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Session 2: Space-time and multi-scales approaches: diagnostic, epidemiology and ecology in the field

When a plant pathogen runs down a river: population genetics of the poplar rust epidemics in the Durance River valley.

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Tracking pathogen movement, identifying source populations and understanding environmental factors, including human activities, that influence pathogen spread are central tasks in disease ecology. Here we focus on the spread of a plant pathogen in a wild pathosystem. Every year we monitored an annual epidemic of the European poplar rust fungus, *Melampsora larici-populina*, in the Durance River valley, in the French Alps. This valley is particularly well suited for the study of recurrent biological invasions: the need of an alternate host plant (larch) to perform its sexual reproduction restricts the resident pathogen population upstream the river, in a poplar-larch sympatry area. Then, a clonal epidemic phase spreads downstream the valley during five months along a ca. 200 km natural riparian stand of black poplar, *Populus nigra*. This landscape also includes a few cultivated stands with poplars carrying qualitative resistances, thus exerting a peculiar selection pressure on pathogen populations. In this study we used epidemiology and population genetics tools to (i) sort *M. larici-populina* individuals according to their wild or cultivated origin, (ii) to describe the spread of the epidemic on the wild poplar stands, (iii) to assess the evolution of the genetic composition of the pathogen populations along the epidemic wave, and (iv) to assess the evolution of life history traits during the epidemic. These results are discussed in the light of recent studies focusing on the relative effects of demographic and selection events on the evolutionary changes accompanying biological invasions.

Keywords: disease ecology, landscape epidemiology, colonization, dispersal, range expansion, wild pathosystem