

OMAR

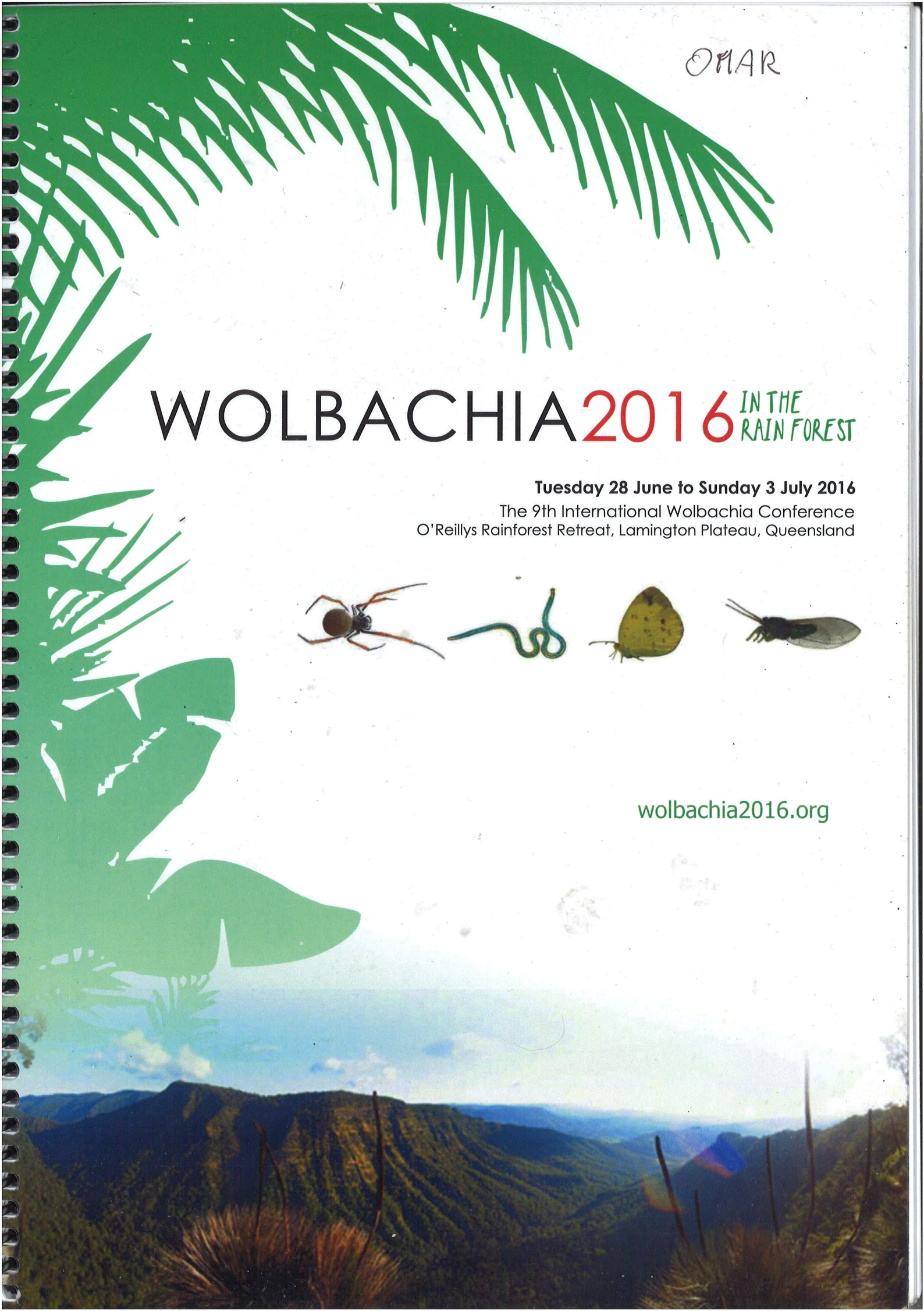
WOLBACHIA2016 IN THE RAIN FOREST

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The 9th International Wolbachia Conference
O'Reillys Rainforest Retreat, Lamington Plateau, Queensland



wolbachia2016.org



Towards a molecular clock of *Wolbachia*

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Timing the evolutionary history of *Wolbachia* is a complex and widely unexplored task. Classical molecular clock techniques have the potential to answer this question, but they are complicated by a general lack of priors needed to calibrate substitutions: absence of fossil records, shortage of generic replacement rates, and host co-divergences that cannot be trusted because of frequent lateral transfer. Regardless of these problems, we are systematically attempting a molecular clock of *Wolbachia* using different approaches. In a first approach we are comparing genomes of *Wolbachia* harboured by closely related sister species hosts: replacements between *Wolbachia* genomes are calibrated with the divergence of the hosts, and the resulting rates are used to calibrate a genome-scaled phylogeny of *Wolbachia*. In a second approach we are calibrating a small dataset of housekeeping genes using known divergence of distant outgroups such as Gammaproteobacteria. We are also attempting to use previously suggested replacement rates for intra-specific *Drosophila* host populations, as well trying to indirectly infer mutation rate by comparing levels of polymorphism in co-hosted mitochondria and *Wolbachia* populations, and by studying the mutation rate of *Wolbachia* genomes integrated in the host genomes. Although our analyses are still ongoing, we aim at discussing the *pro et contra* of our approaches and some preliminary results with the *Wolbachia* community.