[O7]

A *Drosophila* model for the study of *Shigella* virulence factors.

M Kawalec*[1], M Ogawa[2], C Punginelli[2], V Leclerc[1], C Sasakawa[2], J-M Reichhart[1]

[1]IBMC UPR 9022 CNRS, University of Strasbourg, 15 rue Rene Descartes, 67084 Strasbourg, France, [2]Institute of Medical Science, The University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo, Japan

Shigella spp. are very infectious bacterial pathogens transmitted by the fecal-oral route in humans and primates. Majority of bacterial diarrhea incidencies, of which 1.1 million is fatal every year and happen mostly in children below 5 are attributed to *Shigella*. The symptoms of shigellosis (ranging from watery diarrhea to severe dysentery with cramps, fever and mucoid, bloody stools) are due to the complex action of numerous virulence factors. Important part in pathogenesis of shigellosis is played by multiple effectors of the type III secretion system (T3SS) and by the responses that these effectors elicit from host cells.

As the only available model host for shigellosis today are primates, we undertook to develop the fruit fly, *Drosophila melanogaster*, as an alternative host model, with the goal to study the interaction of the T3SS effectors with the host cell. We used the classical Gal4/UAS system to direct the expression of some of these effectors to the *Drosophila* eye during development and obtained several clear phenotypes. The latest results will be discussed.

Keywords: bacterial virulence, T3SS effectors, Drosophila model, Shigella flexneri