MOLECULAR SWITCH MECHANISMS REGULATING NITROGEN FIXATION IN *AZOTOBACTER VINELANDII*

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The oxygen sensitivity of nitrogenase and the considerable energetic input required for dinitrogen reduction necessitates stringent regulation of nitrogen fixation genes at the transcriptional level. This regulation is exerted in response to the redox, fixed nitrogen and carbon status via signalling mechanisms that control the activity of the NifA transcriptional activator. In some representatives of the proteobacteria NifA activity is regulated by the anti-activator NifL. The NifL-NifA system represents a multi-domain signalling complex in which protein-protein interactions are modulated by redox changes, ligand binding and interactions with the signal transduction protein GlnK. Although NifL has a domain architecture similar to that of histidine protein kinases it does not exhibit kinase activity but modulates NifA activity directly by protein-protein interactions. NifL has four domains, two of which are involved in discrete sensing of the redox and nitrogen status. We will present data that reveals how the domains of NifL can collaborate to bring about conformational changes that switch NifL between active and inactive states.