

cAMP signaling in *Dictyostelium*

Complexity of cAMP synthesis, degradation and detection

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Abstract

cAMP plays a pivotal role in control of cell movement, differentiation and response to stress in all phases of the *Dictyostelium* life cycle. The multitudinous functions of cAMP require precise spatial and temporal control of its production, degradation and detection. Many novel proteins have recently been identified that critically modulate the cAMP signal. We focus in this review on the properties and functions of the three adenylyl cyclases and the three cAMP-phosphodiesterases that are present in *Dictyostelium*, and the network of proteins that regulate the activity of these enzymes. We also briefly discuss the two modes of detection of cAMP.

Functions of cAMP

The evolution of signalling in *Dictyostelium discoideum* has particularly favoured cAMP as jack of all trades. The manifold usages of cAMP are summarized in Figure 1 and can be broadly subdivided into its role as first messenger outside the cell and second messenger inside the cell. Outside, cAMP acts as chemoattractant, which coerces amoebae to convert from solitary predators into gregarious community members (Konijn *et al.*, 1967). Outside, cAMP also acts on gene regulation to induce the alterations in phenotype that are required for chemotactic aggregation and for initiation of prespore differentiation (Gerisch *et al.*, 1975; Kay, 1982; Schaap and Van Driel, 1985). As inhibitor of terminal stalk cell differentiation, cAMP plays a critical role in cell-type choice (Berks and Kay, 1988; Hopper *et al.*, 1993a).

Inside, cAMP triggers initiation of development (Schulkes and Schaap, 1995; Mann *et al.*, 1997), maturation of spores and stalk cells (Harwood *et al.*, 1992; Hopper *et al.*, 1993b; Mann and Firtel, 1993) and maintenance of spore dormancy (Van Es *et al.*, 1996). Inside, cAMP also mediates resistance to osmotic stress (Schuster *et al.*, 1996) and contributes to the process of orientation in chemotactic gradients (Wessels *et al.*, 2000).

cAMP synthesis

Until the early 90's the regulation of cAMP production could only be analysed biochemically. cAMP is transiently synthesized upon stimulation of aggregation competent cells with cAMP. The accumulation of

cAMP peaks at 2 min (Devreotes and Steck, 1979) and requires the heterotrimeric G-protein G2 (Kesbeke *et al.*, 1988; Kumagai *et al.*, 1989). In cell lysates, cAMP synthesis requires GTP γ S; the cyclase itself is associated with the membrane fraction, but requires a factor from the cytosol to be active (Theibert and Devreotes, 1986). Genetic screens identified a mutant, *synag 7*, that does not synthesize cAMP and can only aggregate when mixed with wild-type cells. The defective gene was later identified as CRAC (cytosolic regulator of adenylyl cyclase), the essential cytosolic factor for adenylyl cyclase activation (Insall *et al.*, 1994; Lilly and Devreotes, 1994).

The gene for the cAMP-activated adenylyl cyclase *AcaA* was identified by PCR through its homology with the mammalian cyclase domains, and this screen also yielded a second gene, *AcgA*, that was only expressed in spores (Pitt *et al.*, 1992). The third adenylyl cyclase, ACB, was detected biochemically in mutants with a double lesion in *acaA* and *rdeA*, an essential protein for activation of the intracellular cAMP-phosphodiesterase RegA (Chang *et al.*, 1998; Kim *et al.*, 1998a; Thomason *et al.*, 1999). The ACB gene, *AcrA*, was identified from a mutant that was defective in spore maturation (Soderbom *et al.*, 1999).

The catalytic domains of ACA, ACG and ACB classify them as typical eukaryote class III cyclases (Danchin, 1993). This type of cyclase can either be soluble with one or two catalytic domains, membrane-associated with a single transmembrane domain and one catalytic domain or membrane-associated with 12 transmembrane (12TM) domains and two catalytic domains. The catalytic domains are actually half-sites of the catalytic centre and need to form hetero- or homodimers to be active. Optimal juxtaposition of the two domains is usually part of the activation process of the cyclases (Hurley, 1998).

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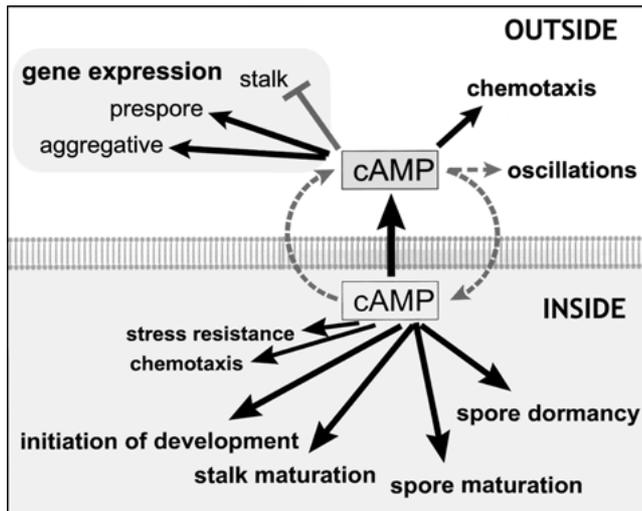


Fig. 1. Functions of intracellular and extracellular cAMP.

Adenylyl cyclase A

ACA is an enzyme with 12TM domains and two cyclase domains. In vertebrates, this type of enzyme is commonly activated by serpentine receptors that couple to heterotrimeric G-proteins. ACA is expressed at high levels during aggregation. During slug formation expression is downregulated at the posterior region and becomes almost exclusively restricted to the tip (Pitt *et al.*, 1992; Verkerke-van Wijk *et al.*, 2001). ACA activity is regulated by a positive and a negative feedback loop, which causes some starving cells to spontaneously produce and secrete cAMP at regular

intervals. The positive loop is caused by self-stimulation of ACA by extracellular cAMP, while the negative loop is due to a cAMP-induced adaptation process (Martiel and Goldbeter, 1987; Tang and Othmer, 1994). cAMP-induced cAMP secretion in neighbouring cells causes propagation of the original pulse as a spiral or concentric cAMP wave through the cell population and chemotactic movement towards the signalling source. The regulation of ACA activity is remarkably complex and requires some factors for which there are as yet no counterparts in regulation of the vertebrate 12TM adenylyl cyclases (Figure 2).

The initial steps involve activation of the heterotrimeric G-protein G₂ by occupied cAMP receptors and formation of a free $\beta\gamma$ dimer (Lilly *et al.*, 1993; Wu *et al.*, 1995). In analogy to vertebrate systems, where the $\beta\gamma$ dimer directly binds to and activates PI3-kinase (Schwindinger and Robishaw, 2001), the *Dictyostelium* $\beta\gamma$ dimer is also supposed to activate a PI3-kinase, which converts the membrane lipid phosphatidylinositol [4, 5] bisphosphate (PIP₂) into the CRAC binding site phosphatidylinositol [3, 4, 5] trisphosphate (PIP₃). PIP₃ then recruits CRAC from the cytosol to the plasma membrane by binding to its pleckstrin homology domain (Dormann *et al.*, 2002). At this location CRAC can participate in ACA activation. This is not the whole story because ACA activation also requires the small G-protein RasC (Lim *et al.*, 2001), a Ras interacting protein, Rip3 (Lee *et al.*, 1999), the Ras nucleotide exchange factor, RasGEF (Insall *et al.*, 1996), the MAPkinase ERK2 (Segall *et al.*, 1995) and a novel factor Pianissimo (Chen *et al.*, 1997). How these proteins interact with each other and with ACA is not clear.

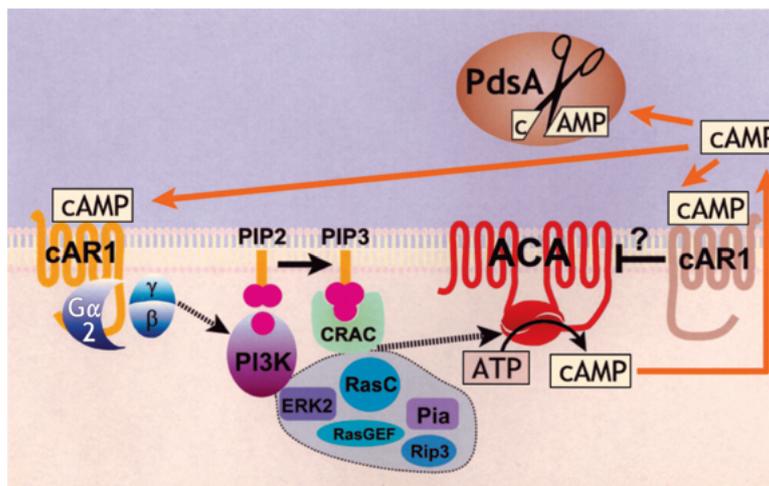


Fig. 2. Schematic of the regulation of adenylyl cyclase A: Binding of cAMP to the serpentine receptor cAR1 induces dissociation of the heterotrimeric G-protein, G₂, into its α and $\beta\gamma$ subunits. The $\beta\gamma$ subunits induce activation of phosphatidylinositol-3 kinase (PI3K) in a manner that is not yet understood. PI3K converts phosphatidylinositol [4, 5] bisphosphate (PIP₂) into phosphatidylinositol [3, 4, 5] trisphosphate (PIP₃). PIP₃ binds to the pleckstrin homology domain of CRAC, the Cytosolic Regulator of Adenylyl Cyclase and recruits CRAC from the cytosol to the plasma membrane, where it can participate in adenylyl cyclase A (ACA) activation. A set of proteins, including the MAPkinase, ERK2, the small G-protein, RasC, the guanine nucleotide exchange factor, RasGEF, the Ras interacting protein, Rip3, and a novel protein, pianissimo (Pia) are also required for ACA activation. The interactions of these proteins with each other and with CRAC and ACA have not yet been clarified. cAMP produced by ACA is rapidly secreted to further activate ACA in a positive feedback loop. Binding of cAMP to cAR1 blocks ACA activation via a negative feedback loop, that is little understood. Extracellular cAMP is degraded by the phosphodiesterase PdsA, which terminates both loops and returns cells to the basal excitable state.

The adaptation process of ACA has also not been resolved. Mammalian adenylyl cyclases are negatively regulated by inhibitory G-proteins (Hamm, 1998) or the activation process is terminated by receptor desensitization. In the case of serpentine receptors this is usually achieved by phosphorylation of the carboxy-terminal cytoplasmic tail and binding of arrestin (Ferguson and Caron, 1998). cAMP receptors are also phosphorylated during ligand binding (Klein *et al.*, 1985), but this does not terminate G-protein-coupled responses (Kim *et al.*, 1997b). A putative candidate for an inhibitory G-protein, G α 9, was recently identified. Deletion of G α 9 augments signalling centre initiation and subsequent aggregation, which suggests that a functional G α 9 negatively regulates ACA activation. However, periodic signalling still occurs in the G α 9 null cells, which indicates that adaptation through G α 9 cannot be the sole mechanism that terminates cAMP accumulation (Brzostowski *et al.*, 2002).

AcaA null cells show a similar phenotype to the previously identified *synag7* mutant. They show no cAMP-induced cAMP production and can only aggregate in synergy with wild-type cells. They fully differentiate into spores in chimeric fruiting bodies, which implies that ACA provides cAMP for extracellular cAMP signalling, but is not required for intracellular cAMP signalling and activation of PKA-dependent responses (Pitt *et al.*, 1992, 1993).

Oscillatory cAMP signalling not only controls aggregation, but is also considered to coordinate multicellular morphogenesis. The waves of cell movement that are the hallmark of oscillatory chemoattractant secretion have also been observed in slugs and fruiting bodies (Siegert and Weijer, 1992). Slug tips function as classical embryological organizers (Raper, 1940), and most likely do so by acting as pacemakers for cAMP oscillations. This is accentuated by high expression of ACA in slug tips (Verkerke-van Wijk *et al.*, 2001).

Adenylyl cyclase G

The *AcgA* gene is expressed in spores and its ablation has little effect on growth and development to fruiting bodies (Pitt *et al.*, 1992). cAMP levels are high in dormant spores and decrease rapidly when spores are activated for germination. High osmolarity prevents this drop in cAMP levels and inhibits the germination process (Virdy *et al.*, 1999). High osmolarity is maintained in the spore head by the presence of more than 100 mM ammonium phosphate (Cotter *et al.*, 1999). ACG is activated by high osmolarity and its activity blocks the germination process through activation of PKA (Figure 3). In *acgA* null mutants inhibition of spore germination by high osmolarity does not occur (Van Es *et al.*, 1996).

Activation of ACG by high osmolarity requires cellular integrity, but the mechanism is still obscure. Histidine kinases are implicated in sensing osmotic stress in bacteria and fungi (Santos and Shiozaki, 2001) and in

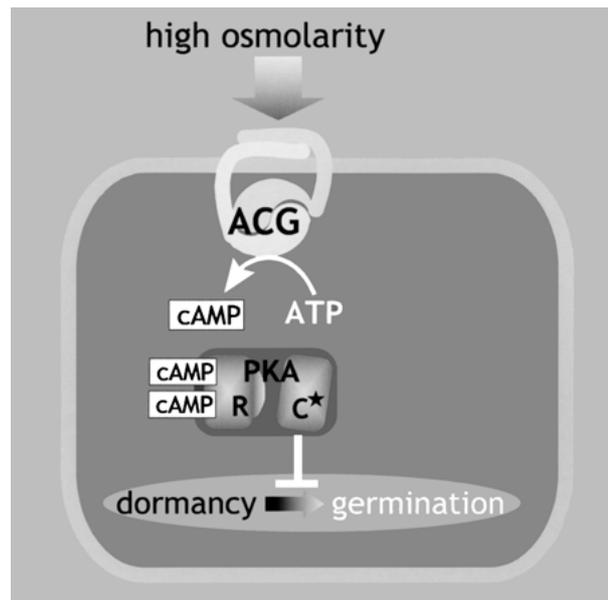


Fig. 3. Regulation of spore germination by high osmolarity: Ambient conditions of high osmolarity in the spore head activate adenylyl cyclase G (ACG) to produce cAMP. cAMP binds to the regulatory subunit (R) of cAMP dependent protein kinase (PKA), causing dissociation and activation of the catalytic subunit (C). Active PKA inhibits the germination process in an unknown manner.

Dictyostelium the histidine kinase DokaA mediates osmotic stress sensing. Osmotic stress causes a DokaA mediated increase in cAMP levels, which is however not achieved by activation of ACG, but by inhibition of the cAMP-phosphodiesterase RegA (Ott *et al.*, 2000). A relationship between ACG and histidine kinase mediated osmosensing is therefore not obvious. When full length ACG was expressed in yeast, it still showed stimulation by high osmolarity. This almost certainly implies that the osmosensor is intrinsic to the ACG protein (Saran and Schaap, preliminary results).

Adenylyl cyclase B

ACB is as yet the most enigmatic of the three adenylyl cyclases. The ACB gene, *AcrA*, is expressed at low levels during growth; transcripts accumulate to high levels after 4 h of starvation, to remain high up to the fruiting body stage. ACB shows greatest sequence and structural homology to the CyaC adenylyl cyclases from the cyanobacteria *Spirulina platensis* and *Anabena spirulensis* (Soderbom *et al.*, 1999). The cyanobacteria utilized their sodium-bicarbonate saturated sea-water habitat for photosynthesis and are considered to be responsible for transforming the pre-Cambrian carbon-dioxide rich atmosphere into the oxygen-rich atmosphere that allowed the Cambrian explosion of animal life (Ohno, 1997). cAMP is considered to play an important role in stimulating metabolic activity in response to light and carbon dioxide/bicarbonate. The two cyanobacterial adenylyl cyclases are activated by light through a dual component phosphorelay system (Yeh *et al.*, 1997;

Kasahara and Ohmori, 1999) and by bicarbonate through direct activation of the catalytic domain (Chen *et al.*, 2000).

Similar to CyaC, the ACB cyclase domain is preceded by a response regulator domain, that is the common target for phosphorelay, and by a histidine kinase domain. The latter domain may not be active in ACB, because it lacks an essential histidine residue for autophosphorylation and is also degenerate in other conserved regions (Soderbom *et al.*, 1999). The AcrA sequence displays two putative hydrophobic transmembrane regions and the ACB enzyme activity is associated with the particulate cell fraction. ACB can readily be measured in cell lysates in the presence of the RegA inhibitor IBMX. In intact cells ACB can only be measured when either RegA or its activator RdeA are absent (Kim *et al.*, 1998a; Meima and Schaap, 1999). ACB differs from most characterized class III ACs in showing higher activity with Mg^{2+}/ATP than with Mn^{2+}/ATP . ACB seems to be active whenever it is expressed and its activity is not influenced by cAMP, GTP γ S, DIF, ammonia or bicarbonate (Kim *et al.*, 1998a; Meima and Schaap, unpublished results). Although the tested signals do not exhaust the list of putative regulators of enzyme activity, the apparent constitutive activity of ACB points to a possibility that cAMP production by ACB is largely controlled by RegA activity.

cAMP breakdown

The inactivation of cyclic nucleotides by hydrolysis is often of greater importance for dynamic signalling than their synthesis. For appropriate regulation of second messenger responses, mammalian cells employ no less than 12 different classes of phosphodiesterases, which each contain several members. The carboxyterminal catalytic centre of these phosphodiesterases is conserved, but the enzymes differ in the sequence and structure of the aminoterminal region, which may contain single or multiple regulatory domains that control enzyme activity and anchoring to scaffolding proteins (Houslay and Milligan, 1997; Mehats *et al.*, 2002). This extensive level of complexity is not present in *Dictyostelium*, but five different cyclic nucleotide phosphodiesterases have presently been identified. Two of those, Pde3 and PdeD, are cGMP-specific phosphodiesterases and will only be briefly discussed. PdsA is a dual-specificity phosphodiesterase that hydrolyses cAMP and cGMP at an equal rate. RegA and PdeE are cAMP phosphodiesterases; RegA does not hydrolyse cGMP at all and PdeE does so at a six-fold lower rate than cAMP.

PdsA

The first enzyme to be biochemically identified and subsequently cloned is PdsA. PdsA is expressed in

starving cells and targeted both for secretion and for display on the extracellular face of the plasmamembrane (Malchow *et al.*, 1972; Gerisch, 1976). The activity of the secreted form of PdsA is regulated by a secreted inhibitor, PDI (Riedel and Gerisch, 1971; Franke and Kessin, 1981; Wu and Franke, 1990). PDI binds only to the soluble form of PDE and changes its K_M for cAMP from 5 μ M to 2 mM (Kessin *et al.*, 1979). Cloning of the PdsA gene revealed that its catalytic domain was unlike that of the mammalian phosphodiesterases, but similar to that of the low-affinity yeast enzyme PDE1 (Nikawa *et al.*, 1987). The *PdsA* gene is regulated by three promoters that control expression during growth, aggregation and multicellular development respectively (Faure *et al.*, 1990). The multicellular (late) promoter element is only active in prestalk cells (Hall *et al.*, 1993). *PdsA* null mutants cannot aggregate (Darmon *et al.*, 1978; Sugang *et al.*, 1997), but aggregation can be restored by expression of *PdsA* from the aggregative promoter, while restoration of slug and fruiting body formation requires expression from the late promoter (Sugang *et al.*, 1997). Overexpression of PdsA accelerates the aggregation process, but arrests tip formation and cell differentiation (Faure *et al.*, 1988). Neither ablation nor overexpression of any of the adenylyl cyclases has such profound effects on aggregation and development (Pitt *et al.*, 1992, 1993; Parent and Devreotes, 1996; Soderbom *et al.*, 1999), which emphasizes the crucial role of opposite regulation of hydrolysis of extracellular cAMP.

RegA

The cAMP-specific phosphodiesterase RegA was identified independently by two laboratories as the defective gene in a sporogenous mutant with accelerated development (Shaulsky *et al.*, 1996, 1998; Thomason *et al.*, 1998). A similar phenotype was found in *rdeC* mutants (Abe and Yanagisawa, 1983), which lack a functional PKA regulatory subunit (Simon *et al.*, 1992) and in *rdeA* mutants, which are defective in a phosphotransfer protein (Abe and Yanagisawa, 1983; Chang *et al.*, 1998). RegA is a remarkable hybrid of a bacterial type response regulator and a mammalian type PDE catalytic domain with a K_M for cAMP hydrolysis of 5 μ M (Shaulsky *et al.*, 1996; Thomason *et al.*, 1998). *RegA* transcripts appear after 4 h of starvation and thereafter remain present at constant levels. The expression of *RegA* is uniform in young slugs, but becomes localized at the prestalk upper cup region during culmination (Shaulsky *et al.*, 1996; Tsujioka *et al.*, 2001). RegA protein is most abundant during aggregation. However, in contrast to *RegA* mRNA levels, RegA protein levels decrease strongly after slug formation (Thomason *et al.*, 1998). This down-regulation appears to be essential for induction of prestalk and prespore genes and involves two scaffolding proteins, CulA and FbxA/ChtA, that target RegA for ubiquitination and degradation (Mohanty *et al.*, 2001).

Both *regA* and *rdeA* null mutants show elevated cAMP levels, which suggests a causal link between the two. This was demonstrated in an elegant series of experiments by Thomason and coworkers. Eukaryote phosphotransfer systems are initiated by an activated histidine kinase which autophosphorylates itself on a conserved histidine residue and relays the phosphate to a receiver aspartate residue within the same protein (Figure 4). In a series of His–Asp phosphotransfer steps, the phosphate is finally delivered to an aspartate in the response regulator domain of the target protein (Santos and Shiozaki, 2001). The V_{max} of the RegA PDE activity is 20-fold increased by phosphorylation of Asp²¹² in its response regulator region (Thomason *et al.*, 1999). RdeA shows a consensus histidine (His⁶⁵) in a region of 20 amino-acids that is conserved in histidine phosphotransfer proteins (Chang *et al.*, 1998). Thomason *et al.* (1999) showed that when RdeA was phosphorylated on His⁶⁵ *in vitro*, the phosphate was carried over to the Asp²¹² of RegA, thereby activating the enzyme activity. Conversely, when RegA was phosphorylated on Asp²¹², it could relay a phosphate to the His⁶⁵ of RdeA. Depending on the relative concentrations of the phosphodonor proteins, the RegA PDE activity can be both positively and negatively regulated by phosphorelay (Thomason *et al.*, 1999). The *Dictyostelium* histidine kinase DhkC may act as a positive regulator of RegA activity (Figure 4A). Similar to *regA* null cells, *dhkC* null cells show rapid develop-

ment, without a migrating slug stage. DhkC is proposed to be activated by ammonia, which induces prolonged slug migration and inhibits terminal differentiation (Singleton *et al.*, 1998). Earlier work indicated that loss of ammonia gas from culminants triggered spore and stalk maturation (Schindler and Sussman, 1977; Wang and Schaap, 1989), supposedly by releasing a block on PKA activity (Harwood *et al.*, 1992; Hopper *et al.*, 1993b). This can now be understood in terms of activation of RegA by ammonia and subsequent inhibition of cAMP accumulation and PKA activation.

DhkA and DhkB are putative negative regulators of RegA. In addition to the histidine kinase domain, both proteins harbour putative transmembrane domains and an extracellular putative sensor domain (Zinda and Singleton, 1998; Wang *et al.*, 1999). The proposed ligand for DhkA is SDF-2, a factor that is secreted by prestalk cells to induce the maturation of spores (Anjard *et al.*, 1998; Wang *et al.*, 1999). *dhkA* null mutants are defective in spore maturation and this defect can be suppressed by abrogation of RegA function or constitutive activation of PKA. This suggests that RegA and PKA act downstream of DhkA in a scenario where binding of SDF-2 to DhkA inhibits RegA (Wang *et al.*, 1999) and thereby permits PKA activation and spore maturation (Figure 4A). The proposed ligand for the sensor domain of DhkB is discadenine (Figure 4B), an inhibitor of spore germination that is released in the spore head (Zinda and Singleton, 1998). The spores of

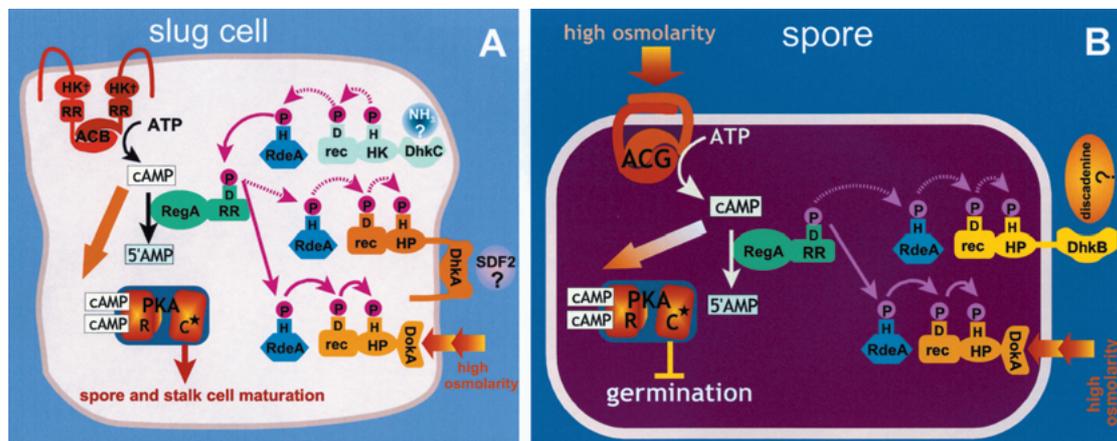


Fig. 4. Network for regulation of terminal differentiation and spore dormancy: (A) In slug cells cAMP is predominantly produced by adenylyl cyclase B, which harbours a single cyclase domain, a response regulator (RR) and a histidine kinase homology domain (HK) that is probably not functional (†). cAMP activates PKA, which will induce the terminal differentiation of spore and stalk cells. cAMP levels are stringently regulated by the cAMP-phosphodiesterase RegA, which is active when phosphorylated on Asp²¹² in its response regulator domain (RR). The phosphorylated state of RegA is controlled by histidine kinases/phosphatases with attached sensor domain. The phosphotransfer protein RdeA acts as intermediate for bidirectional phosphorelay. DhkC functions as a histidine kinase, which is activated by binding of its supposed ligand NH₃ to the sensor domain. DhkC first autophosphorylates itself on a conserved histidine. The phosphate is then relayed to a conserved aspartate in the DhkC receiver domain (rec) and subsequently *via* RdeA to RegA, thereby activating RegA. DhkA and DokA function as histidine phosphatases (HP) when sensing their supposed stimuli SDF-2 and high osmolarity. They reverse the direction of phosphorelay by acting as phosphate sinks and inactivate RegA. (B) In spores cAMP is mainly produced by ACG. RegA also controls cAMP levels at this stage and is negatively regulated by DhkB, which is proposed to act as a histidine phosphatase when bound to discadenine, an inhibitor of spore germination. DokA may act in parallel to ACG at the spore stage to maintain the dormant state under high osmolarity conditions. The phosphate transfers that are indicated by solid arrows in these figures have been confirmed by biochemical methods. The processes indicated by dashed arrows as well as all supposed ligands of the Dhk's are inferred from epistatic relationships, null mutant phenotypes and homologous processes in other organisms.

the *dhkB* null mutant germinate precociously in the spore head. This phenotype can be reversed by constitutive activation of PKA, indicating that also here PKA acts downstream of DhkB (Zinda and Singleton, 1998).

DokA is a third negative regulator of RegA and *dokA* null cells also form fruiting bodies without viable spores. This effect has not yet been pinpointed to either a defect in spore maturation or to precocious germination (Schuster *et al.*, 1996). The *dokA* genetic lesion also affects general cell physiology, because *dokA* null cells cannot withstand hyperosmolarity and do not show the increase in cAMP levels that wild-type cells show in response to osmotic shock. This increase is due to a DokA-triggered and RdeA-mediated inhibition of RegA activity and DokA was shown to dephosphorylate RdeA *in vitro* (Ott *et al.*, 2000). DokA contains a sensor domain, but no putative transmembrane domains and resides most likely in the cytosol (Schuster *et al.*, 1996). The absence of spores in *dokA* null fruiting bodies can have two causes: (i) high osmolarity acts as on DokA as an additional signal for spore maturation (Figure 4A) or (ii) high osmolarity acts on DokA and ACG in parallel to raise cAMP levels and inhibit (precocious) spore germination (Figure 4B). For all negative regulators of RegA, the ligands of the Dhk sensor domains probably act to revert the histidine kinase into a phosphatase, which turns them into phosphate sinks and revert the phosphorelay reaction (Ott *et al.*, 2000).

The identification of RegA and its interacting factors has provided the molecular framework to understand the signalling networks that regulate terminal differentiation and spore germination in *Dictyostelium*. However, it must be realized that the proposed roles of all histidine kinases/phosphatases have thus far only been inferred from epistatic relationships and that all the proposed ligands have yet to be shown to bind to specific Dhk sensor domains and activate catalytic activity.

In addition to effects on gene regulation, RegA null mutants show defects in oscillatory cAMP signalling and in chemotaxis (Wessels *et al.*, 2000). The signalling defect has been attributed to loss of negative feedback on cAMP production (Laub and Loomis, 1998). The chemotaxis defect is due to a failure to suppress lateral pseudopods, which normally contributes to polarized movement of cells in a chemotactic gradient (Wessels *et al.*, 2000). This points to an as yet undocumented role for intracellular cAMP in chemotaxis.

PdeD and PdeE

Two PDEs were identified by screens of the genomic databanks with consensus motifs for cyclic nucleotide binding domains (Goldberg *et al.*, 2002; Meima *et al.*, 2002; 2003) and named GbpA and GbpB by Goldberg *et al.* (2002) and PdeD and PdeE by Meima and coworkers. They both harbour two cyclic nucleotide binding motifs, preceded by a metallo- β -lactamase domain. Truncated proteins containing solely this motif displayed cyclic nucleotide phosphodiesterase activity

(Meima *et al.*, 2002). The *PdeD/GbpA* gene was found to encode the cGMP-stimulated cGMP phosphodiesterase that is lacking in *stmF* mutants (Ross and Newell, 1981; Bosgraaf *et al.*, 2002; Meima *et al.*, 2002). The second cGMP-specific phosphodiesterase, PDE3 is homologous to the mammalian PDEs (Kuwayama *et al.*, 2001). *PdeE/GbpB* encodes a hitherto unidentified cAMP-stimulated cAMP-phosphodiesterase activity, that shows very pronounced expression during aggregation. PdeE has a low affinity for cAMP as substrate ($K_M = 1$ mM), but is about four-fold stimulated by cAMP with a K_A of 3 μ M. PdeE null mutants aggregate and develop normally. They show a modest augmentation of the cAMP relay response, which suggests that PdeE may contribute to the negative feedback loop of oscillatory cAMP signalling (Meima *et al.*, 2003; Bosgraaf *et al.*, 2002).

cAMP detection

cARs

Extracellular cAMP is detected by G-protein coupled serpentine receptors. Four receptors, in order, cAR1, cAR3, cAR2 and cAR4 are expressed during progressively later stages of development (Klein *et al.*, 1988; Johnson *et al.*, 1993; Saxe III *et al.*, 1993; Louis *et al.*, 1994). The major differences in amino-acid sequence between the receptors are localized in the carboxy-terminal cytoplasmic domain. The receptors show a decrease in affinity which correlates with their timing of expression, with the highest affinity receptor being expressed the earliest (Johnson *et al.*, 1992; Kim *et al.*, 1997a). All four cARs can couple to all investigated cAMP-activated signal transduction pathways, such as chemotaxis, ACA and guanylyl cyclase activation, Ca^{2+} influx and gene regulation. It is assumed that the expression of receptors with lower affinity during multicellular development reflects an adjustment to higher ambient cAMP levels in multicellular structures (Milne and Devreotes, 1993; Verkerke VanWijk *et al.*, 1998; Kim *et al.*, 1998b). Serpentine receptors typically use heterotrimeric G-proteins as intermediates for signal transduction and this is the case for cAR-mediated activation of chemotaxis, ACA, guanylyl cyclase and phospholipase C and for induction of aggregative gene expression. cAR mediated induction of Ca^{2+} influx, ERK2 activation, StatA translocation to the nucleus and prespore gene expression do not require heterotrimeric G-proteins (Milne *et al.*, 1995; Wu *et al.*, 1995; Maeda *et al.*, 1996; Araki *et al.*, 1998; Jin *et al.*, 1998). The immediate targets for cARs in these responses are still obscure.

PKA

PKA plays a very dominant role in regulation of development. The *Dictyostelium* PKA holoenzyme consist of one catalytic (PKA-C) and one regulatory

domain (PKA-R) (Mutzel *et al.*, 1987). This differs from the vertebrate enzymes, which consist of dimers of each domain. Disruption of the *PKA-C* gene or overexpression of a dominant-negative form of *PKA-R* under constitutive or cell-type specific promoters has shown that PKA is required for the growth to development transition (Schulkes and Schaap, 1995; Endl *et al.*, 1996; Mann *et al.*, 1997), the control of developmental timing (Simon *et al.*, 1992), the differentiation of prespore cells (Hopper *et al.*, 1993b), the terminal maturation of spores and stalk cells (Harwood *et al.*, 1992; Mann *et al.*, 1994) and the control of spore germination (Van Es *et al.*, 1996). For most of these responses, the activation of the PKA-C is achieved through binding of cAMP to PKA-R, followed by dissociation of the R-C complex. However, at the onset of starvation PKA-C activity is also controlled by regulation of its translation. During growth, the translational regulator PufA binds to conserved motifs at the 3' end of the PKA-C transcript, thereby inhibiting PKA-C translation (Souza *et al.*, 1999). Growing cells secrete the prestarvation factor PSF at a constant rate and use the level of accumulated PSF to measure nutrient status relative to cell density (Clarke and Gomer, 1995). The high levels of PSF that accumulate when cells start to starve trigger the transcription of a protein kinase, YakA, which inhibits the function of PufA, allowing PKA-C to accumulate. YakA also induces cell cycle arrest independently from its effects on PufA. The two effects cause the cells to stop growing and initiate multicellular development (Souza *et al.*, 1999).

Recent work shows that YakA can be directly activated by a variety of stress factors, including heat and oxidative stress, which results in growth arrest and PKA activation (Taminato *et al.*, 2002). In combination with earlier work showing that osmotic shock can cause PKA activation both through RegA repression (Ott *et al.*, 2000) and ACG activation (Van Es *et al.*, 1996), these data highlight that *Dictyostelium* development is in essence a stress response.

Future challenges

Gene regulatory pathways

Recent years have seen major advances in understanding the interpretation of cAMP as a chemotactic signal by the cell and the cytoskeletal reorganization that is instrumental for coordinated cell movement. With respect to the control of gene expression by extracellular cAMP our knowledge is still fragmentary. Tagged mutagenesis has proven to be an excellent tool to uncover many novel components of the gene regulatory pathways (Kuspa and Loomis, 1992), but it has not yet been possible to reconstruct a single pathway from cAR activation to gene transcription. Screens for suppressor mutants have been used to great advantage to find interacting partners in signal transduction (Shauly

et al., 1996; Bear *et al.*, 1998; Souza *et al.*, 1999) and the use of DNA microarrays may systematically identify all proteins with altered expression in a specific mutant or during a specific gene induction response (Van Driessche *et al.*, 2002). In combination with more classical molecular genetic-, immunological- and biochemical tools to detect protein-protein interactions, these strategies should allow us to find the missing links within the next 10 years.

Targets for PKA and compartmentalization of signalling

Despite the prominent role for PKA at virtually all stages of development, the direct targets are thus far unknown. There is genetic evidence for the regulation by PKA of the transcription factor Myb2 and the nuclear factor CudA, but evidence for direct phosphorylation by PKA is lacking (Fukuzawa *et al.*, 1997; Otsuka and Van-Haastert, 1998). PKA activity has been found both in the cytosol and the nucleus (Woffendin *et al.*, 1986), suggesting compartmentalization of cAMP signalling. In metazoans, PKA is targeted to different subcellular locations by a family of A-kinase anchoring proteins (AKAPs), that bind to the dimerization domain of PKA-R, and to a wide variety of other signalling molecules (Houslay and Milligan, 1997; Feliciello *et al.*, 2001). For example, muscle-selective AKAP forms a signalling module in which the activity of the cAMP-specific phosphodiesterase PDE4D3 is regulated by the anchored PKA holoenzyme (Dodge *et al.*, 2001). In *Dictyostelium*, there is biochemical evidence for the presence of cAMP signalling modules. PKA-R binds to RegA and stimulates its activity at least 18-fold (Shauly *et al.*, 1998). RegA only weakly affects cAMP production by ACA, but effectively annihilates the levels of cAMP produced by ACB, suggesting a close proximity between ACB and RegA (Kim *et al.*, 1998a; Meima and Schaap, 1999). It is tempting to suggest the presence of a signalling complex of these enzymes that would allow tight control of cAMP production until the proper signals for terminal differentiation are detected. No AKAPs have been identified in the *Dictyostelium* genome so far and the *Dictyostelium* PKA-R subunit lacks the dimerization domain, that is essential for binding to AKAPs. However, the different vertebrate AKAP families show similarity in secondary structure rather than in protein sequence (Feliciello *et al.*, 2001). Therefore, the presence of functional homologues with different target binding sites in *Dictyostelium* cannot be excluded.

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