

P028 Study of Irr: an iron responsive regulator in *Rhizobium leguminosarum*

Chloe Singleton, Gaye White, Jonathan Todd,

Nick Le Brun, Andrew Johnston

University of East Anglia

Maintaining iron homeostasis by responding to Fe availability is vital to life. Bacteria are known to regulate the expression of genes involved in the uptake and metabolism of Fe. The most studied Fe-responsive gene regulator is Fur found in (for example) *E.coli*, *Pseudomonas* and *Bacillus*. Fur reversibly complexes Fe and in Fe-replete cells Fe-Fur binds to conserved 'fur boxes' on DNA where it acts as a repressor of many genes. In the N₂-fixing α -proteobacterium *Rhizobium leguminosarum* an alternative, more sophisticated method that regulates gene expression in response to physiological forms of Fe has been identified. This involves two different Fe-responsive gene regulators; RirA that represses >100 genes in Fe-replete conditions and Irr that represses a different, but partially overlapping, suite of genes when Fe is scarce. Recent work on free living *Rhizobium* cells indicates that RirA interacts with FeS clusters and Irr acts in response to heme. Due to the cytotoxicity of porphyrins, the heme pathway must be co-ordinated with the cellular Fe level. Irr is believed to play an important role in coupling heme synthesis to Fe availability. This study aims to follow the response of Irr to varying Fe levels *in vivo* and use spectroscopic analysis to investigate its heme-binding properties *in vitro*.