

Chapter 2

Distribution of MACPF/CDC Proteins

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Abstract Membrane Attack Complex/Perforin (MACPF) and Cholesterol-Dependent Cytolysins (CDC) form the MACPF/CDC superfamily of important effector proteins widespread in nature. MACPFs and CDCs were discovered separately with no sequence similarity at that stage being apparent between the two protein families such that they were not, until recently, considered evolutionary related. The breakthrough showing they are came with recent structural work that also shed light on the molecular mechanism of action of various MACPF proteins. Similarity in structural properties and conserved functional features indicate that both protein families have the same evolutionary origin. We will describe the distribution of MACPF/CDC proteins in nature and discuss briefly their similarity and functional role in different biological processes.

Keywords Cholesterol-dependent cytolysins • MACPF/CDC protein superfamily • Membrane attack complex • Perforin • Protein evolution

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Abbreviations

APC- β	Apicomplexan perforin-like proteins C-terminal β -pleated domain
ASTN	Astrotactin
BRINP	Bone morphogenic protein/retinoic acid inducible neural-specific protein
CDC	Cholesterol-dependent cytolysins
MAC	Membrane attack complex
MACPF	Membrane attack complex/perforin
Mpg-1	Macrophage-expressed gene 1
PFN	Perforin

General Overview of Structural Similarity of MACPF/ CDC Protein Families

MACPF and CDC proteins are important effectors in the immune system and bacterial pathogenesis, where their observed effects are primarily mediated through membrane interactions and the formation of transmembrane pores. Their activity is, however, not restricted to membrane interactions and it will be important to determine the exact role and molecular mechanism of action for many representatives. MACPF proteins were initially defined by the sequence similarity among proteins of the Membrane Attack Complex (*MAC*) of the complement system and perforin (*PF*) [59, 83, 93]. These proteins have crucial roles in immune defence against viral and bacterial pathogens and in removal of cancer cells. For example, perforin is the only molecule of the human immune system that allows entry of granzyme into the target cells and initiation of apoptosis. The MAC is the terminal stage of the complement system of innate immunity. On the other hand, CDCs are predominately found in Gram-positive bacteria [29, 94], although a recent report indicates that this protein family may be more widespread as they are at least present in Gram-negative bacteria too [41] and diatoms and plants (see below). Because they were discovered separately, in quite separate niches, there was originally no sequence similarity apparent between the proteins of MACPF and CDC families. The realisation that these two families are evolutionary related was the result of intense structural work on MACPF proteins; in particular crystal structures of Plu-MACPF from bacteria *Photorhabdus luminescens* [77], Bth-MACPF from bacteria *Bacteroides thetaiotaomicron* [104], the MACPF domain of complement components C6 [5] and C8 [35, 62, 85] and mouse perforin (PFN) [57] revealed their similarity to the CDC protein family. Both protein families are now collectively referred to as the MACPF/CDC pore forming proteins [30, 78]. Structure-based alignment allows the identification of very limited sequence conservation of glycines present in all family members [30], which in fact

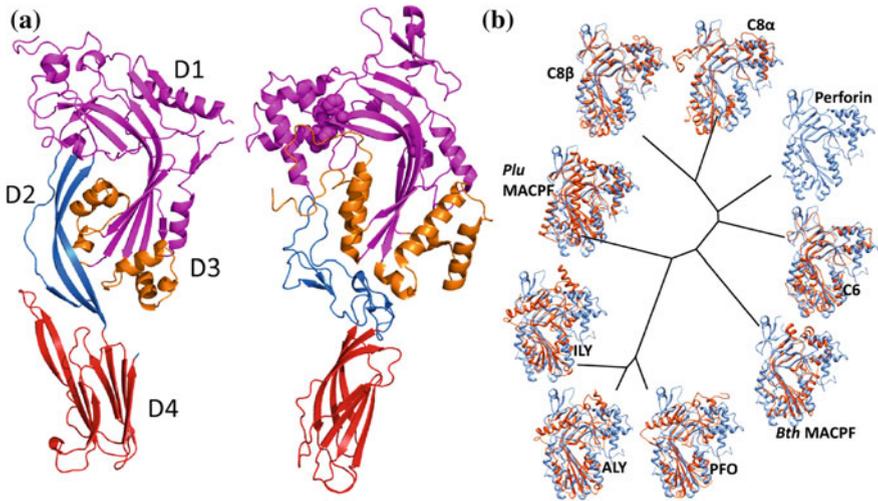


Fig. 2.1 Structure and similarities of CDC and MACPF proteins **a** Crystal structure of perfringolysin O (PFO), the first CDC to have its structure determined (*left*) [79] and mouse PFN (*right*) [57]. The original domains of the CDC are labelled D1–D4. The MACPF/CDC domain is shown in *magenta*, with helical regions that refold to form the transmembrane β -barrel coloured in *orange*. The membrane interacting domains in both proteins, immunoglobulin-like domain in PFO and C2 domain in PFN, are labelled *red*. The conserved MACPF residues in PFN are labelled with *spheres* (see below). **b** Structural phylogenetic tree of determined MACPF and CDC structures. The PFN structure is shown in *blue* and each MACPF/CDC structure in *orange*. The figure was adapted from [30]

represent a continuum in sequence space (see below) and several other shared features can be identified (see also [Chap. 4](#)).

The structure of CDCs is traditionally divided into four domains, each with particular functions during the pore-forming process (Fig. 2.1a) [29, 94]. The C-terminal domain 4 is used for the attachment of the protein to the lipid membrane, domain 1 is primarily used for contacts between the monomers, domain 3 is used for the formation of the final transmembrane β -barrel pore and domain 2 is a linking structure that provides flexibility needed during the process of pore formation (Fig. 2.1a) [29, 42]. See [Chaps. 4](#) and [5](#) in this volume for description of a detailed understanding of the CDC mechanism of action. Structural similarity between MACPFs and CDCs is centred on the central bent β -sheet composed of four strands and flanked on the sides by clusters of α -helices (the MACPF/CDC domain) [35, 77] (Fig. 2.1). From the structural comparisons it seems that domains 1 and 3 of CDCs could be seen as a single functional unit with a fold that is conserved throughout the tree of life (Fig. 2.1b). The universally-conserved glycines permit conformational rearrangements of this region of the protein to allow insertion of part of it into the lipid membrane, forming a transmembrane pore.

Distribution of MACPF Proteins

The MACPF protein family (Pfam PF01823) is the biggest family of eukaryotic pore-forming proteins and the current version of the Pfam database (version 27.0) [75] contains 1,329 unique sequences. The MACPF-containing proteins are widespread in nature and may be found in all domains of life [30]. Proteins with the MACPF domain are most abundant in metazoans and many representatives may be found in higher eukaryotes. Some organisms possess large numbers of genes containing MACPF domains—for example amphioxus (*Branchiostoma floridae*) possesses 29 such genes [43]. In this organism approximately 10 % of all genes are defence-related and since MACPF proteins represent an important part of the immune system such a high number is not surprising. MACPF proteins are also abundantly represented in Apicomplexans, where they have a crucial role in tissue and cell invasion and egress [47]. MACPF proteins were even found in anguillid herpesvirus 1 [96].

Prokaryotic representatives, primarily from the taxonomic groupings Chlamydia, Proteobacteria and Bacteroidia, may be found in various habitats and come from the following genera: bacteria of the human microbiome (*Alistipes*, *Bacteroides*), bacteria from the sea (*Dokdonia*, *Leeuwenhoekiella*, *Plesiocystis*, *Zunongwangia*), from land waters (*Beggiatoa*), plant pathogens (*Calvibacter*, *Ralstonia*), bioluminescent pathogens of insects (*Photorhabdus*), human pathogens (*Chlamydia*, *Chlamydophila*, *Chryseobacterium*, *Filifactor*, *Porphyromonas*), cyanobacteria (*Trichodesmium*), etc.

MACPF proteins are abundantly represented in mammalian genomes. In the human genome, for example, there are at least 12 genes that code for a MACPF domain (Fig. 2.2). Complement proteins C6, C7, C8 α , C8 β and C9, perforin and macrophage-expressed gene 1 (Mpg-1) have important roles in the immune system, while astrotactins (ASTN) 1 and ASTN2 and bone morphogenic protein/retinoic acid inducible neural-specific protein (BRINP) 1, BRINP2, and BRINP3 have important roles in the neuronal system (see below). Some of these MACPF-containing proteins have relatively simple domain structures, for example Mpg-1 and the BRINPs have a MACPF domain at the N-terminus and a C-terminal region of unknown structure and function. Mpg-1 is an interesting example of a MACPF protein that is permanently tethered to the membrane in contrast to other well-known MACPF proteins such as complement proteins and perforin. Some of these have a complex structure containing many different associated domains (see Chaps. 6 and 10 for a detailed domain organisation of complement proteins and perforin, respectively), while ASTN1 and ASTN2 are the largest human MACPF proteins with multiple domains. They are composed of two N-terminal transmembrane helices, three epidermal growth factor-like domains in the central part followed by the MACPF domain and finally a fibronectin type-III domain on the C-terminus.

Although family membership is simply identified, there is in fact only limited sequence conservation in the MACPF family, as the sequences are around 20 %

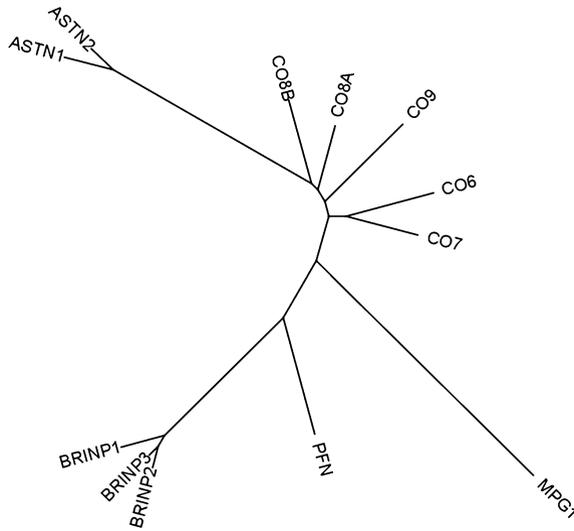


Fig. 2.2 Maximum-likelihood phylogenetic tree of human MACPF proteins. Protein sequences from UniProtKB (www.uniprot.org) were aligned using PSI-Coffee on T-Coffee server [51] and the phylogenetic tree was constructed with RAxML BlackBox [87]. The tree was depicted using *Archaeopteryx* [37]. *Sequence names* ASTN1 (Astrotactin 1, O14525), ASTN2 (Astrotactin 2, O75129), CO8B (complement component C8 β , P07358), CO8A (complement component C8 α , P07357), CO9 (complement component C9, P02748), CO6 (complement component C6, P13671), CO7 (complement component C7, P10643), MPG1 (macrophage-expressed gene 1 protein, Q2M385), PFN (P14222), BRINP1 (BMP/retinoic acid-inducible neural-specific protein 1, O60477), BRINP2 (Q9C0B6), BRINP3 (Q76B58)

identical (Fig. 2.3a). The most conserved amino acids are within the so-called MACPF motif [73] (Fig. 2.3b). This motif may be found in the structure at the top of the twisted β -sheet and particularly conserved are two glycine residues at the hinge between the upper and lower segment of the β -sheet (Fig. 2.1a). Other amino acid residues are not so well conserved (Fig. 2.3b). Thus the low sequence conservation presents a great challenge in discovering novel MACPF-containing proteins, as is highlighted by the fact that the original discovery of MACPFs in mammals and of CDCs in Gram-positive bacteria hid their deep evolutionary relationship until their structures were solved. This is demonstrated nicely by our recent analysis of MACPF proteins in fungi detailed in the next section.

MACPF Proteins in Fungi

Proteins with a MACPF/CDC domain are present in fungi as well. It is believed that more than 1.5×10^6 fungal species exist, with diverse lifestyles. They are important pathogens, saprophytes and symbionts. A huge expansion of available fungal

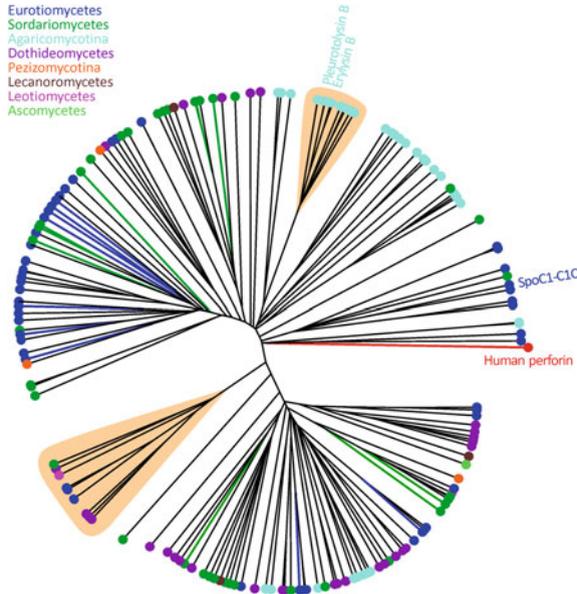


Fig. 2.4 Grouping of putative fungal MACPF proteins in relation to taxonomy, neighbour-joining tree without distance corrections was constructed after aligning sequences by using MAFFT algorithm. Taxon representation is according to JGI Mycosom [32]. The distribution of 9 putative MACPF proteins from *Aspergillus wentii* is marked with blue branches and 11 putative MACPF proteins from *Fusarium graminearum* in green. Orange background highlight branches of MACPF protein-containing genes that are in neighbourhood of aegerolysin protein. The position of functionally characterised proteins is denoted by names

fungi with a filamentous growth form (Fig. 2.4). A short signature sequence Y/F-G-X₂-F/Y-X₆-G-G was identified in 151 of the putative MACPF-containing proteins (Fig. 2.3b), verifying their identity. Some MACPF coding genes have a large number of introns, 8–13, in comparison to two introns in an average fungal gene and, consequently, annotation was difficult (interestingly, note that the MACPFs of Api-complexans are all mono-exonic except one, PPLP1/SPECT2, which has seven exons). The phylogenetic evolutionary tree was generated by using MAFFT [48] and a Neighbor-Joining approach. The sequences fall into two groups (Fig. 2.4). The first contains primarily sequences confirmed by Pfam and they are grouped together with PFN. In the second group are mostly sequences confirmed only by PHYRE2 but containing the typical MACPF/CDC signature as well.

We found the distribution of putative MACPF proteins in filamentous fungi uneven and with no clear correlation to taxonomy (Fig. 2.4). For example, in Agaricomycotina MACPF proteins were identified in 45 % of species, while in Eurotiomycetes they were present in 69 % of species (Table 2.1). The numbers of putative MACPF proteins present in a single fungal species are from one and up to nine. Some MACPF/CDC proteins within one species group together in the phylogenetic tree, while some do not, as is marked on Fig. 2.4 for 9 putative

Table 2.1 Taxonomic distribution of MACPF proteins in fungi

Taxon	Number of species in taxon	Number of species with MACPF sequence	Percent of species with MACPF sequence (%)	Number of MACPF sequences
Agaricomycotina	37	17	45	38
Pezizomycotina	4	3	75	3
Eurotiomycetes	42	29	69	60
Dothideomycetes	39	18	46	34
Lecanoromycetes	1	1	100	3
Leotiomycetes	6	2	33	2
Sordariomycetes	35	16	46	40
Ascomycetes	1	1	100	1

MACPF proteins from *Aspergillus wentii* (blue branches on Fig. 2.4) or for 11 putative MACPF proteins from *Fusarium graminearum* (green branches).

Among the strains with putative MACPF domains are those with declared pathogen lifestyles, like plant pathogens *Cochliobolus carbonum* (Northern Corn Leaf Spot), *C. heterostrophus* (Southern Corn Leaf Blight), *C. miyabeanus* (Brown Spot of rice), *C. victoriae* (Victoria Blight of oats), *Fusarium graminearum* (Wheat head blight), *F. oxysporum* (Panama disease) and *Moniliophthora perniciosa* (Witches'-broom disease), or animal pathogens like: *Arthrotrichy oligospora* (Nematode trapping), *Cordyceps militaris* (Caterpillar fungus), *Trichophyton equinum* (Horse ringworm), *T. rubrum* (Athlete's foot) and *T. tonsurans* (Scalp ringworm). Some are also saprophytic, like soil fungus *Chaetomium globosum* and *Aspergillus nidulans*, *Postia placenta* (Brown rot) or edible Oyster mushroom *Pleurotus ostreatus* (White-rot), *Pleurotus eryngii* (Boletus of the steppes) and food producing *Aspergillus oryzae* (Yellow koji).

SpoC1-C1C from *Aspergillus nidulans* is among those rare fungal MACPF proteins with assigned function, as a conidium-specific member of the SpoC1 gene cluster [33]. It has been shown for some fungal MACPF proteins, like pleurotolysin B or erylysin B, that they act in concert with additional smaller proteins, the aegerolysins [71, 82, 92]. It is interesting to note that in some cases these two components are found as neighbouring genes in the genome. The subsets of MACPF proteins with an aegerolysin component as a neighbour are denoted by an orange background on Fig. 2.4. The interactions between the components and pore-forming capacity of fungal MACPF proteins are described in detail in Chap. 14.

In conclusion, only a little is known about the function of MACPF proteins in filamentous fungi. From the taxonomic distribution one can clearly conclude that they are definitely not part of the core proteome. Fungal MACPF proteins most probably contribute to different specific processes, while some of them were found in secretomes (without a typical signal sequence recognised) [18], others being intracellular, and some of them may be involved in pathogenesis, however, most probably not all of them. Large intron number, sporadic taxonomic distribution, and different numbers of diverse MACPF proteins per fungal species may imply involvement of horizontal transfer mechanisms in specific environmental niches.

Domain Organisation of MACPF Proteins

In most cases one MACPF/CDC domain exists per protein, although some examples with two or even three MACPF/CDC domains have been identified [30]. It is not however uncommon for other protein domains to be associated with MACPF proteins. The domain architecture is quite simple in bacteria, where MACPFs are located N-terminally to other domains and as a rule there is only one additional domain present. Metazoan MACPF/CDC proteins have much more complex architectures and several other domains may be present on either side of the MACPF domain. These domains are quite often involved in molecular interactions needed to exert the biological function of a particular MACPF protein. For example many MAC proteins contain additional domains that are important for regulation of MAC assembly at the surface of the target cell (see the details in Chap. 6). Many MACPF-containing proteins are involved in membrane interactions and pore formation and, therefore, there is quite a large number of small β -sheet rich domains associated with membrane interactions. For example, the C2 domain is present at the C-terminus of PFN and is used for calcium-specific membrane attachment [74, 99]. In other proteins such domains may facilitate cell attachment through interactions with sugars, such as the MIR domain, Jacalin domain (a mannose-binding lectin domain), B-lectin domain, MABP domain, etc. Apicomplexan MACPF proteins contain 1–3 so-called APC- β domains (Apicomplexan Perforin-like proteins C-terminal β -pleated domains) [47]. These are small modules of ~ 55 amino acids and, according to sequence comparisons at least, are unique to apicomplexan proteins (though see discussion in Chap. 4). For many of these cases the functional significance of particular domains for cell-surface interactions remains to be verified.

There are, however, many MACPF-containing proteins that do not possess additional domains (such as torso-like protein from *Drosophila melanogaster*). In such cases it needs to be determined whether these proteins are able to interact with lipid membranes and if such interactions are needed at all to exert their physiological activity. However, it is known that some MACPF proteins associate with other components in order to successfully complete formation of pores. For example, complement monomers of C9 associate with the C5b-8 complex [4, 5, 36, 62] (see Chap. 6). The MACPF protein pleurotolysin B from the fungus *Pleurotus ostreatus* needs a smaller component, pleurotolysin A for efficient membrane interactions and pore formation [71, 92] (see Chap. 14); also, an interesting combination of disulphide linked MACPF and lectin domains was reported recently [23].

Functional Properties of MACPF Proteins

Some of the described functions of MACPF-containing proteins are listed in Table 2.2. The most studied and understood role is that of MAC proteins and perforin in the immune system. These proteins help with the removal of unwanted

Table 2.2 Functions of MACPF proteins

Biological process	Function	Examples
Immunity	Membrane attack complex of vertebrates	C6, C7, C8 α , C8 β , C9
	Killing of unwanted cells	Perforin
	Killing of bacteria and innate immune defence in invertebrates	Mpg-1 and homologues
	Pathogen-induced immune response	CAD1
Development	Neuronal development	Astrotactin1, BRINP proteins
	Insect embryo development	Tsl
	Sea urchin embryo development	Apextrin
Pathogenesis	Tissue invasion and cell egress	Apicomplexan MACPF proteins
	Bacterial pathogenesis	Plu-MACPF
	Toxins	PsTX-60A

For references see text.

cells from the organism, either microorganisms [72], virally infected cells or cancer cells [98]. The removal is achieved through efficient formation of transmembrane pores at the cell membrane surface or within endosomes and is described in detail elsewhere in this book (Chaps. 6 and 10). In plants a MACPF protein CAD1 was shown to have a role in plant responses induced by pathogens [67].

The MACPF protein family is, however, characterised by a variety of functions that may not always be linked to pore formation or membrane association (Table 2.2). One prominent role of MACPF-containing proteins is in the development of insects [88], sea urchins [34] and mammalian neurons [1, 49, 106]. In apicomplexans MACPF proteins are implicated in parasite invasion of tissues and egress from cells [47] (see also Chap. 12 for a more detailed description of MACPF protein function in apicomplexan parasites). In bacteria it was proposed that they are important for pathogenic bacteria (e.g. *Chlamydia*), however their role in pathogenicity is not yet entirely understood [73, 77] (see also Chap. 13 for the role of MACPF protein in *Chlamydia*). MACPF-containing proteins were also suggested to have a role in protein secretion, nutrient uptake systems or to have a preventive role through molecular mimicry [104].

Involvement of MACPF proteins in the native immunity of lower eukaryotes and as a toxic arsenal for water-borne organisms is described in more detail in the following sections.

Macrophage-Expressed Gene 1 (Mpg-1)

Mpg-1 protein, termed also perforin-2, was originally identified by differential screening of a murine macrophage cDNA library. It showed macrophage and

differentiation stage-specific expression and its expression was increased upon transition of murine fetal liver hematopoietic cells into macrophages [86]. Mice contain another Mpg-1 homologue, termed EPCS50, which is primarily expressed in trophoblast giant cells in the ectoplacental cone and the parietal yolk sac [39]. It was also shown that Mpg-1 is increased in prion-inoculated brain tissue of mice, however the physiological function of Mpg-1 in mice brains was not clarified and is not known [55]. Thus, very little was known about the function of Mpg-1 until recently, where two studies demonstrated its importance for the killing of intracellular bacteria. In one, it was shown that Mpg-1 has an important role in elimination of intracellular bacteria [64] because the expression of its mRNA in mouse embryonic fibroblasts and a fibroblast NIH-3T3 cell line was shown after exposure of cells to several cytokines (IFN- α , IFN- β and IFN- γ). The same study showed that Mpg-1 mRNA was induced by exposure of fibroblasts to *Escherichia coli* and *Mycobacterium smegmatis*. Increased levels of Mpg-1 mRNA were associated with increased bactericidal activity and Mpg-1 also increased the susceptibility of intracellular bacteria to lysozyme. The second recent report showed that Mpg-1 is needed for elimination of intracellular *Chlamydia trachomatis* cells in macrophages [25]. *Chlamydia* infection caused an increase in Mpg-1 mRNA and in protein levels of Mpg-1 in murine macrophages. Production of Mpg-1 mRNA could also be induced by heat-killed *Chlamydia* in HeLa epithelial cells but not with viable bacteria and this led to the realisation that *Chlamydia* can actively suppress the production of Mpg-1 mRNA in such cells. This study also showed that Chlamydiae were susceptible to killing by ectopically expressed Mpg-1. In summary, these results demonstrated that expression of the Mpg-1 gene can be induced in other cells than macrophages, i.e. fibroblasts and HeLa cells, and that it is required for elimination of intracellular bacteria.

Mpg-1 represents an important constituent of innate immune defence in evolutionarily lower organisms. For example it was discovered in the sponge *Suberites domuncula* [103], cnidarians [65], the planarian *Schmidtea mediterranea* [6], molluscs, oysters [38] and abalones [52, 63, 100]. The Mpg-1 protein is evolutionarily very conserved, for example sponge and human Mpg-1 share 46 % similar and 28 % identical residues [103]. However, the evolutionary history of Mpg-1 is not clear, as it is not found in the genomes of *Drosophila* or *Caenorhabditis*. Its presence in gastropods and bivalves indicates that it may originate from an ancient ancestral gene that was lost in insects and nematodes [38]. Recent studies on perforin evolution are in agreement with this proposition and suggest that Mpg-1 is the precursor of perforin, which arose from duplication of an ancient Mpg-1 gene [21].

Marine invertebrates are in constant contact with bacteria and many genome-encoded effectors are an important constituent of their innate immunity. Haemocytes are specialised blood cells of the mollusc's cellular immune response. They circulate in the hemolymph and are able to recognise foreign antigens through specific pattern recognition motifs. Pathways for pathogen destruction include specific transduction pathways that are similar to vertebrate pathways [44]. It was observed that Mpg-1 is kept at very low levels in haemocytes and is upregulated

upon stress or infection with bacteria [52]. In different experimental settings the up-regulation of Mpg-1 was found upon challenge with bacteria [38, 52, 100, 101], ostreid herpesvirus 1 [76], parasite *Schistosoma mansoni* [45] or lipopolysaccharides in sponges and planarians [6, 103], further indicating its important and ancient role in innate immunity. Kemp et al. also showed that the protein levels of Mpg-1 were upregulated upon stress with bacterial exposure and that protein levels were upregulated in a similar manner to mRNA levels [52]. This was shown also for Mpg-1 protein from sponge [103]. Some Mpg-1 homologues have been expressed, purified to homogeneity and tested for antibacterial activity. Mpg-1 from Pacific oyster *Crassostrea gigas* was shown to possess antibacterial activity against Gram-positive and Gram-negative bacteria [38], while recombinant Mpg-1 protein from sponge exhibited antibacterial activity against Gram-negative bacteria [103].

Toxins with the MACPF Domain

MACPF proteins were described also as a part of the toxic arsenal of lower eukaryotes. Cnidarians evolved special organelles called cnidocysts, which are considered as one of the most complex cellular secretory products. It is widely believed that cnidocysts serve for storage and active delivery of toxic compounds in cnidarian venom [53, 61, 91]. Many different cytolytic protein families were identified in Cnidaria [9, 11, 28]; for example Nagai et al. have reported isolation of two toxins, PsTX-60A and PsTX-60B, from the nematocysts of the sea anemone *Phyllodiscus semoni*. These two proteins represent major venom toxins and were haemolytic (ED₅₀ values 300 and 600 ng/ml using 0.8 % suspension of sheep red blood cells) and lethal to shrimps (LD₅₀ value around 800 µg/kg for intraperitoneal injection) [68]. A similar protein was purified from the nematocyst venom of another sea anemone *Actinaria villosa*. This toxin, termed AcTX-60A, was lethal to mice (minimal lethal dose for intraperitoneal injection less than 250 µg/kg). Its primary structure was determined from mRNA and for the first time these proteins were recognised as members of the MACPF family [70]. A subsequent report of the full length sequence of PsTX-60B reconfirmed similarity to MACPF domains [80]. Proteins similar to PsTX-60A were found by proteomic analysis also in nematocyst venom from the jellyfish *Olindias sambaquiensis* [102] and similar proteins were found in the genomes of the hydrozoan *Hydra magnipapillata*, sea anemone *Nematostella vectensis* and in coral *Acropora millepora* [65]. Furthermore, EST clones, publicly available in GenBank, of sea anemones *Aiptasia pallida* [89] and *Metridium senile* also contain PsTX-60A homologues. It was shown previously that *M. senile* contains an 80 kDa polypeptide cytolytic metridiolysin, reminiscent of CDCs based on functional and structural properties [14] and it is tempting to suggest that metridiolysin belongs to the MACPF protein family. It seems that MACPF-containing protein toxins are not only restricted to sea anemones, but are present also in other cnidarians and they clearly represent another family of cnidarian pore-forming toxins [11].

The domain organisation of cnidarian MACPF domain-containing toxins resembles that of perforin. A MACPF domain is placed at the N-terminus and it is followed by an EGF-like domain. There is, however, a notable exception that the C2 domain is missing at the C-terminus and it will be interesting to determine the molecular details of membrane attachment and which parts of the protein allow initial interaction with the membrane. The PsTX-60A protein has also a typical signal sequence and a propeptide at the very N-terminus, a structural organisation that is shared by other nematocyst toxins [10]. However, it is not clear if all cnidarian MACPF-containing proteins are toxins expressed in cnidocysts. As noted by Miller et al. it is unclear if Hy-MAC, a homologue of PsTX-60A in *Hydra*, is an orthologue, since the overall sequence identity is low [65]. Furthermore, expression of Hy-MAC was restricted to gland cells in the endoderm and not nematocytes [65]. In another study, a differentially expressed PsTX-60A homologue gene, termed *anklet*, was also shown to be expressed in the newly differentiated gland cells of the basal disk and it was suggested that this gene is involved in the formation and maintenance of the basal disk in *Hydra* by exerting a cytotoxic role [7].

Another toxin that contains the MACPF domain was reported recently in an aquatic snail [23]. Protein PcPV2 from *Pomacea canaliculata* is a perivitellin involved in egg defence against predation. PcPV2 is a neurotoxin with strong lethal effects against rodents and is used for defence purposes [23]; it is glycosylated and is composed of four 98 kDa heterodimers yielding a 400 kDa complex. The smaller 31 kDa component is similar to tachylectin-1, while the larger 67 kDa domain is similar to the MACPF domain [23]. Both domains are linked with a disulphide bond [27] and since the tachylectin-1 component of PcPV2 allows binding to cells this domain combination resembles the A-B toxin combination found in bacterial and plant lectins [23].

Distribution of CDC Proteins

CDCs (Pfam PF01289) were originally identified in a number of Gram-positive bacteria from the genera *Bacillus*, *Clostridium*, *Streptococcus* and *Listeria* where they are associated with invasion of and replication within animal hosts [29, 94]. The most well-known such CDCs include perfringolysin O from *Clostridium perfringens*, streptolysin O from *Streptococcus pyogenes*, pneumolysin from *Streptococcus pneumoniae* and listeriolysin O from *Listeria monocytogenes* [29, 94]. In each case the CDC has a distinctive role. Perfringolysin O is responsible for *Clostridia* gaining access deep into tissue to protect anaerobic respiration, leading to gangrene [40], pneumolysin is required for pneumococcal virulence via the effects it has on cell membranes that permit host invasion [97], and listeriolysin O is used to enable invasion and growth within cells [17]. There are, however, many less well-known examples and to snapshot the current state of knowledge we performed a protein sequence database search using the whole

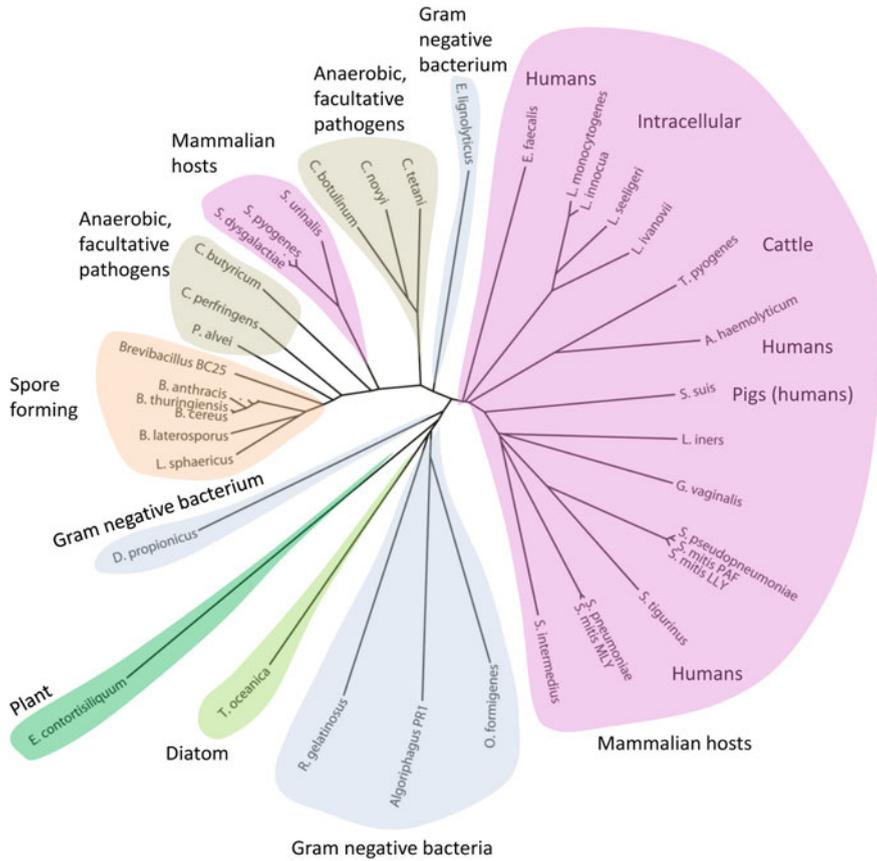


Fig. 2.5 Sequence-based phylogenetic tree of CDC proteins, *B. mycoides* and *B. weihenstephanensis* are not shown but share a branch with *B. anthracis*. *S. canis* shares a branch with *S. dysgalactiae*

perfringolysin O sequence, on the UniprotKB (<http://www.uniprot.org>). Of the 1,000 hits studied we found 40 unique sequences, and subsequently added the enterolysin from the Gram negative bacterium *Enterobacter lignolyticus* as identified alongside the CDC from *Desulfobulbous propionicus* by Tweten and colleagues [41], and the CDC identified in *Enterolobium contortisiliquum* (a member of the pea family, from South America) [26]. We pre-aligned the sequences in Uniprot and then used Clustal Omega [84] to perform alignments of the amino-terminal region of each protein (up to the end of the MACPF-homologous domain). We used the output alignments to construct phylogenetic trees using ClustalW2 Phylogeny [31, 56], which we then depicted using the program DRAWTREE (part of the PHYLIP package) [24] (Fig. 2.5). There are a number of interesting observations to be made on the basis of this analysis.

Firstly, in addition to the previously-identified CDCs from *E. lignolyticus* and *D. propionicus* we identified three more Gram-negative organisms which possess family members: one, *Oxalobacter formigenes* is a commensal human bacterium which relies on the degradation of oxaloacetate for most of its energetic and carbon needs and which (at 2,100 genes) has one of the smaller bacterial genomes [54]. By contrast, *Rubrivirax gelatinosus* and the *Algoriphagus* species PR1 are aquatic organisms; *R. gelatinosus* is a photosynthetic and nitrogen-fixing aquatic beta-proteobacteria [69], while *Algoriphagus* PR1 (*marchipongonensis*) is distinguished by the fact it is the prey of the choanoflagellate *Salpingoeca rosetta* [2, 3]. Choanoflagellates are the closest known relatives of animals, species of eukaryote of which some are unicellular and some multicellular colonies [95]. Even more surprisingly, we identified a form of CDC produced by the diatom *Thalassiosira oceanica* [60], which, after enterolobin from *E. contortisiliquum* is the second identified eukaryotic CDC. Genomic analysis of this species demonstrates 5 % gene acquisition from diverse taxonomic groups and so is consistent with the acquisition of a CDC by horizontal transfer from an aquatic bacterium [60]. The percent identity between the CDC of *T. oceanica* and that of *D. propionicus* is 23.9 %, that with the *Algoriphagus* PR1 26 % and that with *C. perfringens* perfringolysin 27.5 %. Its identity with the human-specific intermedilysin from *S. intermedius* is 25.2 % and to enterolobin, its neighbour in the phylogeny, is 13.9 % (see Fig. 2.6 for examples of alignment). The greater difference between the CDCs in *T. oceanica* and *E. contortisiliquum* reflects the much more developed evolutionary history of the plant versus the diatom, and the relative stasis in lifestyle and selective pressure experienced by bacterial lineages. The fact that sequences of CDCs in prokaryotic organisms which have not encountered each other for millions of years remain relatively stable at ~25 % identity suggests a strong selective pressure which is also, of course, reflected in the much greater conservation demonstrated by the MACPF/CDC fold [30]. The fact that the *T.oceanica* CDC is not more similar to those of bacteria nearby in ecological niche and within the phylogenetic tree than it is to those of bacteria much more distant phylogenetically and in ecology suggests that the diatom either acquired its CDC from the nuclear genome of its ancestor heterotrophic eukaryote, or due to an endosymbiotic event, or that any horizontal gene transfer that occurred was very ancient.

How ancient was the acquisition of a CDC by an ancestor of *T.oceanica*? A version of this phylogeny lacking just enterolobin did not present a single root, but instead a series of branches from a central common line. It is very interesting that this phylogenetic analysis based solely on sequence positions the diatom and plant CDCs adjacent to one another, and branching from a single point close to the origin of species. This leads to four of the five Gram negative CDCs alongside the diatom and plant CDCs forming a clade distinct from all other known family members, rooted at the origin of the tree. The absence of CDC proteins in many species argues against its presence in the genome of the last universal common ancestor and, therefore, the CDC gene transfer to diatoms and plants appears to have occurred from (endosymbiosis of) an ancestor of these Gram negative species

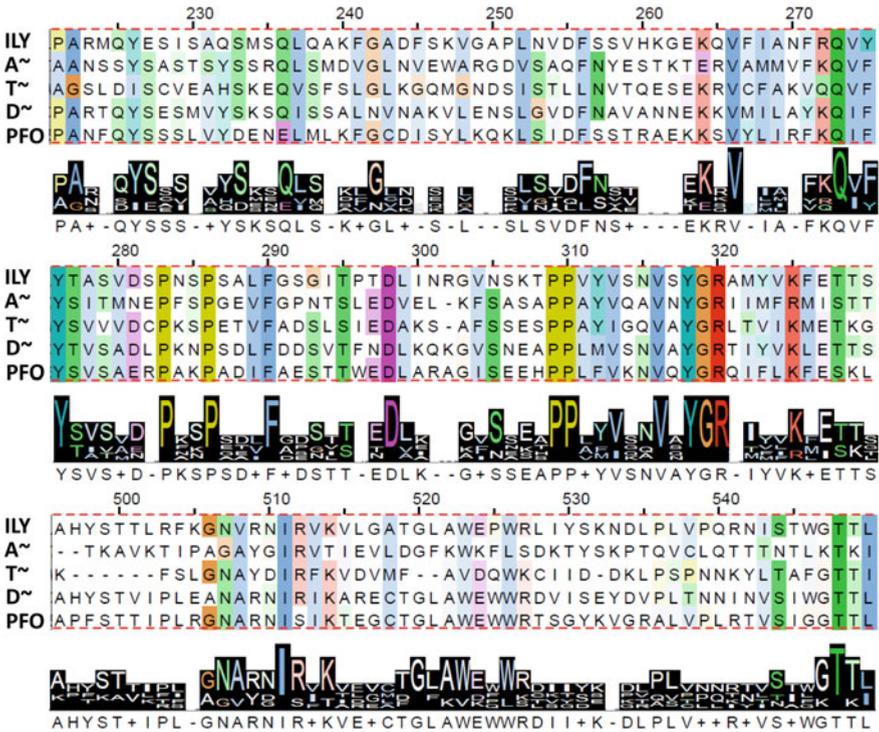


Fig. 2.6 Two regions of CDCs aligned. The first two sets of sequence comprise the core of the MACPF homology domain including the TMH helices; then final sequence comparison encompasses the carboxy-terminal domain (domain 4) undecapeptide. *ILY* intermedilysin from *S. intermedius*; *A~* the *Algoriphagus* species CDC; *T~* the *Thalassiosira oceanica* CDC; *D~* the *Desulfolobus* CDC and *PFO* perfringolysin O from *C. perfringens*

of which the evolutionarily closest example now known is *D. propionicus*. Another possibility is that a CDC was present in the last universal common ancestor as some sort of a housekeeping gene and was subsequently lost if not needed in particular species.

Diatoms evolved via a two-stage endosymbiotic process [12]. First, a cyanobacterium was captured by a eukaryotic heterotroph and this generated the origin of plants and red and green algae. Second, a red alga was captured by a different eukaryotic heterotroph and this gave rise to the stramenophile lineage that includes diatoms (emerging about 250 million years ago), macroalgae and plant parasites. Since our plant and diatom examples of CDCs derive from a single root this suggests that the CDC in diatoms (and in *E. contortisiliquum*) derives from the first endosymbiosis and thereby from an original cyanobacterium which shared a common (non-photosynthetic) ancestor with *D. propionicus*. In their paper on the *D. propionicus* and *E. lignolyticus* CDCs, Tweten and colleagues [41] discuss the possibility that a CDC may have helped to fend off endocytosis of primitive

bacteria. It seems plausible that diatoms and plants result from a successful endosymbiotic event involving a prokaryote possessing a CDC.

Overall, the pore-forming (MACPF) domain phylogeny for CDCs shows a structure strongly consistent with the lifestyles adopted by the producing organisms. Thus, one clade encompasses the majority of the *Streptococcal* species (those of the *mitis* grouping) [19, 66, 105] alongside others infecting humans such as *Gardnerella vaginalis* and *Lactobacillus iners*. Here, *S. mitis* stands out as a species of bacterium expressing three different CDC proteins: lectinolysin, mitilysin and the platelet aggregation factor. Its clade shares a common root to the centre of the phylogeny with other bacteria with similar or the same hosts (*Arcanobacterium haemolyticum*, first isolated from Pacific islanders, and *T. pyogenes*) [16, 90] and separate branches containing the intracellular *Listeria* bacteria and the originally commensal bacterium *Enterococcus faecalis* now found also as a drug resistant pathogen [58]. The position of the *mitis* grouping of *Streptococci* at a location distant from the pyogenic group (*S. pyogenes*, *S. canis*, *S. urinalis* and *S. dysgalactiae*) [20] is in line with their relative distance based on a published analysis of seven housekeeping genes that confirmed the phylogenetic positioning of the *dysgalactiae* species, among others [46].

Interposed between the two groups of *Streptococci* lie an isolated Gram negative example (from *E. lignolyticus*) and anaerobic bacteria (*Clostridium novyi*, *C. botulinum* and *C. tetani*) which can also cause human disease [40]. This common grouping matches the shared anaerobic ecological niche of *E. lignolyticus* and the Clostridial species. The *Clostridium* producers of CDC proteins also include *P. alvei*, *C. perfringens* and *C. butyricum* which are similarly anaerobic and associated with plants, humus and rotting material and again are potential human pathogens. These share an ecological niche with the spore-forming bacilli infecting livestock (*B. anthracis*) and insects (*B. thuringiensis*, *L. sphaericus*, *B. laterosporus* and *Brevibacillus*) [15, 22].

Evolutionary Implications

While CDCs are primarily cytolytic proteins, not all MACPF proteins have lytic activity and other biological functions are possible. This echoes the situation with eukaryotic proteins of the Bcl-2 family, which are similar to bacterial colicins. Although some Bcl-2 proteins are able to interact with membranes and form pores they do not all exhibit lytic activity and function at different stages of apoptosis—some to promote it, others to inhibit [8]. Various proteins that contain the MACPF domain are clearly evolutionary extremely conserved. For example Mpg-1 is present in sponge where it has a clear role in the immune response [103]. Similarly apextrins are widespread in cnidaria, echinoderms and apicomplexans [65]. Interestingly, apextrins seem to be specifically expressed in the ectoderm during metamorphosis in two distant evolutionary groups, cnidaria and echinoderms [65]. It is, however, extremely difficult to reconstruct the evolutionary history of the

MACPF/CDC superfamily with the current set of available genomic information and protein structures (see for example the distribution of MACPFs in fungi in section “[MACPF Proteins in Fungi](#)”). Until recently there were no examples of the two protein families that could be retrieved by sequence searches. However, now one can find MACPFs and CDCs with 20 % identity. For example the CDC of the diatom *Thalassiosira oceanica* is 22 % identical in its MACPF/CDC domain to the MACPF of *T. pseudonana*. The former was identified as a CDC by searching with the perforingolysin O sequence, the latter as a MACPF by searching with a *Plasmodium yoelii* perforin-like protein.

When reconstructing a CDC phylogeny we have identified not only known prokaryotic examples but also examples of eukaryotic proteins which, in our view, are likely to have arisen due to an endosymbiotic event. Mirroring the finding of eukaryotic CDCs, a preliminary phylogenetic study of 82 examples of MACPFs from unique genera highlights several bacterial examples of MACPFs as well as examples in coelacanths, a sea squirt, fungi (*Arthrotrichy oligospora* and *Fusarium oxysporum*) and even the diatom *T. pseudonana*. Indeed, the bacterium *Enterococcus faecalis* appears to have a MACPF-lineage protein 19.9 % identical to its CDC (data not shown). This level of similarity alongside a pairwise alignment of the CDC from *T. oceanica* and the MACPF from *T. pseudonana* that suggests 22 % sequence identity indicates the possibility of constructing a single sequence-based phylogeny for the MACPF/CDC superfamily but this is outside the scope of this chapter. The analysis we have been able to perform does, however, show that there was indeed one original protein domain now found in at least two different sequence families, and that it was present at a point in extreme antiquity before the lineages giving rise to current bacteria, diatoms, plants, animals and fungi diverged.

Although MACPF/CDC proteins may belong to at least two different sequence families, they belong to one structural class, which has been conserved throughout evolution. Understanding why the structure has been so deeply conserved will require further work but to a first approximation it is reasonable to conclude that the capacity it has to refold from an aqueous monomeric conformation into an oligomeric membrane-inserted conformation lies at the heart of the matter. The CDCs and MACPFs may not be considered as “just” toxins or even exclusively toxins: in many cases of pathogenic bacteria, for example, they are not the distinctive protein at the heart of the mechanism of disease (e.g. not in anthrax, not in botulism). Perhaps we should, after all, think of the MACPF/CDCs as house-keeping genes, genes that conferred the capacity to remodel membranes in fundamentally helpful ways, for example in establishing colony formation and as seen today in developmental processes, and that only subsequently did they get co-opted as agents of attack and defence in bacteria, apicomplexans and humans, among other cases [30].

Elsewhere we have reported a structural phylogenetic analysis [30] and it is worth highlighting the fact that however useful such an analysis is in terms of tying together shared fold and function, it does not provide a measure of evolutionary distance in time. In that case, because there is no simple concept of a

“mutational clock” in play (as there is in the sequence data we have studied here, albeit one running faster or slower in different organisms with different nucleotide base biases, accuracies of genome replication and environments) it is very hard to know what the meaning of a tree branch length is. The sequence analysis we describe here gives a more informative measure of the evolutionary process; alongside each other the sequential and structural phylogenies provide a compelling case for understanding the unity of the CDC and MACPF families. Further structural work and novel genomic information will aid in understanding further the evolutionary history of this interesting protein superfamily.

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