

In the spring of 1993, a terrifying outbreak of a rapidly progressive, frequently fatal cardiopulmonary disease, occurring among healthy adults in the southwestern United States, brought immediate attention to a new hantavirus, harbored by rodents (rodents are mice or rats) identified as animals which carry the virus some decade earlier. That a hantavirus would be responsible for this previously unrecognized respiratory disease, now known as hantavirus cardiopulmonary syndrome (HCPS), was beyond the collective wisdom and imagination of clinicians, epidemiologists and medical virologists. The frightening prospect of species jumping from animals to man has again reared its head with the recent discovery of genetically distinct hantaviruses in multiple species of shrews and moles (those animals albeit similar are not rodents), in widely separated geographic regions. These newfound hantaviruses challenge long-held conventional views about the host range of hantaviruses and raise concerns about their pathogenic potential to infect humans. Although no human disease has yet been associated with these newly discovered, so called “orphan” hantaviruses, studies are urgently needed to investigate their ecology, transmission dynamics and infectivity, before the next outbreak of a hitherto unknown hantavirus disease.

Our *long-term goal* is to better understand the host range of hantaviruses and the clinical spectrum of hantavirus-associated diseases. The *principal objective* of the proposed 3-year basic research project is to clarify the ecology and human-health relevance of hantaviruses harbored by shrews, moles and bats in Poland. Our *central hypothesis* is that hantaviruses occurring in diverse hosts share an ancient and dynamic evolutionary history and that genetic changes and host switching events in the distant and recent past may account for their differential pathogenicity for humans. The *immediate impact* of this basic research will be the acquisition of new knowledge about the genetics and biology of nonrodent hantaviruses to develop diagnostics for future life-threatening outbreaks caused by emerging hantaviruses. The objective will be achieved by the following specific aims.

*Specific Aim 1. Determine the spatial and temporal distribution and phylogenetic relationships between hantaviruses harbored by shrews, moles and bats in Poland.*

*Specific Aim 2. Determine the transmission dynamics of hantaviruses harbored by shrews, moles and bats in Poland.*

*Specific Aim 3. Determine the infectivity of non-rodent-borne hantaviruses in humans, specially those who are in close contacts with animals (hunters, foresters).*

A multidisciplinary, team-science approach, which integrates state-of-the-art molecular biology techniques with fieldwork and robust computational analysis, will be employed to gain new knowledge about the genetic diversity, transmission dynamics and infectivity of novel soricomorph- and chiropteran-borne hantaviruses circulating in Poland. Preliminary data about the co-circulation of shrew- and mole-borne hantaviruses in central Poland provides a solid foundation on which to base the proposed research. Moreover, the many months of planning and the well-established working relationship between Polish and U.S. scientists ensure the on-schedule completion of the proposed project.

The proposed research is *innovative* in that it opens a new frontier in hantavirus research, one which focuses on uncovering vital new knowledge about the ecology of non-rodent-borne hantaviruses in Poland. Furthermore, the scientific impact goes far beyond the proposed research in that the repository of well-curated tissues collected from shrews, moles and bats, as well as serum samples from humans with various febrile illnesses and chronic diseases, will serve as a precious resource for other unanticipated pioneering investigations.