

Poster presentation

## From biochemical and structural studies of soluble guanylate cyclase toward drug design

Emmanuelle Laffly\*, Jane Macdonald and Elsa Garcin

Address: Department of Chemistry and Biochemistry, University of Maryland Baltimore County, Baltimore Maryland, USA

Email: Emmanuelle Laffly\* - [elaffly@umbc.edu](mailto:elaffly@umbc.edu)

\* Corresponding author

from 4th International Conference of cGMP Generators, Effectors and Therapeutic Implications  
Regensburg, Germany. 19–21 June 2009

Published: 11 August 2009

BMC Pharmacology 2009, 9(Suppl 1):P39 doi:10.1186/1471-2210-9-S1-P39

This abstract is available from: <http://www.biomedcentral.com/1471-2210/9/S1/P39>

© 2009 Laffly et al; licensee BioMed Central Ltd.

The heterodimeric haemoprotein soluble guanylate cyclase (sGC) is the direct sensor and mediator of nitric oxide (NO) signal transduction via the NO-sGC-cGMP pathway. Aberrant sGC-dependent signalling may be fundamental to the aetiology of a wide variety of cardiovascular pathologies. As a consequence, compounds that activate cGMP production by sGC have a considerable therapeutic potential.

To date, x-ray structures of independent sGC domains HNOX, HNOX-A and GC have been solved. Nevertheless, the determination of the full-length sGC x-ray structure would provide additional clues to understand the structural basis for the mechanism of sGC assembly and regulation and should facilitate the design of these therapeutic agents.

To achieve this goal, I developed a heterologous expression system of full-length bovine sGC (Fl-sGC). Early attempts to produce recombinant bovine sGC in *E. coli* resulted in misfolded protein accumulation. Indeed, producing soluble protein in *Escherichia coli* is still a major difficulty in the sGC field. By using fusion technology, I successfully overexpressed both  $\alpha$  and  $\beta$  subunits in a soluble heme-bound active form. Optimization of expression levels by varying bacterial growth conditions including temperature, media, additives and induction, will be followed by purification and characterization of Fl-sGC. So, a crucial step has been achieved, allowing us to pursue structural studies to probe the structure and

mechanism of sGC and promote the discovery of stimulators of this physiologically important enzyme.