Chapter 6
Biotechnologies from Marine Bivalves

Paola Venier, Marco Gerdol, Stefania Domeneghetti, Nidhi Sharma, Alberto Pallavicini, and Umberto Rosani

Abstract Bivalve molluscs comprise more than 9000 extant species. A number of them are traditionally farmed worldwide and are fundamental in the functioning of benthic ecosystems. The peculiarities of marine bivalves have inspired versatile biotechnological tools for coastal pollution monitoring and several new biomimetic materials. Moreover, large amounts of sequence data available for some farmed bivalve species can be used to unveil the organism's responses to environmental factors (e.g. global climate change, emergence of new infectious agents and other production problems). In bivalves, data from genomics and transcriptomics increases more quickly than data from other omics, and permit new bioinformatics inferences, real comparative genomics and the study of molecules suitable for biotechnological innovations. Bivalves (and their microorganism communities) produce a variety of bioactive peptides, proteins and metabolites. Among them, the numerous families of antimicrobial peptides identified in the Mediterranean mussel likely contribute to its vigour and could assist with the identification of molecular scaffolds for innovative pharmaceuticals, nutraceuticals and constructs suitable for other applications.

海水双壳贝类相关的生物技术 双壳类软体动物由9, 000多种现存物种组成。其中一些全球分布物种有着比较悠久的养殖历史, 并且是底栖生态系统的基础物种。海水双壳贝类的生长及生理学特性为海岸污染监测和创新仿生物材料研发提供了多种多样的生物技术工具。受到海水双壳贝类生物学特性的启发, 研究人员研发了一些用于沿海污染监测的通用生物技术工具及数种新仿生材料。此外, 大量的养殖双壳贝类的测序数据可以用来揭示生物体对环境因素变化的响应(如全球气候变化, 新型传染病和其他养殖问题)。双壳贝类

P. Venier (✉) · S. Domeneghetti · U. Rosani
Department of Biology, University of Padova, Padova, Italy
e-mail: paola.venier@unipd.it; stefania.domeneghetti@unipd.it; umberto.rosani@unipd.it

M. Gerdol · A. Pallavicini
Department of Life Sciences, University of Trieste, Trieste, Italy
e-mail: mgerdol@units.it; pallavic@univ.trieste.it

N. Sharma
Regional Centre for Biotechnology, NCR Biotech Science Cluster, Faridabad, Haryana (NCR Delhi), India

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的转录组学和基因组资源比其它组学数据的增长要快得多，从而使针对这一动物类群的新的生物信息学预测、真正的比较基因组学和适用于生物技术创新的分子研究成为可行。双壳贝类（及其微生物群落）会产生多种生物活性肽、蛋白质和代谢物。其中，在地中海贻贝中鉴别出多种可能有助于增强贻贝活力的抗菌肽家族成员，为开发新型药物、营养制品等提供了分子骨架模 板.

Keywords Marine bivalve molluscs · Biotechnology · *Mytilus* · *Crassostrea* · *Ruditapes* · DNA microarray · High-throughput sequencing · Byssus · Biomimetic · Antimicrobial

关键词 软体双壳贝类 • 生物技术，贻贝 • 牡蛎；蛤 • DNA微阵列 • 高通量测序 • 足丝 • 仿生 • 抗菌剂

6.1 Introduction

Technologies based on the peculiarities of marine bivalves not only provide services and products of current use but are expected to grow in the future, owing to the great exploration power of current omics strategies (high-throughput production of different sorts of molecular data aimed at the complete interpretation of biological structures, functions, and dynamics) and to the surprising advances of life sciences, material and nanomaterial sciences and microelectronics engineering. Undeniably, the growing number of bivalve-inspired innovations add value to animal species already identified as fundamental components of marine benthic ecosystems and regarded as a strategic food resource for the future (the European aquaculture production of marine molluscs reached 572,957 tons, nearly 3.5% of the global amount, with an estimated value of 972,987 USD in 2016) (FAO 2018).

6.2 Living Monitors and Source of Versatile Biotechnological Tools

Since the mid ‘70s, filter-feeding bivalves such as mussels and clams started to be used as pollution sentinels because they integrate in space and time the contaminant mixtures present in the surrounding water and sediments, respectively (Goldberg and Bertine 2000). Complementary to the analysis of toxicants in the soft tissues (Guéguen et al. 2011; Melwani et al. 2014), various pollution biomarkers have been developed and a number of them has been validated (Moore et al. 2006; Banni et al. 2007; Bolognesi and Hayashi 2011) and combined (Pytharopoulou et al. 2008; Okay et al. 2016) to rank coastal sites according to the intensity of toxicant-induced adverse effects.

Table 6.1 Gene expression datasets and DNA microarray platforms available for selected marine bivalves

	Datasets	Microarrays
Crassostrea gigas	833	20[a,b]
Crassostrea virginica	668	3[b]
Mytilus galloprovincialis	480	20[a]
Ruditapes philippinarum	340	10[a]
Mytilus californianus	196	5[a]
Mytilus edulis	163	5[a]
Ruditapes decussatus	141	7
Mytilus trossulus	122	2[a]
Pinctada maxima	89	4
Pinctada fucata	34	3
Mercenaria mercenaria	32	1
Chamelea gallina	32	1
Pinctada martensii	22	2

From Gene Expression Omnibus at Aug 2018 (www.ncbi.nlm.nih.gov)

[a]GPL22172 probes from *Crassostrea angulata, Crassostrea ariakensis*, *C. gigas*, *C. virginica*, *M. californianus*, *Mytilus chilensis*, *Mytilus coruscus*, *M. edulis*, *M. galloprovincialis*, *M. trossulus* and *Venerupis (Ruditapes) philippinarum*

[b]GPL3994 probes from *C. gigas* and *C. virginica*

Over time, the increasing availability of nucleotide sequence data inspired the production of DNA microarrays, adaptable biotechnological tools made of spotted DNA/cDNA or *in situ* synthesized oligonucleotides (Table 6.1). Such predefined assemblies of molecular probes allow the multiple and quantitative assessment of gene expression levels, among other purposes.

The hybridization of processed RNA samples on DNA microarray slides could discriminate *Mytilus* mussels and *Ruditapes* clams sampled at different distance from a petro-chemical district in the Venice lagoon area (Venier et al. 2006; Milan et al. 2015), supporting the use of transcriptional profiles in environmental monitoring and suggesting an innovative way to assess quality and the possible illegal origin of traded stocks.

Tissue- stage- and sex-specific transcript profiles obtained by DNA microarrays can assist management actions and sustainability plans in the farming of bivalves. For instance, they have been used to understand the partial sterility of triploid oysters and genes related to growth and reproduction (Dheilly et al. 2014; Guan et al. 2017; Tong et al. 2015) or the oyster response to pathogens and stress factors negatively impacting the production rates (Venier et al. 2011; Anderson et al. 2015; Romero et al. 2015; Pardo et al. 2016). Relevant to the growth of the pearl oyster *Pinctada fucata*, gene expression profiles obtained during larval development highlighted new aspects of shell formation mechanisms (Liu et al. 2015).

Both high-throughput sequencing and a DNA microarray were used to investigate the early mussel response to algal toxins with the aim of developing new

monitoring tools for okadaic acid, a heat-stable phosphatase inhibitor causing diarrhetic shellfish poisoning (Suarez-Ulloa et al. 2015). A total of "1,066,985" nucleotide sequences (at 10.08.2018) and "3,478" GEO datasets (at 10.08.2018) are available at NCBI for Bivalvia (10 Aug 2018) and the genomes of nine marine bivalves (oysters: *C. gigas*, *C. virginica*, *P. fucata martensii*; mussels: *Bathymodiolus platifrons*, *M. galloprovincialis, Modiolus philippinarum*, *Limnoperna fortunei*; scallops: *Mizuhopecten yessoensis*; clam *Ruditapes philippinarum*) have been completed or drafted (Zhang et al. 2012; Takeuchi et al. 2012; Murgarella et al. 2016; Mun et al. 2017; Sun et al. 2017; Wang et al. 2017a, b; Du et al. 2017).

Different from the DNA microarray analysis, high-throughput sequencing can lead to gene discovery and to the validation of population genetics markers for breeding programmes. The identification of single nucleotide polymorphisms (SNPs, codominant-inherited molecular features very abundant in animal genomes) in bivalves is just a preliminary step, before starting to validate their association with valuable quantitatively inherited traits or with stress-responsive genes, and to proceed with fine linkage mapping and population genetics analyses (Coppe et al. 2012; Ge et al. 2015; Nie et al. 2015; Dong et al. 2016; Fan et al. 2016; Wang et al. 2016a, b; Qi et al. 2017; Gutierrez et al. 2017; Azéma et al. 2017).

Although proteomics, metabolomics and epigenetics studies in marine bivalves are at their onset (Gómez-Chiarri et al. 2015; Digilio et al. 2016; Dineshram et al. 2016; Vincenzetti et al. 2017), in the near future they could reinforce and widen the existing assortment of bivalve services and products. In essence, the comprehensive knowledge of the vital processes in marine bivalves is a fundamental research strategy, consistent with the growth of a sustainable and innovative blue economy for the future. To confirm the continuous attention to marine bivalves and their expanding roles, they have been proposed in Northern Europe as living monitors of multidrug-resistant *Escherichia coli* and other *Enterobacteriaceae* spp. (Grevskott et al. 2017).

In the following section, we present a paradigmatic case which illustrates how the natural properties of bivalve byssus has guided the development of new materials of practical use.

6.3 Byssal Threads and Adhesive Plaques as Archetypes for New Biomimetics

Some freshwater and marine bivalves such as *Dreissena polymorpha*, *Perna viridis* and *Mytilus* spp. anchor themselves to hard substrates by means of silk-like byssus threads, having remarkable mechanical properties, and adhesive plaque proteins, functioning as an underwater superglue.

Descriptions of the general structure and microscopical anatomy of mussel byssus date back to 1711 and 1877, respectively, but only in the early 1950s investigations based on mechanical, chemical and enzymatic assays, histological and histochemical techniques, polarized light and X-ray diffraction, paved the way to bivalve-inspired materials for medical and non-medical applications (Fig. 6.1)

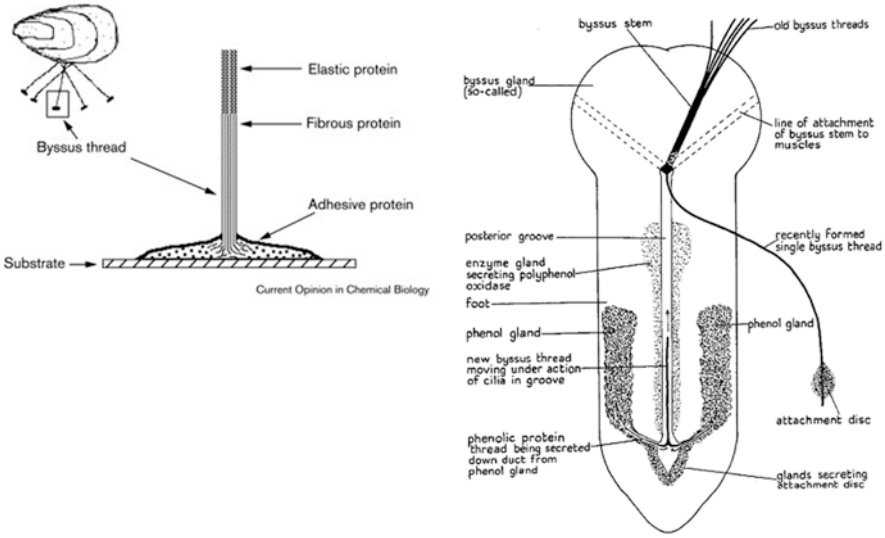

Fig. 6.1 Graphical representations of mussel byssus threads (**left**, as reported in Deming 1999) and anatomy of the byssus production in *Mytilus* (**right**, as reported in Smyth 1954). Gland tissue cells, detectable in precise zones of the mussel foot, emit a thread-like protein secretion along the foot groove whereas cells coating the foot groove secrete the protein components of the terminal adhesive plaque (disk). The byssus thread is released when it occupies the whole groove length

(Brown 1952; Smyth 1954; Deming 1999; Lee et al. 2011; Kord Forooshani and Lee 2017).

The proteinaceous byssus fibers comprise a proximal stem region, a mid-thread region and the terminal adhesive plaque. Mussel byssogenesis occurs in the post-larval stages within minutes by coordinated secretion and extracellular solidification of a composite fluid released by three pedal glands into the distal depression and ventral groove of the foot organ (Silverman and Roberto 2010; Priemel et al. 2017). More than ten types of secreted proteins compose the mussel byssus, including fibrillar collagens, non-collagenous thread matrix proteins and polyphenolic proteins of the thin cuticle surrounding the stretchy fibrous core and the adhesive plaque. As a result of post-translational hydroxylation of tyrosine, L-3,4-dihydroxyphenylalanine (L-DOPA) is a main component of the latter proteins, commonly named mussel foot proteins (Mfp, not to be confused with other proteins with the same acronym) or mussel adhesive proteins.

The unusual resistance of such fibrous and adhesive structure against predators and the mechanical force of waves and currents has considerably stimulated multidisciplinary investigations aimed to develop innovative biomimetic materials (Degtyar et al. 2014; Reinecke et al. 2016; Priemel et al. 2017). In the byssus thread, non-covalent protein–metal interactions stabilize the main constituent proteins and contribute to their tensile strength and self-healing properties. In detail, the thread core is made by bundles of collagenous proteins (preCols) having a central collagen domain with a typical Gly-X-Y triple helical repeat and flanking domains. Among

other features, all preCols have N- and C-termini enriched in histidine, the amino acid most likely involved in coordination bonds with transition metal ions such as Zn and Cu. In essence, highly directional and dynamic protein–metal coordination bonds generate cross-linking and hierarchical structuring of byssal protein blocks, with the metal site geometry and activity governed by local charges, helical dipoles and other conformational protein elements. Rupture and rapid restructuring of coordination bonds between histidine residues and Zn^{2+} sustain the self-healing of byssus and, as expected, such self-healing can be inhibited by removing metal ions with ethylenediaminotetraacetic acid or by lowering the pH, a condition known to hamper histidine–metal bonding (Degtyar et al. 2014; Reinecke et al. 2016).

In the byssus plaque of *Mytilus* species, at least six Mfp rich in DOPA and cationic amino acids contribute with specialized roles to the adhesion in wet conditions to hard substrates (Table 6.2). The catechol moiety of L-DOPA permits the formation of hydrogen bonds and the interactions with other aromatic rings and with positively charged ions such as Cu^{2+}, Zn^{2+}, Mn^{2+} and Fe^{3+} among others. At sea water pH (mildly basic), these chemical events result in stable coordination complexes (e.g. DOPA oxidation coupled with the reduction of coordinated Fe^{3+} ions) and cross-linking (e.g. catechols oxidized to quinones can react with various nucleophilic groups and produce intermolecular/interfacial covalent bonds). After secretion, the spontaneous DOPA-Fe cross-linking in the byssus coating acts like a protective varnish as a result of attained hardness and extensibility. The local distribution of different Mfp and the significant presence of positively charged ions in the byssus plaque additionally stabilize its foamy structure and boost cohesive interactions and, hence, enhance the strong (wet) adhesion to hard surfaces (Lee et al. 2011; Reinecke et al. 2016; Kord Forooshani and Lee 2017; Priemel et al. 2017).

Using Mf3 as an example, the multiple alignment of 36 protein sequences available in GenBank highlights fully conserved amino acid residues and variable sequence traits (Fig. 6.2).

In essence, the byssus threads and their terminal plaques have emerged as a model for the development of self-healing polymers and water-resistant adhesive materials (Holten-Andersen et al. 2011; Danner et al. 2012; Guerette et al. 2013; Park et al. 2013; Liu et al. 2014; Fullenkamp et al. 2014; Schmidt et al. 2014; Wu et al. 2014; Nichols 2015; Ryu et al. 2015; Grindy et al. 2015; Miller et al. 2015; Tian et al. 2015; Krogsgaard et al. 2016; Liu et al. 2016; Xu et al. 2016; Zhang et al. 2017b; Waite 2017). In both cases, the coordination of metal ions plays a fundamental role; however, the occurring chemical events and final material properties depend on metals and ligands, their molar ratio, pH and redox reactions. Actually, catechols are regarded as suitable anchoring groups for surface modification, although their metal-binding strength depends on the oxidation status. Other byssogenic bivalves produce somewhat different foot proteins yet capable of strong adhesion, e.g. pvfp-1 from *Perna viridis* contains C(2)-mannosyl-7-hydroxytryptophan, Man7OHTrp, instead of DOPA, and trimerized chains instead of monomeric chains (Hwang et al. 2012). Deep understanding of the complex chemico-physical processes underlying the byssus formation as well as comparative data deriving from the omics technologies (Schultz and Adema 2017) should provide additional hints for a step-by-step

Table 6.2 Some data on the mussel foot proteins (from Kord Foreooshani and Lee 2017)

	Mfp-1	Mfp-2	Mfp-3	Mfp-4	Mfp-5	Mfp-6
Molecular weight (Kda)	108[a]	42–47[a]	5–7[a,b]	90–93[c]	8.9	11[c]
Isoelectric point[c]	10.5	9.5	nd	nd	9	9.5
Secondary structure	Very little	Highly repetitive motifs; 6 mol % Cys	No repeats; 30–35 variants rich in DOPA (>20 to 28 mol %): MFP-3f and Mfp-3s are rich in Gly (25–29 mol %), MFP-3f is highly hydrophililic; MFP-3s is polar but hydrophobic	His-rich decapeptide tandeml y repeated more than 36 times	Just 2 closely related variants; rich in DOPA (30 mol%), cationic ami no acids (27.7 mol %) and phosphoserine (≈4.8 mol%); hydrophilic	Rich in Tyr (20 mol %) mostly not converted in DOPA (3 mol %) and in Cys (11 mol%); the richest in charged aminoacids (23 mol% cationic, 16 mol% anionic)
Proposed role	Protective coating	It is the most abundant protein (≈25 wt %); its disulphide bonds support plaque integrity	It contributes to adhesion at the plaque-surface interphase	Exceptional binding to transition metal ions, functional bridge between thread (PreCol) and plaque proteins	It contributes to adhesion at the plaque-surface interphase	It contributes to adhesion at the plaque-surface interphase; it likely controls the redox chemistry of DOPA in the other plaque proteins

[a]in *Mytilus edulis*
[b]in *Mytilus californianus*
[c]*from* Lee et al. (2011)

development of useful novelties. As long as the new materials mimic natural substances and processes, they should have a great chance to be efficiently produced in environmentally friendly conditions and to be biodegradable. The development of wet adhesive materials using molluscan models could enable the development of new surgical adhesives, artificial joints, contact lenses, dental sealants and hair and skin conditioners (Wu et al. 2014; Nichols 2015; Ryu et al. 2015; Grindy et al. 2015; Miller et al. 2015; Tian et al. 2015). Moreover, byssus-inspired bioadhesive polymers, polymer blends and micro- or nano-structures have been proposed to fabricate new drug delivery or diagnostic systems including the encapsulation of

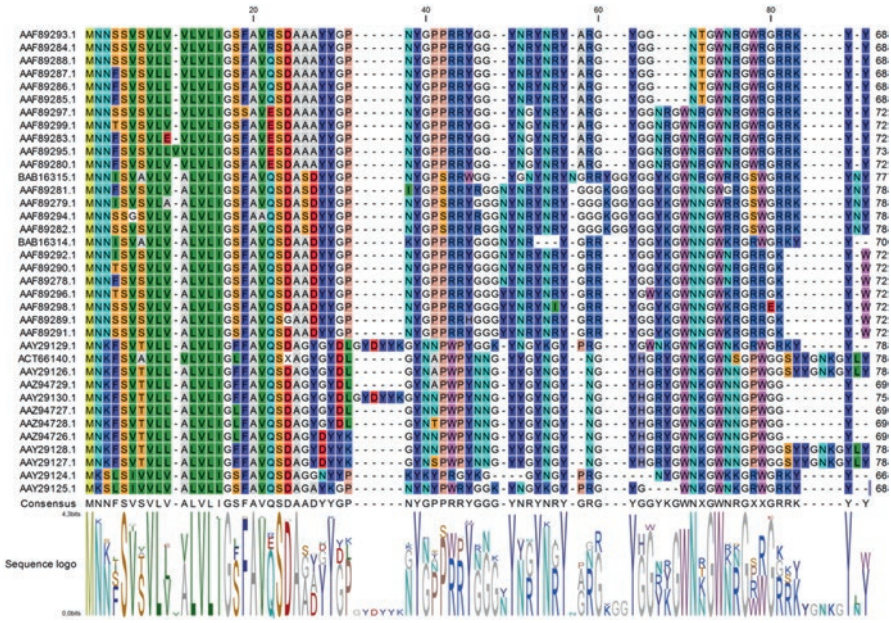

Fig. 6.2 Multiple alignment of amino acid sequences of 36 mussel foot proteins (Mfp 3). GenBank accession number, consensus sequence and sequence logo (i.e. graphical representation of the conservation extent of each protein residue) are reported

therapeutic, prophylactic, diagnostic agents to deliver bioactive components expected to be released upon contact with mucosal tissues of aquatic organisms. One could also imagine the development of biodegradable and nutritionally attractive feed formulations containing biocidal or antibiotic compounds and/or microbes, for the prevention and control of invasive non-indigenous species or for selective nutritional feed ingredients for more efficient growth of farmed species (Ma et al. 2016; Wang et al. 2016a, b, 2017a, b; Li et al. 2017; Luo and Liu 2017; Zhang et al. 2017a). Patents describing byssus-inspired inventions are exemplified in Table 6.3.

Reversing the scope, new lubricant-infused coatings are now suggested as an effective strategy to prevent the mussel adhesion and, hence, to mitigate marine biofouling (Amini et al. 2017).

6.4 Antimicrobials and Other Bioactive Molecules from Marine Bivalves Are Valuable Assets

The search of bioactive molecules of marine origin dates back to the past century but continues to generate pharmaceutics of human use and new compounds (1340 in 2015) (Liu et al. 2009; Mayer et al. 2010; García-Fernández et al. 2016; Kwon et al. 2016; Anjum et al. 2017; Blunt et al. 2017; Kang et al. 2017).

Table 6.3 Examples of patents describing byssus-inspired inventions (from Google patents)

Patent	Registration date	Pubblication date	Candidate Appointee	Title
US5049504	30/05/1990	17/09/1991	Genex Corporation	Bioadhesive coding sequences
US5202236	25/05/1990	13/04/1993	Enzon Labs Inc.	Method of producing bioadhesive protein
US6987170B1	09/08/2004	17/01/2006	Battelle Energy Alliance, Llc.	Cloning and expression of recombinant adhesive protein Mefp-1 of the blue mussel, Mytilus edulis
WO2005056708A2	09/12/2004	23/06/2005	Spherics, Inc.	Bioadhesive polymers with catechol functionality
WO2007002318A2	23/06/2006	04/01/2007	Spherics, Inc.	Bioadhesive polymers
CA 2864891A1	21/02/2013	29/08/2013	Advanced Bionutrition Corporation and others	Compositions and methods for target delivering a bioactive agent to aquatic organisms
US20160115196A1	28/05/2014	28/04/2016	Ramot At Tel-Aviv University Ltd.	Self-assembled micro-and nanostructures

Marine species including plants, animals and microorganisms (mostly unculturable and unknown) are a rich source of gene-encoded products and metabolites whose molecular moieties mediate biological activities potentially exploitable for new inventions or for the repositioning/reinvention of known bioactive components (pharmaceuticals and nutraceuticals, among others). For instance, inhibitors of proteases and voltage-gated ion channels have been isolated from marine venomous animals such as sea anemones and *Conus* snails and are currently studied for their therapeutical and biotechnological potential (Liu et al. 2009; García-Fernández et al. 2016; Kwon et al. 2016). In the '90s, the cloning of the green florescent protein from the jellyfish *Aequoria victoria* and production of mutants opened the way to use these chromo proteins as probes in cell and tissue imaging (Prasher et al. 1992; Verkhusha and Lukyanov 2004; Chen et al. 2013). Both discoveries have driven significant advancements in the field of life sciences. In the discovery phase, the bioactivity is often claimed following *in vitro* demonstration of antibacterial/ antifungal/ antiviral, anti-proliferative and anti-tumor properties, although the latter must be demonstrated *in vivo* with adequate study design and high costs. It should be noted that different human ethnic groups have traditionally used molluscs and mollusc extracts for their anti-inflammatory, immune-modulatory and wound healing properties. Molluscan species were estimated to be the source of more than 1145 products by 2014. Liprinol® and Biolane Seatone from the green-lipped mussel *Perna canaliculus* exemplify marketed products of current use, the potent analgesic ziconotide from *Conus* snails has been clinically tested and approved by the Food and Drug Administration whereas other compounds are under trial (Ahmad et al. 2018).

Owing to their filtering activity, marine bivalves interact with putative pathogens including bacteria and viruses, and, thus, are expected to possess effective defence mechanisms. Nowadays, bioinformatic approaches accelerate the identification and guide the functional characterization of bioactive molecules from non-model bivalve species. In *Mytilus galloprovincialis*, the Mediterranean mussel, many families of putative cysteine-stabilized antimicrobials have been described. Mytilins, defensins, myticins and mytimycins were reported in the '90s (Hubert et al. 1996; Charlet et al. 1996) whereas big defensins, mytimacins, CRP I and the linear myticalin peptides were more recently discovered (Gerdol et al. 2012; Gerdol et al. 2015; Leoni et al. 2017). Among all of them, myticin C displayed high gene transcript polymorphism, constitutive and microbe-inducible expression, chemokine-like and antiviral activities. Although the action mode of myticin C is still unclear, an engineered construct with superior antiviral activity has been developed (Pallavicini et al. 2008; Novoa et al. 2016). As additional example, Mytichitin CB from *Mytilus coruscus* is a chitotriosidase-like antimicrobial which displays antifungal activity whose recombinant production should permit its full characterization (Qin et al. 2014; Meng et al. 2016).

While no mussel antimicrobial peptide (AMP) has been commercially exploited yet, some pilot studies have been carried out over the years, demonstrating the potential biotechnological applications of engineered peptides. Indeed, synthetic mytilin-derived peptides were capable or reducing mortality in virus-infected shrimp (white-spot syndrome) (Dupuy et al. 2004). Interesting antiviral, antibacterial and antiprotozoan activities also have been demonstrated for engineered defensin and mytilin variants (Dupuy et al. 2004; Liu et al. 2010).

Additional bivalve molecules could be regarded as having therapeutic potential. For instance, the mussel MytiLec-1 is a galactose-binding lectin able to inhibit the growth of both Gram-positive and Gram-negative bacteria (Hasan et al. 2016) and, at the same time, able to bind Burkitt's lymphoma and breast cancer cells expressing globotriose on their surface, significantly inducing apoptosis (Hasan et al. 2015; Liao et al. 2016; Chernikov et al. 2017). These remarkable properties have led to the computational design of an artificial β-trefoil lectin, named Mitsuba, capable of recognizing globotriose-expressing cancer cells, as an initial step for the development of effective MytiLec-1-based cancer treatment or diagnostics tools (Terada et al. 2017).

Other molluscan lectins with biotechnological potential are two C-type lectins from *C. gigas* (CgCLec-4, CgCLec-5), which exhibited anti-microbial (agglutinating) activity against bacteria and fungi (Jia et al. 2016). One extrapallial protein (C1Q-domain containing protein) of the mussel hemolymph serum (MgEP) was also demonstrated to act as an opsonin and to promote interactions between a suspected *Vibrio* pathogen and *Mytilus* hemocytes (Canesi et al. 2016).

In addition to ethanolic extracts, hydrolysates obtained by enzymatic digestion from bivalves and other marine invertebrates, revealed tens of antioxidant peptides which could benefit health or be used to produce novel food products (Chai et al. 2017; Odeleye et al. 2016; Wu and Huang 2017). Almost certainly, there are many

more bioactive mollusc/bivalve components yet to be investigated. Regardless of the current state of knowledge of molluscan bioactives, we should never forget the possibility of toxic substances co-occurring in the same biological matrix.

6.5 Conclusions and Perspectives

This paper has presented a historical and conceptual timeline of the products and services provided by marine bivalve molluscs, focusing the attention to biotechnological innovations for a sustainable future. Marine bivalves with their associated microorganisms are central in the marine trophic networks, from the shoreline to the deep ocean. Bivalve species are traditionally fished and farmed worldwide as seafood since ancient times whereas their use as water pollution sentinels was established far more recently. Our time testifies great progresses in life sciences and, accordingly, further research on marine bivalves will likely confirm them as rich source of bioactive compounds and as interesting models for technological innovations (Imhoff et al. 2011; Desriac et al. 2014; Newman 2016). Today, the CRISP/CAS genome editing biotechnology represents a new revolutionary strategy also to engineer and implement bivalve-inspired products (Mojica and Montoliu 2016; Singh et al. 2018). As our knowledge base expands based on a multifaceted blue economy, there is little doubt that discoveries in this field will lead to societal and economic benefit in the near future.

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