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YOU ARE INVITED TO ATTEND THE

DEFENSE OF THE DOCTORAL

DISSERTATION

"Structure-function studies of the *Bacillus subtilis* Ric proteins identify the Fe-S cluster-ligating residues and confirm their roles in development and RNA processing"

by

Felix Adusei-Danso

Infection, Immunity and Inflammation Program

B.S., University of Science & Technology, Kumasi, Ghana, 2000

M.S., University of Cape Town, South Africa, 2006

Thesis Advisor, David Dubnau, Ph.D.
Professor
Public Health Research Institute (PHRI)

Tuesday, September 10th, 2019
11:00 A.M.
ICPH Auditorium, First Floor

ABSTRACT

In *Bacillus subtilis*, the RicA (YmcA), RicF (YlbF) and RicT (YaaT) proteins accelerate the phosphorylation of the transcription factor Spo0A, contributing to genetic competence, sporulation and biofilm formation and are also essential for the correct maturation of several protein-encoding and riboswitch RNAs. These proteins form a stable complex (RicAFT) that carries two $[4Fe\text{-}4S]^{+2}$ clusters. We show here that the complex is a 1:1:1 heterotrimer and we present the X-ray crystal structures of a RicAF heterotetramer and of a RicA dimer. We also demonstrate that one of the Fe-S clusters (cluster 1) is ligated by cysteine residues donated exclusively by RicT and can be retained when the RicT monomer is purified by itself. Cluster 2 is ligated by C167 from RicT, by C134 and C146 located near the C-terminus of RicF and by C141 at the C-terminus of RicA. These findings imply a novel arrangement; the adjacent RicT residues C166 and 167 ligate clusters 1 and 2 respectively, while cluster 2 is ligated by cysteine residues from RicT, RicA and RicF. Thus, the two clusters must lie close to one another and at the interface of the RicAFT protomers. We also show that the cluster-ligating cysteine residues, and therefore most likely both Fe-S clusters, are essential for *cggR-gapA* mRNA maturation, for the regulation of *ricF* transcript stability and for several Ric-associated developmental phenotypes including competence for transformation, biofilm formation and sporulation. Finally, we present evidence that RicAFT, RicAF, RicA and the RicT monomer may play distinct regulatory roles *in vivo*.