The Institute for Animal Health’s contribution to the eradication of rinderpest

IAH’s contribution to rinderpest eradication was in three main and closely linked areas: the advancement of knowledge about the virus; the development of new diagnostic techniques; and the implementation of training and monitoring systems to improve national and international control programmes. In the later stages of the campaign, when it was formalized as GREP, IAH acted as FAO’s World Reference Laboratory (WRL) for rinderpest, providing diagnostic services, training and advice to many countries, and information to OIE and FAO to assist the coordination of international activities.

IAH’s work on rinderpest began in earnest about 1980 with the arrival of William Taylor. During this period, IAH contributed as both a rinderpest vaccine manufacturer and a resource for vaccine training skills. In collaboration with FAO, quality assurance tests were conducted on vaccines obtained from African manufacturers. Concern about the variable results of these tests provided the impetus for developing FAO’s PANVAC. Another vital contribution at this time was the gathering of rinderpest virus (RPV) strains and demonstration of the varying virulence of different isolates in sets of cattle belonging to the same breed.

Another very important contribution was development of the rinderpest ELISAs used throughout GREP for sero-monitoring and sero-surveillance (first with the indirect ELISA and then with the monoclonal antibody-based competitive ELISA). This work was carried out by John Anderson and colleagues in the 1980s, and allowed virus neutralization tests – which were time-consuming, difficult to standardize and technically demanding – to be replaced by much simpler and more robust ELISA test kits. The first ELISA was field tested and validated during work in the United Republic of Tanzania, led by Anderson and funded by the EU. Anderson then went on to collaborate with the IAEA/FAO Joint Division on establishing the rinderpest laboratory network, which played an important part in PARC. IAH ran training courses and annual coordination meetings for the network, and provided trouble-shooting support for national and regional laboratories in implementing the ELISAs, which became essential tools for sero-monitoring and later sero-surveillance. Anderson and others at IAH continued this training and trouble-shooting role as rinderpest control programmes extended into the Middle East and Asia. In 1990, he developed the competitive ELISA as a more specific and sensitive test that can be applied across many host species, including wildlife.
Throughout the eradication programme, IAH manufactured and supplied ELISA kits, working closely with local users to ensure that the kits functioned and were reliable, even under difficult local conditions. Based on its development of these tests, its work to support and develop the rinderpest network and its experience of rinderpest control, IAH became the FAO WRL for rinderpest in the early 1990s. Anderson and Anke Bruning also developed a rapid pen-side test for diagnosis of rinderpest in the field, which was based on lateral flow technology and allowed diagnosis from an eye swab within ten minutes. Availability of this field test greatly assisted in identifying the remaining foci of infection in Pakistan and detecting the clinically mild rinderpest strain present in the United Republic of Tanzania.

The basic biology of RPV was studied at IAH from the late 1980s, led by Tom Barrett, who was joined later by Michael Baron. This work resulted in the complete sequencing of the virus (both virulent and vaccine strains) and the development of a system for making recombinant RPVs. The system led to the creation of numerous modified RPVs, which contributed greatly to knowledge about the virus’s biology and creation of a number of differentiating infected from vaccinated animals (DIVA) or “marker” vaccine candidates. The molecular basis for the attenuation and stability of the Plovrigh vaccine was discovered, the virus receptor was identified, and the functions of the different viral non-structural proteins were explored.

The vaccines based on recombinant RPVs were not used in the field, but provided important information that will be of use in work to control peste des petits ruminants virus (PPRV). Recombinant pox virus-based vaccines were also created and tested, and the knowledge these provided on the nature of the protective immune response to morbillivirus infection has already helped in designing DIVA vaccines for control of PPRV.
Knowledge of the sequence of the virus allowed Barrett to develop rinderpest-specific polymerase chain reaction (PCR) primer pairs, which provided the basis for the PCR-based diagnostic tests used in the WRL. These tests were coupled with deoxyribonucleic acid (DNA) sequencing and phylogenetic analysis of the virus isolates, which led directly to the identification of the separate African and Asian lineages of RPV. The ability to identify and track the origin of a virus isolate became increasingly important in the later stages of the eradication campaign, and was crucial in identifying the existence of low-virulence strains circulating in areas thought to be free of disease. The PCR tests were used extensively at the WRL to improve diagnostic assay throughput, replacing the need for virus isolation and characterization. They were also passed on to other regional and national reference laboratories, with support from the IAEA/FAO Joint Division.

An important factor in this work was that IAH, both before and after its establishment as the WRL for rinderpest, acted as a large, secure collection point for RPV isolates from around the world. The availability of a large number of distinct isolates in one place greatly facilitated the comparison of strains in terms of their pathogenicity under defined conditions, and enabled the development of the sequence database that underpinned the phylogenetic analysis described in previous paragraphs. Many historic samples that are no longer available in their countries of origin are still stored at IAH Pirbright. It is hoped that these isolates will eventually be completely sequenced, to preserve the historical record of the virus, now that it has been eradicated from the wild.

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