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Salle de réunion + visio

SCHISTOSOMIASIS, HYBRIDIZATION AND ZOONOSIS: TOWARDS AN INTEGRATIVE VIEW OF THE PATHOSYSTEM

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- Schistosomiasis is second only to malaria in terms of human heath and social-economic impacts worldwide. This debilitating parasitic disease affects the poorest communities around the world, mainly in Africa. Molecular techniques have substantially improved our understanding of schistosomes transmission patterns but have also shed light on new challenges that remain to be addressed. Whatever historic or recent, an increasing number of human-infecting schistosomes are now identified with signatures of interspecific hybridization and introgression. In particular, hybrids between *Schistosoma haematobium* and *Schistosoma bovis*, two species causing urogenital or intestinal schistosomiasis in human and livestock, respectively, are widespread in several African foci. Importantly, in 2013, these last hybrid forms where involved in the emergence of schistosomiasis in Europe (Corsica, France). The biological invasion of a hybrid strain hitherto limited to tropical and subtropical areas raises several questions about the invasive capacities, virulence and the health risks of such hybrid pathogens in Europe or on the African continent.
- During this presentation, I will first present the complex and unexpected epidemiological case study of the Corsican outbreak as well as the molecular characterization of the parasites involved. I will then focus on our current understanding of the eco-evolutionary and public heath consequences of such admixture on the parasites' life history traits. Starting from the field, an experimental evolution protocol allowed us to generate several hybrid lines with different introgression levels using crosses and backcrosses from both parental species. Several life history traits modifications (regarding the parasites interactions with their intermediate hosts and an experimental vertebrate host) and molecular features (genomics and transcriptomics) have been compared between parental species and their natural hybrids from Corsica. Our results suggest that hybridization may represent a major evolutionary force for parasites. First, mating choice experiments and molecular characterisation of homo- vs. hetero-specific pairs show that hybridization between *S. haematobium* and *S. bovis* may be common. Second, hybrids display heterosis across the parasite's life cycle, increasing their transmission both towards intermediate snail hosts and the experimental vertebrate host. However, hybrids are also more virulent and cause increased morbidity compared to parental strains. These results underlie (i) the potential risk of disease spread and emergence out of its endemic range where suitable fresh water molluscs may be present and (ii) the importance of host pathology which cannot be disregarded in zones where two parasite species may hybridize.

At last, I will briefly expose my current (CBGP Postdoctoral project) and future project (IRD proposal) that both aim for an integrated "One health" view of the pathosystem as well as the implementation of adequate procedures allowing a sustainable control of the disease.

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