid karyotypes were close to the progenitors (Rodriguez-Romero & Gasca-Montes, 1995; 1998). Chromosomal examination of parents and offsprings in hybridization experiments may contribute to the confirmation of a hybrid status.

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