Guanylyl cyclases with the topology of mammalian adenylly cyclases and an N-terminal P-type ATPase-like domain in Paramecium, Tetrahymena and Plasmodium

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We cloned a guanylyl cyclase of 280 kDa from the ciliate Paramecium which has an N-terminus similar to that of a P-type ATPase and a C-terminus with a topology identical to mammalian adenyl cyclases. Respective signatory sequence motifs are conserved in both domains. The cytosolic catalytic C1a and C2a segments of the cyclase are inverted. Genes coding for topologically identical proteins with substantial sequence similarities have been cloned from Tetrahymena and were detected in sequences from Plasmodium deposited by the Malaria Genome Project. After 99 point mutations to convert the Paramecium TAA/TAAG-Gln triplets to CAA/CAG, together with partial gene synthesis, the gene from Paramecium was heterologously expressed. In SF9 cells, the holoenzyme is proteolytically processed into the two domains. Immunocytochemistry demonstrates expression of the protein in Paramecium and localizes it to cell surface membranes. The data provide a novel structural link between class III adenyl and guanyly cyclases and imply that the protozoan guanyly cyclases evolved from an ancestral adenyl cyclase independently of the mammalian guanylyl cyclase isoforms. Further, signal transmission in Ciliophora (Paramecium, Tetrahymena) and in the most important endoparasitic phylum Apicomplexa (Plasmodium) is, quite unexpectedly, closely related.

Keywords: adenyl cyclase/cGMP/guanyly cyclase/Paramecium/Plasmodium

Introduction

cAMP is used universally as a second messenger. Therefore, the existence of at least three phylogenetically separate classes of adenyl cyclases (ACs) is surprising. The membrane-attached ACs from Gram-negative bacteria (class I ACs) possess no sequence or topological similarity to the class II AC toxins from Bordetella pertussis or Bacillus anthracis. Both class I and II ACs are equally distant from the class III isoymes, which are found in mammals as well as in slime molds and many prokaryotes. The class III ACs share sequence similarity in their catalytic domains and, to a lesser extent, with the catalytic regions of mammalian soluble and membrane-bound guanyly cyclases (GCs) (for a review see Barzu and Danchin, 1994). The currently accepted topology of mammalian ACs comprises two hydrophobic membrane casettes of six α-helical transmembrane spans (TM), designated M1 and M2, and a catalytic center formed by two conserved cytoplasmic domains of ~250 amino acids, C1a and C2a, which are localized downstream of M1 and M2, respectively (see Figure 1B for a schematic representation). C1a and C2a precede poorly conserved cytosolic segments of variable length, designated C1b and C2b. Initially it was speculated that the prominent membrane anchors of the ACs might entertain an independent transport activity because their topology is reminiscent of the multidrug resistance gene, the cystic fibrosis gene, various membrane transporters and voltage-gated channels (Krupinski et al., 1989). Yet, all attempts to demonstrate such a secondary function of class III ACs failed. Mammalian ACs have a low basal activity and their hormonal stimulation is mediated predominantly by G-proteins in conjunction with other effectors (for a review see Sunahara et al., 1996).

We reported that in the protozoans Paramecium and Tetrahymena, cAMP and cGMP formation are biochemical correlates of electrophysiological events. Thus, the control of cAMP levels in Paramecium is linked to a K⁺ outward current because K⁺ channel blockers such as tetraethylammonium, Cs⁺ and quinine inhibit hyperpolarization-activated cAMP formation, and because a mutant, restless, with a defect in the K⁺ resting conductance is unable to control cAMP formation (Schultz et al., 1992). This raised the possibility that within the AC protein from Paramecium the function of an ion pore which is intimately linked to the regulation of enzyme activity may have been preserved. Indeed, the purified AC of 97 kDa, i.e. comparable in size with the prototypical mammalian versions, displayed both an AC activity and cation conductance (Schultz et al., 1992).

cGMP levels in Paramecium and Tetrahymena are regulated by a Ca²⁺ inward current (Schultz et al., 1986). Paramecium mutants with defects in Ca²⁺ channel regulation such as pawn or pantophobia show deficits in cGMP regulation. To understand the molecular properties of Paramecium ACs and GCs, we wished to clone and express candidate cDNAs. As a start, we used a 328 bp genomic DNA sequence from Paramecium which presumably coded for a partial sequence of a mammalian-type AC (Hinrichsen et al., 1995), and expected to clone an AC in which the bulky membrane anchors had retained an ancestral ion conductance. To our surprise, we discovered a GC which is disguised in the topology of mammalian ACs and has an extended N-terminal domain with topological and amino acid sequence similarity to P-type ACs...
ATPase ion pumps. After 99 point mutations for conversion from the ciliate to the universal DNA code and partial resynthesis of the cDNA, the gene was heterologously expressed. Similar genes were identified by cloning in *Tetrahymena* and in *Plasmodium* by searching the data released by the Malaria Genome Project. Our data provide a novel view on the evolution of mammalian ACs and GCs and suggest the existence of a new type of signal transduction in these protozoans which employs P-type ATPase-like structures as receptor.

**Results**

**Cloning of a Paramecium cyclase with a mammalian AC topology**

The sequence of a 328 bp PCR product from genomic DNA of *Paramecium* which displayed 29% amino acid identity to the catalytic C2a region of the rat type III AC was kindly provided by C.Russel and R.D.Hinrichsen (Hinrichsen *et al.*, 1995). Using specific primers, we amplified a 219 bp piece which was used as a probe to screen a *Paramecium* cDNA library prepared with poly(A)+ mRNA. We obtained two cDNA clones of 4.5 and 7.2 kb, both with a 3′ poly(A) tail. The open reading frame (ORF) was identical in both clones and ended at a TGA stop codon 47 bp upstream of the poly(A) tail. The 7.2 kb clone contained an ORF of 2408 amino acids; an ATG start codon was not identifiable. A genomic DNA (gDNA) library prepared from EcoRI-digested DNA and a new probe located at the 5′ end of the clone were used to obtain the ATG start. The genomic sequence unequivocally identified an ATG as start just 12 bp upstream of the 5′ end of the 7.2 kb cDNA clone because of an in-frame TGA stop only a further 24 bp upstream. The ORF coded for a protein of 2412 amino acids with a calculated molecular mass of 282.6 kDa (Figure 1). Hydrophobicity analysis indicated five hydrophobic regions with 22 putative TMs. Similarity searches demonstrated that the protein consisted of two large units: an N-terminal half of 1319 amino acids (115 kDa) with similarity to P-type ATPases and a C-terminal half of 982 amino acids (125 kDa) with a topology identical to that of the prototypical mammalian AC (Figure 1A). Both units were linked by a polypeptide of 111 amino acids. To exclude the possibility that we did not...

**Fig. 1.** (A) Sequence of the *Paramecium* guanylyl cyclase. Transmembrane regions are shaded; the four consensus blocks in the P-type ATPase-like domain and the two catalytic domains of the guanylyl cyclase region are in bold. (B) Suggested topology of the guanylyl cyclase. The 22 putative transmembrane spans are depicted as barrels, and cytosolic portions of the protein are shown as a duck head-like shape for P-type ATPases (Toyoshima *et al.*, 1993; Zhang *et al.*, 1998) and as a doughnut shape for the C1a/C2a heterodimer of the cyclase (Tesmer *et al.*, 1997; Zhang *et al.*, 1997). As in several mammalian adenylyl cyclases, a distinct C2b region is absent in the cloned guanylyl cyclase. For the C-terminal cyclase, the short-hand nomenclature used for mammalian adenylyl cyclases is adopted. M1/2 designate two membrane cassettes of six transmembrane spans, C1a, C1b and C2a domains coalesce as a cytosolic catalytic center.
cloned a cDNA which was joined accidentally during library preparation, we cloned a 2.5 kb EcoRI fragment from gDNA which was intronless, and we fully covered the intradomain region. Thus we unequivocally established the presence of this gene at the gDNA level.

The Paramecium cyclase unit contained hydrophobic M1 and M2 regions with six TMs each which were followed by C1a- and C2a-positioned domains with sequence similarity to the catalytic loops of metazoan ACs (Figure 1B). The C1a-positioned domain was followed by a hydrophilic stretch of 221 amino acids reminiscent of the C1b region in mammalian ACs; a distinct C2b region was absent. All mammalian ACs have GDCY as a signature sequence in the C1a-positioned domain (2276–2279), i.e. close to the C-terminus. Similarly, the motif TYMA is invariant in all C2a regions of mammalian ACs whereas in the ciliate cyclase it was located in the C1a-positioned domain (2276–2279), i.e. close to the C-terminus (amino acids 1121–1131; Figure 1A; Stokes et al., 1994; Zhang et al., 1998). In the cytosolic domains of the P-type ATPase family which has >150 members, several sequence blocks are conserved (Henikoff and Henikoff, 1992). Four of these align to corresponding cytosolic regions of the Paramecium GC. DKTGT(L/I)T, which is located within the large cytoplasmic loop, is an invariant signature sequence in all P-type ATPases. For ion transport to occur, the aspartate must be phosphorylated (Allen and Green, 1976). In the Paramecium GC, DKTGTLLT was conserved at the equivalent position (amino acids 461–467). A conserved GDGXXND motif present in the hinge region of P-type ATPases was 1025GDSFSF1030 in the Paramecium gene, and the (TSND)GE (SNT) block in the transduction domain was retained with a significant E to N change at 240SGNT243 virtually excluding ATPase function (Clarke et al., 1990a; Fagan and Saier, 1994). Finally, the ATP-binding domain in nearly all eukaryotic P-type ATPases involves an indispensable aspartate in a block of moderately conserved amino acids (Clarke et al., 1990b). The corresponding amino acid in the Paramecium P-type ATPase-like domain was Glu848. These decisive deviations of the Paramecium sequence from the ATPase consensus imply that this GC domain has adopted another function.

Expression of Paramecium GC

Transfection of Paramecium is not yet established. However, heterologous expression of Paramecium genes is impossible because it uses the universal stop codons TAA and TAG for glutamine (Prer et al., 1991). Therefore, we painstakingly changed all 99 TAA and TAG codons to CAA/CAG by site-directed mutagenesis (Deng and Nickoloff, 1992). The ‘corrected’ ORF was inserted into the bicistronic expression vector pRESlneo (Rees et al., 1996). However, upon transfection, no HEK293 cells survived the G418 selection. Using a green fluorescent protein (GFP)-based reporter assay (Trouet et al., 1997) with the cyclase domain, we realized that HEK293 cells did not transcribe a functional mRNA compared with cells transfected with a vector containing a bovine type VII GC.
AC cDNA (data not shown). Assuming that the problem may be caused by the high AT content of the Paramecium GC gene (66%) and in order to localize the problem, we used the bovine AC as a scaffold to test for proper transcription of individual protozoan cDNA segments. We separately inserted six cDNA sequences of the cyclase domain (N-terminal amino acids, 1380–1420; M1, 1421–1589; C1a-positioned, 1590–1806; C1b-positioned, 1807–1996; M2, 1997–2178; and C2a-positioned, 2179–2412) at the corresponding positions of the bovine type VII AC cDNA using appropriately generated restriction sites. No expression of the GFP reporter gene was observed when M1 or M2 of the protozoan cyclase replaced the respective bovine membrane cassettes. Therefore, we resynthesized the ciliate cDNA coding for M1 and M2 using the standard mammalian codon usage. This introduced a 58% G/C content into ~34% of the Paramecium GC domain. The partially synthetic gene in pIREsneo was again transfected into HEK293 cells and yielded a G418-selectable cell population. Using an antibody directed against the C1b-positioned domain (K1811–2007), a set of bands at ~95 kDa was stained specifically in Western blots, indicating protein expression of the M1380–Q2412 GC domain (data not shown). Cell homogenates had membrane-bound GC activities of up to 150 pmol/mg/min (Figure 3A). The $K_m$ for MgGTP was 50 µM. The GC activity was unaffected by 50 µM Ca$^{2+}$, 1 mM EGTA or by Paramecium Ca$^{2+}$/calmodulin. AC activity was not observed with MgATP as a substrate, yet it was detectable using Mn$^{2+}$ as a metal cofactor (Figure 3A). Forskolin did not enhance enzyme activity. These results proved that the cyclase domain of the cloned gene constituted a GC in the disguise of what hitherto had been considered to be a prototypical mammalian AC topology. We were unable to express the holoenzyme cDNA in HEK293 cells. In the hope of obtaining higher expression levels of the GC domain and an expression of the full-length clone, we turned to Sf9 cells and the baculovirus system for expression.

Expression of the Paramecium GC domain in Sf9 cells was equally efficient whether the ciliate cDNA (stop codons removed) or the partially synthetic cDNA clone (see above) was used for infection. GC catalytic activities were ~10-fold higher than in HEK293 cells (Figure 3B). The $K_m$ for MgGTP was 32 µM. AC activity was negligible using MgATP as a substrate, yet it was substantial with Mn$^{2+}$ as a divalent cation (Figure 3B). In a competition assay with 75 µM GTP and 1 mM ATP in the presence of 5 mM Mg$^{2+}$ as the physiologically relevant divalent cation, GC activity was diminished by only 25%, i.e. the Paramecium cyclase domain truly is a GC. The expression of the GC domain was monitored by Western blotting using an antibody directed against the C1b-positioned region (Figure 4, lane 4). The calculated mass of the GC domain was 115 kDa. The slightly lower apparent molecular weight is probably due to the hydrophobic transmembrane regions, as similar effects have been reported for proteins with large transmembrane domains (Hauser et al., 1998; Mons et al., 1998). Variable glycosyl-
Table I. Immunogold labeling of *Paramecium* cellular structures with anti-GC antibody or anti-ATPase antibody

<table>
<thead>
<tr>
<th>Structures analyzed</th>
<th>Au grains per 100 µm membrane length</th>
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<tr>
<td></td>
<td>Anti-GC</td>
</tr>
<tr>
<td>CM/OASM</td>
<td>37.9</td>
</tr>
<tr>
<td>IASM</td>
<td>34.5</td>
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<tr>
<td>CiM</td>
<td>17.6</td>
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<tr>
<td>TM</td>
<td>0.0</td>
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<td>OMM</td>
<td>0.4</td>
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CM/OASM, cell membrane/outer alveolar sac membrane complex; IASM, inner alveolar sac membrane (facing cell center); CiM, ciliary membrane; TM, OMM, trichocyst or outer mitochondrial membranes.

...ation may account for the appearance of closely spaced bands.

We were unable to express the full-length *Paramecium* GC gene in SF9 cells as determined by Western blotting. Again we reasoned that this may have been due to the high A/T content of the gene, in particular to two stretches of seven and nine As in the ATPase-like region. Multiple As in an mRNA may constitute a signal for premature mRNA degradation, and slippage may occur during replication and transcription (Laken *et al.*, 1997). Therefore, we resynthesized four DNA segments of the ATPase-like domain comprising 46% of this gene portion (nucleotides 1–436, 1012–1387, 1973–2363 and 3303–3991). The G/C content of the synthetic DNA was 56%; the amino acid sequence remained unchanged. Nevertheless, for reasons not yet understood, we were unable to express only the ATPase-like domain in SF9 cells as determined by Western blot analysis. However, upon infection with the partially synthetic gene coding for the holoenzyme, expression in SF9 cells was achieved (Figure 4, lanes 2 and 3), although we never detected a product corresponding to the full-length protein of 280 kDa. Using affinity-purified polyclonal antibodies directed either against a 20 kDa cytosolic portion of the P-type ATPase-like domain (L549–M718; anti-ATPase antibody), the 23 kDa C1b-positioned segment of the cyclase domain (K1811–A2007; anti-GC antibody) or a peptide antibody directed against the N-terminal hexadecapeptide R5–N20, we labeled specific bands of lower molecular mass in a Western blot. Because SF9 membrane proteins up to 350 kDa were blotted successfully as visualized by Ponceau S staining, and because inclusion of a cocktail of protease inhibitors during cell lysis had no effect, the result most likely reflected protein processing in the SF9 cells. The anti-GC antibody recognized proteins with an apparent molecular mass of mainly 85 kDa up to 100 kDa (Figure 4, lane 3). In the same membrane preparations, the anti-ATPase antibody and the N-terminal peptide antibody specifically detected a 120 kDa band (Figure 4, lane 2, and data not shown). Any unspecificity and cross-reactivity of the antibodies was excluded by respective pre-blocking experiments (data not shown). The proteolytic processing in SF9 cells must have occurred in the area linking the ATPase-like and the GC domains because of the size of the two generated proteins and because GC activity was obtained (Figure 3B). This conclusion was supported by the isolation of mRNA from infected SF9 cells and the unequivocal demonstration by RT–PCR that a correct and uninterrupted mRNA existed (data not shown). In SF9 cells infected with the gene for the holoenzyme, GC activity was ~50% of that obtained with the GC domain expressed alone. All enzymatic properties of this proteolytically processed holoenzyme corresponded to those of the expressed GC domain. This finding indicated that the physical presence of the ATPase-like protein in the membrane did not affect GC activity per se.

Localization of *Paramecium* GC

Using anti-GC or anti-ATPase antibodies, we detected the GC immunocytochemically in cross-sectioned *Paramecium* using gold conjugates of F(ab)2 as a second antibody (Table I; Figure 5). Both primary antibodies labeled the same membranes, i.e. the GC was present in the ciliary membrane, in the complex formed by the cell membrane and the outer alveolar sac membrane (CM/OASM), on the inner alveolar sac membrane (IASM), on a cilium cross-section (Ci) and on a ‘grazing’ section along the membrane of an emerging longitudinally cut cilium (upper right).
Background without the first antibody was negligible (Table I). In semi-quantitative evaluations with both antibodies, we subtracted background labeling determined for probably irrelevant membranes such as outer mitochondrial and trichocyst membranes (Table I). The differences in the labeling intensity were probably caused by differential accessibilities or different affinities of the antigenic sites for the respective primary antibodies.

Chimeras between Paramecium GC and mammalian AC

The GC domain is topologically identical to mammalian ACs. Therefore, we investigated whether a mammalian membrane anchor would be compatible with the GC catalytic domains derived from Paramecium. First, we replaced the mammalian C1a, C1b and C2a regions of a bovine type VII AC (Völk et al., 1996) by the C1a-positioned, C1a,b-positioned and C2a-positioned regions of the Paramecium GC domain, i.e. using the mammalian AC as a scaffold for the Paramecium catalyst (Figure 6, constructs I and II). Secondly, we generated a construct with an inverse order of the C1a- and C2a-positioned regions from Paramecium because, as outlined above, these two regions seem to have been switched in the Paramecium GC domain (construct III). The constructs showed substantial and similar GC activity and a minor AC activity when assayed with MnATP (Figure 6). We conclude that the Paramecium GC catalytic center comprised of C1- and C2-positioned loops is expressed and active in the frame of a mammalian AC irrespective of the origin of the C1b region and, surprisingly, of the arrangement of the catalytic subdomains.

Tetrahymena guanylyl cyclase

The heterologous expression of Paramecium GC holoenzyme in Sf9 cells did not reveal if and how the GC activity is regulated by the P-type ATPase-like domain. Therefore, we wished to clone a GC from the related ciliate Tetrahymena for sequence comparisons. A PCR with primers designed to recognize a protozoan C1a-positioned region and cDNA as a template yielded six different PCR products with a high degree of amino acid identity (Figure 7). One fragment was chosen arbitrarily as a probe to clone the corresponding full-length gene from a Tetrahymena cDNA library; 9.7 kb of genomic sequence was obtained by chromosome walking. The 3’ end of the ORF was completed by vectorette PCR (Gonzalez and Chan, 1993) and the introns were identified unambiguously by PCR using Tetrahymena cDNA as a template. The protein encoded by the 8.4 kb ORF had exactly the same topology as the Paramecium GC: an N-terminal P-type ATPase-like domain of 168 kDa, followed by a 146 kDa GC domain with mammalian AC membrane topology. As in the Paramecium GC, the C1a- and C2a-positioned regions were inverted compared with mammalian ACs. The amino acids decisive for substrate specificity (E1808 and S1885 in C1a and R2734 in C2a) unequivocally identified the encoded protein as a GC. Interestingly, the P-type ATPase-like domain resembled the general ATPase consensus sequence much less than this region from the Paramecium GC. In the Tetrahymena sequence, the extremely conserved DKTGTLT phosphorylation site evolved to 485SKSGTLM490. This proves that the protozoan P-type ATPase-like domains lack the capacity for an active ion transport. Further, the consensus sequence GDGXND was 1180GSNSID1185 in Tetrahymena and the conserved (TSND)GE(SNT) box was changed to 234QGSN237. An attempt to compare the 22 putative transmembrane spans of the Paramecium GC with those of the Tetrahymena clone revealed a potentially significant conservation in TM5 and TM4, where the YXXL5PXYX3D motif, and in TM5, a (F,Y)RSF motif, were conserved between Paramecium and Tetrahymena. Because no similarity exists to the corresponding transmembrane spans in true P-type ATPases, the functional importance of this remains to be evaluated. We note that amino acids in TM6 which supposedly are crucial for cation binding in P-type ATPases were absent in the ciliate GCs (Zhang et al., 1998). Since Tetrahymena also uses the universal stop codons TAA and TAG for glutamine, no attempt was made to express the cloned Tetrahymena gene.

A guanylyl cyclase disguised as an adenylyl cyclase

Fig. 6. Guanylyl cyclase and adenylyl cyclase activities of chimeras between the Paramecium GC domain and bovine type VII AC. Regions from the Paramecium AC are shaded, type VII AC domains are open boxes. Compatible restriction sites (AvrII, Sall, XhoI and AciI) were introduced as shown and used for domain shuffling. The locations of the restriction sites in the Paramecium GC were: XhoI at 4765; AvrII at 5986; Sall at 6532; and AciI at the 3’ terminus; and in the bovine type VII AC: Sall at 1183; MluI at 2032; AvrII at 2350; and XhoI at 3022. GC activity was assayed with 75 µM GTP and 5 mM Mg2+. AC activity with 75 µM ATP and 2 mM Mn2+.

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<th>Construct</th>
<th>M1</th>
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<th>C1b</th>
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<td>C2a</td>
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<table>
<thead>
<tr>
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Fig. 7. Alignment of C1a-positioned regions of guanylyl cyclases from Paramecium, Tetrahymena and Plasmodium. The sequences of the Paramecium and Tetrahymena GCs are from the full-length clones (DDBJ/EMBL/GenBank accession Nos AJ238859 and AJ238858, respectively); other Tetrahymena (TetraGC) or Paramecium (ParaGC) sequences are PCR fragments of the C1a-positioned domains (DDBJ/EMBL/GenBank accession Nos: AJ242491 for ParaGC2; AJ242492 for ParaGC3; AJ242493 for ParaGC4; AJ239077 for TetraGC2; AJ239078 for TetraGC3; AJ239079 for TetraGC4; AJ239080 for TetraGC5; and AJ239081 for TetraGC6); the Plasmodium sequence is translated from chromosome 13.

Identical amino acids are inverted, the consensus glutamate and serine (alanine in Plasmodium) residues which are involved in defining GTP as a substrate are indicated by arrows.

Guanylyl cyclase isoforms from Paramecium and Tetrahymena

The variety of AC isoforms is almost a hallmark of the mammalian cAMP signaling system, and often a single cell expresses several isoforms concomitantly. So far, nine membrane-bound isozymes have been identified in mammals which share extensive sequence identities in their catalytic regions, yet are highly diverged elsewhere. The protozoan GCs have the topology of mammalian ACs. Therefore, we wanted to know whether multiple isoforms of this peculiar GC are expressed in Paramecium and Tetrahymena. Further, we wished to find out whether protozoan cyclase genes may exist which at the crucial substrate-specifying positions contain amino acids which would endow the protein with a preference for ATP as a substrate. Using several slightly degenerate oligonucleotide primer pairs covering the C1a-positioned region, and genomic and cDNA from Paramecium and Tetrahymena, respectively, as templates, we identified three further DNA fragments from Paramecium and another five from Tetrahymena. All fragments coded for 60–75 amino acids of the C1a-positioned domain and had a serine, not an aspartate, as one of the three crucial amino acids which specify GTP as a substrate, i.e. these genes coded for GCs (Figure 7). The extremely conserved regions around the GTP-specifying serine (–20 to +2) were nearly identical in all protozoan variants and highly conserved with respect to the corresponding region in mammalian ACs. The anterior 40 amino acids were diverged (21–93% identity) and had approximately the same extent of diversity as that observed in the corresponding C2a domains of the nine mammalian AC isoforms (24–83% identity; Sunahara et al., 1996). From an evolutionary point of view, it is noteworthy that the fully cloned Paramecium GC shared 95% amino acid identity with one of the Tetrahymena isoforms (Figure 7, TetraGC2). We conclude that in both ciliates, a family of GC isoforms exists comparable in size with that of mammalian ACs, and that some of the GC isoforms have been highly conserved in these protozoans, indicating a conservation of function.

Guanylyl cyclase isoforms in Plasmodium falciparum

We searched databases to determine whether GCs with this architecture were present in other organisms, particularly in other protozoans. In DDBJ/EMBL/GenBank database, we found a 2.797 bp fragment designated as an AC from chromosome 11 of Plasmodium falciparum (deposited by D.J. Carucci and D.C. Warhurst; PFAC, accession No. U33118). The ORF codes for six TMs (M2) and a C2a-positioned domain. At nucleotide 1966, a substrate-specifying arginine is encoded, which strongly indicates that this gene, contrary to the given definition, codes for a GC with mammalian AC topology. A C1a-positioned domain is absent in this clone. Further, searching the data which have been released, but not yet edited, from the Malaria Genome Project, we discovered an unequivocal GC sequence on chromosome 13 of P. falciparum. It was possible to assemble a complete putative ORF which exactly matched the Paramecium GC topology, i.e. it contained a P-type ATPase-like domain fused with a GC of mammalian AC topology with the C1a and C2a positions inverted. The alignment of the C1a-positioned region with the Paramecium and Tetrahymena GCs clearly identified GTP as the substrate (Figure 7).

Discussion

We have cloned a GC from Paramecium which has an N-terminal P-type ATPase-like domain and a C-terminal cyclase domain. So far, mammalian GC catalysts are either homodimers fused to an extracellular receptor by a single TM, or soluble heterodimers linked to a nitric oxide-binding site (Schulz et al., 1991; Yu et al., 1996; Tang and Hurley, 1998; Koesling and Friebe, 1999). The ciliate GC domain differs. It has the unmistakable topology of a
mammalian AC complete with catalytic C1a and C2a regions and two prominent membrane anchors, M1 and M2, with six TM5s each. Therefore, the ciliate GC is not related to metazoan GCs but is a close relative of metazoan ACs. A striking difference between the ciliate GCs and their mammalian AC congeners was the switch of the C1a and C2a positions. The preference for GTP could be rationalized by looking at three amino acids which determine the nucleotide specificity in the catalytic pocket. In metazoan ACs, glutamine, lysine and aspartate define ATP as a substrate, whereas in GCs the respective positions are taken by arginine, glutamate and cysteine and define GTP as a substrate (Sunahara et al., 1998; Tucker et al., 1998). In the protozoan GCs, we have arginine, glutamate and a serine instead of a cysteine residue. According to molecular modeling of mammalian GCs, the cysteine SH group interacts with the O6 of the guanine ring via a hydrogen bridge (Tucker et al., 1998). A serine at this position has a similar space requirement and potential for interaction.

Another remarkable feature of the ciliate GC domain was the successful expression of chimeras with the bovine type VII AC. The catalytic activity of the Paramecium GC did not depend on a specific order of the C1a- and C2a-positioned segments, and was completely unaffected by the origin of the C1b region or the M1 and M2 membrane anchors and suggests a considerable mobility of the membrane-anchored loops to form an active heterodimer. Such a cross-compatibility has not yet been reported for mammalian ACs.

In the two fully sequenced ciliate GCs, the C1b and M1/M2 regions displayed no sequence similarity. This was not surprising since the catalytic loops of ciliate GCs were quite insensitive to the origin of the membrane anchors or C1b segments, as demonstrated by the active chimeras. This does not exclude the existence of regulatory functions which depend on C1b or even on M1/M2, but so far those must have escaped detection. The existence of a couple of almost identical GCs in Paramecium and Tetrahymena leads to two conclusions. First, this isoform must have evolved before Paramecium and Tetrahymena segregated. Secondly, the existence of several GC isozymes is not an indication of redundancy, rather it defines functional peculiarities which were retained during ciliate evolution. This is not unlike the situation concerning the mammalian AC isoform variety.

The biochemical properties of the recombinant Paramecium GC differed from those reported earlier (Schultz and Klumpp, 1982). We were unable to demonstrate an effect of Ca2+. The reasons for this discrepancy may be: (i) the expressed GC is a minor isoform in late-log Paramecium cells; (ii) the calcium dependence is conferred by a protein which has no homolog in HEK293 or S9 cells or by a post-translational modification which occurs in Paramecium cells only; or (iii) a Ca2+ dependence may only be demonstrable in the holoenzyme which we consistently failed to express in S9 cells due to the inevitable proteolytic processing. The latter may also be responsible for the failure to demonstrate a function for the 155 kDa N-terminal domain with its topology identical to the family of P-type ATPases. Sequence similarity was restricted to four conserved cystolic regions. We have reasons to believe that these domains do not operate as transporters because decisive amino acid deviations preclude an ATPase function. The most conclusive proof comes from an aspartate invariant in all P-type ATPases. Mutation of this Asp to Glu or Asn completely abrogates enzyme activity (Clarke et al., 1990b). In the Paramecium and Tetrahymena GCs, the equivalent positions (848 and 1005, respectively) are taken by Glu, thus excluding ATPase activity provided the structure–function relationships which were established for conventional P-type ATPases can be extrapolated to the N-terminal domain of the ciliate GCs. In addition, two genes coding for canonical P-type ATPases have been cloned from Paramecium which possess all the structural hallmarks required for an ion transport activity (Elwess and van Houten, 1997; Hauser et al., 1998).

With regard to a potential function of the ATPase-like domains in the GCs, we may get a hint by examining the pore and cation-binding helices TM4, 5 and 6. TM4 and TM5 are significantly conserved in the ciliates, yet differ substantially from the corresponding helices of ion transporters, and the ciliate TM6 lacks amino acids which supposedly are involved in cation binding (Zhang et al., 1998). We tentatively propose that the protozoan ‘pore region’ does not bind inorganic ions. Perhaps it associates with organic molecules as does another family of P-type ATPases, the putative aminophospholipid transporters. The protozoan P-type ATPase-like domains would then constitute a receptor-like entity reminiscent of the atrial natriuretic receptor–guanylyl cyclase couple in mammals. However, at present this must remain purely speculative.

Finally, the data allow us to discuss the evolutionary steps which most likely have occurred during the development of these cyclases. The fact that cyclases exist with C1a and C2a arranged in both ways strongly supports the hypothesis that initially membrane-anchored monomers formed a homodimeric AC. This structure is still in existence in several bacteria and may actually represent a common ancestor of mammalian and ciliate nucleoside triphosphate cyclases (Coudert-Cavalli et al., 1997; Tang and Hurley, 1997). Upon gene duplication, independent evolution led to the formation of a heterodimeric AC in eukaryotes before the monomers were fused in a single peptide chain. Evidently, the order of monomer linkage has occurred in either way. Only after this event did the ciliate GC evolve by a few point mutations in the purine-binding pocket from an ancestor AC module. All 10 GC isoforms detected in Paramecium and Tetrahymena by PCR are most likely to have evolved from a common ancestor because the sequences surrounding the substrate-determining serine are almost identical. On the other hand, the soluble heterodimeric GCs in mammals must have diverged from an ancestral cyclase homodimer even before the bulky membrane anchors were added and before heterodimers evolved, because the GCs have retained identical amino acids at positions which determine substrate specificity and at equivalent positions of a non-catalytic pocket (see Figure 2; Tesmer et al., 1997). In summary then, the ciliate GCs evolved from a membrane-anchored, heterodimeric AC with inverted catalytic centers, whereas mammalian GCs most probably descended from a primordial cytosolic cyclase homodimer. The aquisition by the protozoan GCs of an ATPase-like domain
may have occurred before or after the change in substrate specificity.

Recently, the ciliates *Paramecium* and *Tetrahymena* were systematically reclassified as belonging to the parvkingdom 2, Alveolata, which is one out of seven protozoan parvkingdoms. The alveolates comprise the phyla Ciliophora, Dinozoa and Apicomplexa (Cavalier-Smith, 1993). The Apicomplexa contain many dreaded parasites such as *Plasmodium*, *Toxoplasma*, *Theileria* and *Babesia*. Currently, the *P. falciparum* genome with an A/T content of ~80% is being sequenced. The database search identified GC isoforms were detected. A cDNA library was established with 8.8 g of poly(A)^+ RNA isolated from stationary phase *P. falciparum* template, a 219 bp fragment suspected to code for a sense primer coding for KTYMAA and the antisense primers for GDTINTA or G(D,N)T(V,I)NV A. Six further primers were created in pBluescriptII SK(−) using the corresponding amino acid sequence (Salomon et al., 1974). The reactions contained 22% glycerol, 50 mM Tris–HCl, pH 8.0, 5.7% sucrose and protease inhibitors. AC activity was determined for 10 min at 37°C with 75 µM [α-32P]ATP (Salomon et al., 1974). The reactions contained 22% glycerol, 50 mM Tris–HCl, pH 7.5, 3 mM creatine phosphate, 0.23 mg of creatine kinase and 2 mM [2-3H]cAMP (1.7×10^4 Bq/µmol). GC assay conditions were identical, except that cAMP and ATP were replaced by [8-3H]cAMP and [α-32P]GTP (Klumpp and Schultz, 1982).

**Expression of Paramecium GC in HEK293 cells**

Site-directed mutagenesis to convert 99 protozoan TAA/TAG-Gln codons to the universal CAA/CAG-Gln triplets was according to Deng and Nicipoff (1982). The 7.2 kb cDNA clone was cut into fragments of 0.2–1.2 kb, ligated into pBluescriptII SK(−) and mutated separately. A 0.6 kb fragment at the 5’ end was amplified by PCR using specific primers which introduced a 5’ *EcoRI* restriction site, a Kozak sequence and the bases for the four N-terminal amino acids not found in the 7.2 kb cDNA clone. Similarly, a 0.2 kb fragment of the 3’ end was amplified to eliminate the 3’-UTR region and generate a 3’ *ApaI* restriction site. The ORF was reconstituted in pBluescriptII SK(−). A list of the primers used in this study is available from J.E.S. on request.

Five DNA stretches (nucleotides 1–436, 1012–1387, 1973–2363, 3303–3991, 4261–4764 and 6001–6377) were redesigned for chemical synthesis by reverse translation of the corresponding amino acid sequence using the most common mammalian codon usage as defined by the Lasergene software package. The sequences were edited manually to remove potential strong secondary structures and RNA splice sites. Restriction sites were designed as needed for ligating the synthetic fragments to neighboring sequences. Synthesis was carried out by annealing, elongation and amplification with 0.1 µM template oligonucleotides and 0.5 µM amplification primers (Chio et al., 1994). Twenty-one PCR cycles were run with an annealing temperature of 56°C. Synthetic stretches of the P-type ATPase-like domain were generated with 0.5 µM template primers without amplification primers. Eleven PCR cycles were run with an annealing temperature of 54°C. The synthetic DNA fragments were joined to the TAA/TAG-corrected parts of the ORF. The DDBJ/EMBL/GenBank accession No. of the synthetic gene is AJ239047.

The GC domain (nucleotides 4141–7239) was cloned into pBluescriptII SK(−) via the 5’ BamHI site at position 4141 and a 5’ *ApaI* site. Using the oligonucleotide GCTAGCCGACCATGAGTACC, we concomitantly created a start ATG preceded by a Kozak sequence and a 5’ *NheI* site. The ORF was excised from pBluescriptII SK(−) via the *ApaI* and *ApaI* blunt ligated into the *EcoRI* site of pRE31neo (Clontech).

HEK293 cells were grown at 37°C in minimum essential medium (Gibco-BRL; #31095-029) containing 10% fetal calf serum (FCS) and 20 µg/ml gentamycin. For transfection, the calcium phosphate method was used with 10 µg of plasmid DNA/100 mm dish (Kingston et al., 1992). Cells were selected with 1 µg/ml G418 starting 3 days after transfection. After 2 weeks, cells were rinsed once with phosphate-buffered saline (PBS; 137 mM NaCl, 2.7 mM KCl, 10 mM Na_2_ HPO_4_, pH 7.4), suspended in 5 ml of PBS and collected. Cells were lysed by freeze–thaw in 20% (v/v) glycerol, 1% (v/v) thioglycolic, 20 mM KCl, 20 mM Tris–HCl, pH 7.5. The homogenate was used for cyclic assays.

**S9 cell culture and recombinant baculoviruses**

S9 cells were grown at 27°C in TC-100 medium with 10% FCS, 200 U/l penicillin and 200 µg/l streptomycin as a monolayer or in suspension (90 r.p.m., 0.1% pluronic F68). The ORF of the *Paramecium* GC holoenzyme, consisting of the partially resynthesized ATPase-like domain and the GC domain alone were inserted into pFastBac1, respectively. The BAC-TO-BAC baculovirus expression system from Gibco-BRL was used to produce recombinant virus.

Membranes were prepared from S9 cells 48 h after infection (m.o.i. 0.1). Cells were lysed in 3 mM EDTA, 3 mM EGTA, 12 mM HEPES pH 8.0 containing a protease inhibitor cocktail (1 tablet/10 ml Complete Mini from Roche Diagnostics) by two freeze–thaw cycles and repeated passages through a 0.45 mm needle. After removal of nuclei, membranes were pelleted, washed and resuspended in 1 mM EDTA, 16 mM HEPES pH 8.0, 5.7% sucrose and protease inhibitors.

**Enzyme assays**

Activity was determined for 10 min at 37°C with 75 µM [α-32P]ATP and 2 mM [2-3H]cAMP (1.7×10^4 Bq/µmol). GC assay conditions were identical, except that cAMP and ATP were replaced by [8-3H]cAMP and [α-32P]GTP (Klumpp and Schultz, 1982).

**Antibodies and Western blot analysis**

Rabbit antibodies were generated against a synthetic N-terminal peptide (R5–N20), a cytosolic region of the ATPase-like region (LS49–M718) and the C1b-positioned region (K1811–A2007) of the GC domain. Corresponding cDNAs were cloned in pqEs (Qiagen) and expressed in...
Escherichia coli M15[pREP4]. Peptides were affinity purified on Ni-NTA and by SDS-PAGE and used for immunization. Antibodies were affinity purified with antigen linked to NHS-agarose (Bio-Rad). A 10–20 μg aliquot of cell membrane protein was incubated in sample buffer for 2 h at 37°C prior to SDS-PAGE. Proteins were blotted onto nitrocellulose, transiently stained with Ponseau-S, incubated with the respective antibodies and detected by chemiluminescence.

Construction of functional Paramecium GC/type VII AC chimeras

In the remodeled ORF of the Paramecium GC domain, restriction sites were created by site-directed mutagenesis: Spel at position 4528 with an L1421S change, XhoI at position 4765, AvrII at position 5986 with a K1997R change, Sall at position 6532 with a N2179D change and a 3′-terminal AscI site by extension of the ORF with the sequence GAGGCGCGCCAA. For constructs II and III (Figure 6), an MfuI site was generated at position 5446 with an I817R change. Compatible sites for an I833L/D834E change. Chimeras were generated by assembling the appropriate restriction fragments. Chimeric ORFs were cloned into the EcoRV site of pRES1neo and expressed in HEK293 cells.

Immunocytochemical localization of guanylyl cyclase in Paramecium

Cells were fixed in 4–8% formaldehyde and 0.1% glutaraldehyde and 1 mM CaCl2. After ethanol dehydration and cooling, cells were embedded in hydrophilic metacrylates (Unicryl, British BioCell, or LR Gold, London Resin Co., London, UK) and UV polymerized at –20 or –35°C, respectively. Identical results were obtained with both methods and data were pooled. Ultrathin sections were incubated with affinity-purified anti-GC or anti-ATPase antibodies followed by incubation with gold conjugates of F(ab)2 (5 nm, Au 5 ) from goat anti-rabbit antibodies (Aurion, Wageningen, The Netherlands). For further details, see Grothe et al. (1998). On electron micrographs of uranyl acetate-stained sections, gold particles per unit membrane length were determined by the hit point method (Plattner and Zingsheim, 1983).

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References


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