

What can endosymbionts tell about the *Harmonia axyridis* invasion?

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Maternally-inherited endosymbiont bacteria are widespread among arthropod species (Hurst and Jiggins, 2000; Zchori-Fein and Perlman, 2004; Hilgenboeker *et al.*, 2008). Recent studies on large samples of ladybirds showed that 52% of the species were infected with *Wolbachia*, *Rickettsia* or *Spiroplasma* (Weinert *et al.*, 2007). To maintain themselves in their host population, these bacteria can dramatically alter their host's reproduction strategy by inducing parthenogenesis or cytoplasmic incompatibility, by feminization or by selectively killing infected males (O'Neill *et al.*, 1997). Alternatively, an increasing number of studies show that endosymbionts can mediate pathogen resistance in their hosts (Brownlie and Johnson, 2009).

Understanding the factors determining the invasion success of alien species is a major challenge of invasion biology. *Harmonia axyridis*, with its widespread distribution and the rapidity, at which it expanded its geographic range, is the ideal system to study the role of intrinsic and extrinsic traits on invasive potential. Extensive human-mediated movement of *H. axyridis* poses limitations to population genetics methods (microsatellites) used to characterize its invasion routes (Lombaert *et al.*, 2010). Sequence information of *Helicobacter pylori*, a chronic gastric pathogen of human beings was successfully used to answer unsolved questions about human migrations in the past (Falush *et al.*, 2003). The great genetic diversity among bacterial populations and the limited linkage disequilibrium between polymorphic nucleotides within genes because of frequent recombination between bacterial strains (Baldo *et al.*, 2006) suggest that sequence information of bacteria associated with insect species may provide valuable information on the host's population genetics.

In a collaborative project we are currently combining endosymbiont incidence and prevalence data with endosymbiont phylogenies to i) describe the endosymbiont community in the native and invaded range of *H. axyridis*, ii) assess the direction of spread of *H. axyridis*, iii) estimate the number of introduction events and iv) evaluate the role of endosymbionts on the invasive success of the Asian ladybird.

We believe that this study will shed light on the invasion success of *H. axyridis* and provide valuable information on the potential of endosymbionts as additional molecular tools.

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