Characterization and expression profiling of microRNAs associated to host-plant adaptation in Lepidopteran pests of corn

S. GIMENEZ, Y. Moné, S. Nhim, F. Legeai, I. Seninet, H. Parrinello, N. Nègre, E. d'Alençon Diversity, Genomes and Insect - Microorganisms Interaction (DGIMI), Univ. Montpellier, INRAE, 34095 Montpellier, France sylvie.gimenez@inrae.fr

A change in the environment may impair development or survival of living organisms leading them to adapt to the change. The resulting adaptation trait may reverse, or become fixed in the population leading to evolution of species. Deciphering the molecular basis of adaptive traits can thus give evolutionary clues. In phytophagous insects, a change in host-plant range can lead to emergence of new species. Among them, *Spodoptera frugiperda* is a major agricultural lepidopteran pest consisting of two host-plant strains having diverged 3 MA, based on mitochondrial markers. In this work, we addressed the role of microRNAs, important gene expression regulators, in response to host-plant change and in adaptive evolution.

Using small RNA sequencing, we characterized miRNA repertoires of the corn (C) and rice (R) strains of *S. frugiperda*, expressed during larval development on two different host-plants, corn and rice, in the frame of reciprocal transplant experiments. We provide evidence for 76 and 68 known miRNAs in C and R strains and 139 and 171 novel miRNAs. Based on read counts analysis, 34 of the microRNAs were differentially expressed in the C strain larvae fed on rice as compared to the C strain larvae fed on corn. Twenty one were differentially expressed on rice compared to corn in R strain. Nine were differentially expressed in the R strain compared to C strain when reared on corn. A similar ratio of microRNAs was differentially expressed between strains on rice. We could validate experimentally by QPCR variation in expression of the most differentially expressed candidates. We used bioinformatics methods to determine the target mRNAs of known microRNAs. Comparison with the mRNA expression profile during similar reciprocal transplant experiment revealed potential mRNA targets of these host-plant regulated miRNAs

In summary, we performed the first systematic analysis of miRNAs in Lepidopteran pests feeding on host-plants. We identified a set of the differentially expressed miRNAs that respond to the plant diet, or differ constitutively between the two host plant strains. Among the latter, the ones that are also deregulated in response to host-plant are molecular candidates underlying a complex adaptive trait.