Structural Proteomics of Proteins Coded by the *cag* PAI of *Helicobacter pylori*

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H. pilory is a Gram-negative bacterium that colonizes the stomach of probably half of the human population. It is associated with gastritis, peptic ulcers and mucosa-associated lymphoid tissue lymphomas. Many factors contribute to the virulence of *H. pylori* [1]. Among them, the enzyme urease, the Neutrophil Activating Protein, NAP [2] and the secreted protein toxin VacA. However, the major genetic difference in HP isolates is the presence or absence of a specific pathogenicity island, named *cag*-PAI. It is a 40-kb locus that contains about 30 ORFs, whose function is unknown, with few exceptions.

We have cloned, expressed, and purified several proteins of the *cag* pathogenicity island of *H. pylori*. They all have been expressed in *E. coli*. We have already solved the structure of CagZ, using the Se-Met method [3] and the structure will be described in detail. We have also obtained crystals of a second protein, CagS, and its structure determination is in progress, along with crystallization tests on other *cag* proteins. Our final goal is to determine, in collaboration with other groups [4], most of the proteins coded by the *cag*-PAI island.

[1] Covacci, et al., *Science*, 1999, **284**, 1328. [2] Zanotti, et al., *J. Mol. Biol*., 2002, 323, 125-130. [3] Cendron L., Seydel A., Angelini A., Battistutta R., Zanotti G., *J. Mol. Biol.,* 2004, **340,** 881. [4] *The Helicopter Structural and Molecular Biology Consortium.*

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