

P009 cGMP signalling in epithelial transport
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cGMP signalling, like cAMP signalling, is central to many physiological processes. However, the *in vivo* roles for cGMP, and mechanisms of spatio-temporal control of cGMP, are still relatively poorly understood. In order to address the complexities of organotypic roles for cGMP signalling, a transgenic approach using the model organism, *D. melanogaster*, can be useful. Recent curation and characterisation of the *Drosophila* PDE family show that six PDEs are encoded, including the cAMP-specific PDE, *dunce*. Several of the novel *Drosophila* PDEs are close homologues of vertebrate PDEs which act on cGMP, including *Dm* PDE1, *Dm* PDE6 and *Dmp*PDE11.

Targeted expression of an endogenous cGMP-specific PDE (cG-PDE), PDE6, and ectopically expressed bovine cG-PDE (PDE5A), *in vivo*, show that cG-PDEs are localised to the apical membrane of the *Drosophila* Malpighian (renal) tubule principal cells. *Dm*PDE6 has also recently been shown to directly modulate active transport of cGMP by the tubule. Furthermore, endogenous *Drosophila* cGMP-dependent kinases are specifically localised to either the apical / basolateral membranes or in the cytosol of tubule cells and differentially affect stimulated fluid transport. Thus, the localisation of cG-PDEs/cGKs allows for specificity of cGMP signalling in epithelial cells; and so must direct epithelial function.