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Necker-Pasteur Clinical Metagenomics: Part 2. Contribution to Pathogen Discovery

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BACKGROUND

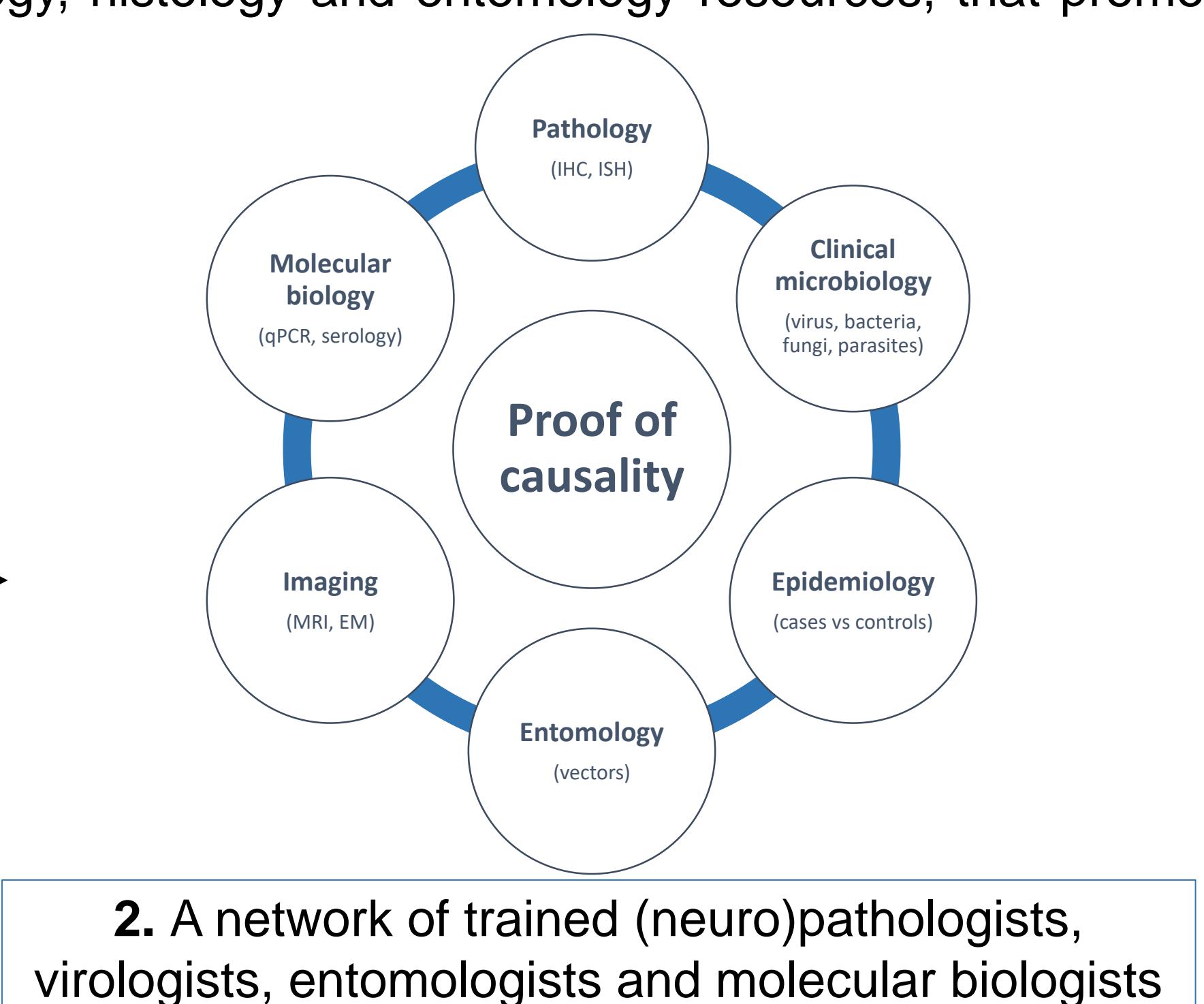
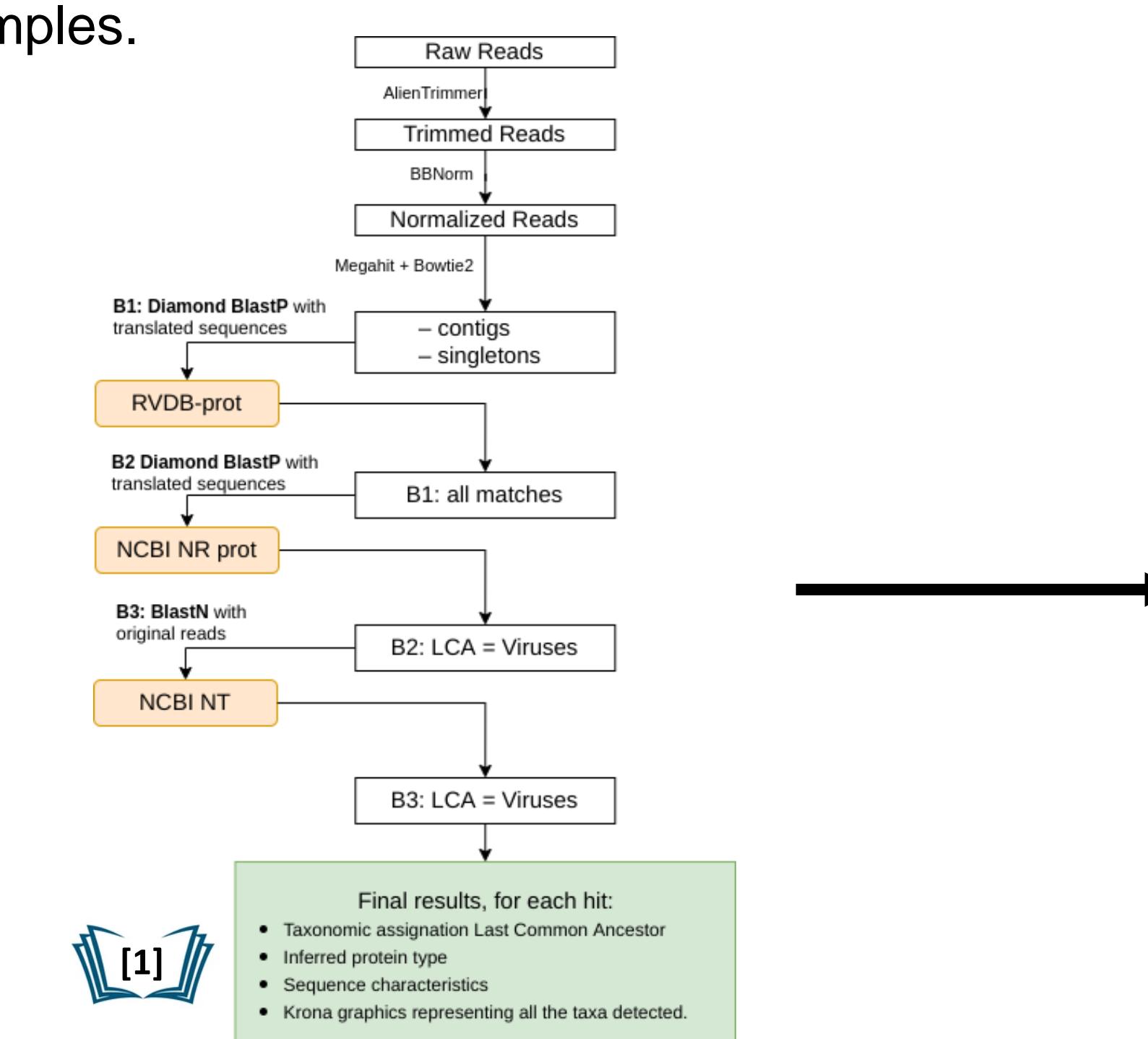
Clinical metagenomics fuels pathogen discovery but a comprehensive research environment is required to address critical questions such as imputability, physiopathology of novel identified infectious agents, and development of new diagnostic tools. The Institut Pasteur, in close collaboration with specialized hospital clinical services and laboratories including (neuro)pathologists, along with other academic labs, seeks to address these topics.

METHODS

We present the research environment, including sequencing and analyzing tools, molecular and cellular biology, virology, histology and entomology resources, that promotes the exploration of novel or unexpected pathogens identified from patient samples.



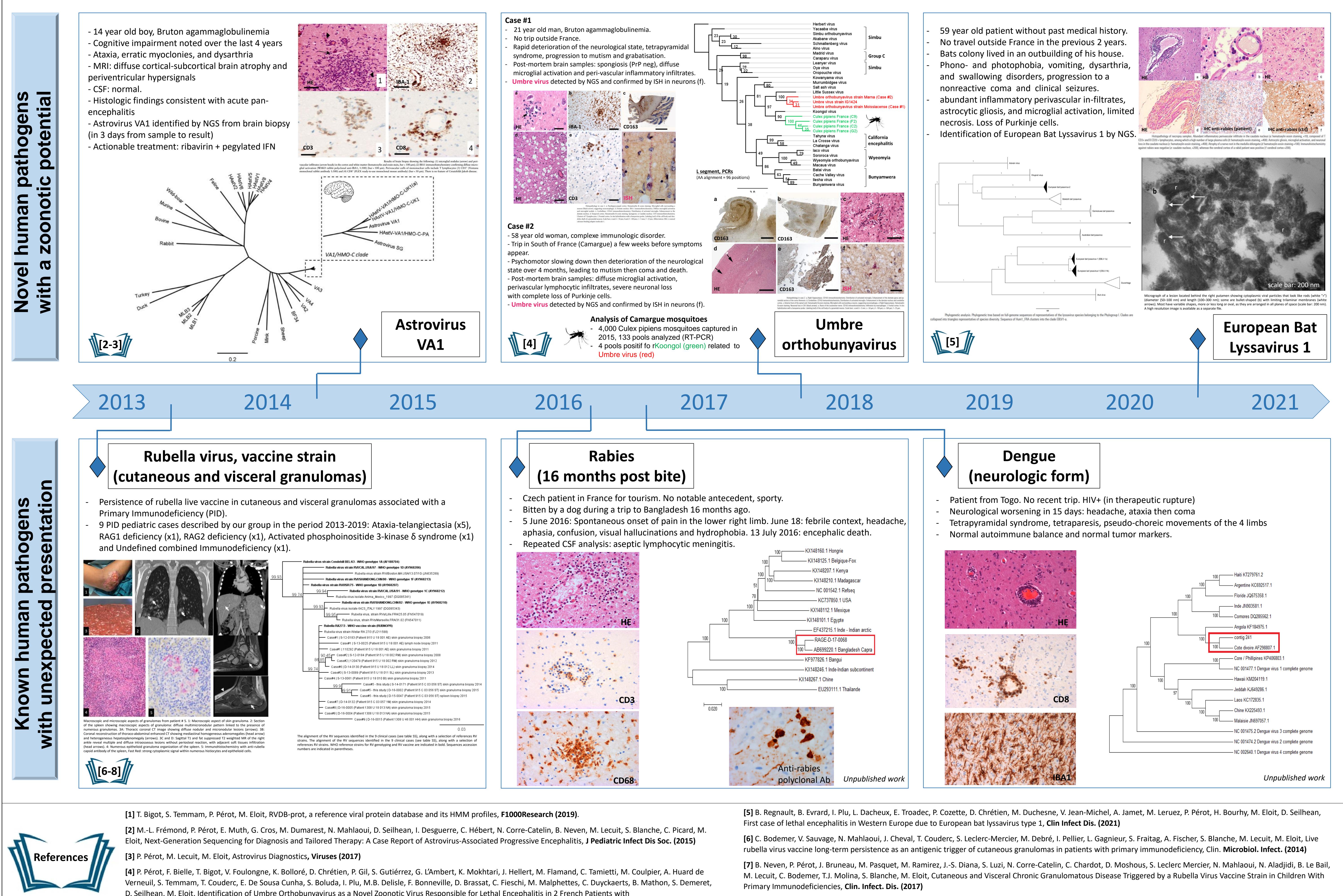
1. A dedicated sequencing platform,
BioIT infrastructure and pipeline



2. A network of trained (neuro)pathologists,
virologists, entomologists and molecular biologists

RESULTS

We review some of the major identifications done in the course of our historical partnership with hospitals, by highlighting the place and the contribution of research works following identification of new or unexpected microorganisms. The list includes novel human pathogens with a zoonotic potential (Astrovirus VA1, Umbre orthobunyavirus, European Bat Lyssavirus 1) and known pathogens with unexpected or atypical presentation (Rubella virus, Rabies, Dengue).



CONCLUSION

Pathogen discovery includes the identification and characterization of new or unexpected infectious agents and the demonstration of their causality, with the objectives of understanding their biology and fostering the development of novel diagnostic or therapeutic tools. The goal of the Pasteur-Necker initiative in the coming years is to become a national center for clinical metagenomics combining patient care and fundamental research with potential for medical applications, for the benefit of science and patients.