Outbreaks and epidemics of acute viral diseases can have enormous costs that extend beyond those of just the infected individuals. These costs disproportionately affect lower-middle income areas of the world, as healthcare systems may already be stretched by a lack of resources. Recent outbreaks, notably the West African Ebola epidemic, South American Zika outbreak, MERS-CoV and SARS-CoV, have highlighted the need for rapid, real-time characterisation of viral genetic diversity to provide critical epidemiological information to guide control and interventions. Our team was an integral part of the international group of scientists and epidemiologists that came together during the Ebola outbreak to provide rapid, in-country sequencing support in both Sierra Leone and Guinea, and helped demonstrate the utility of sequencing to an outbreak response. Subsequently, the group has established the ARTIC network, which has brought together experts in outbreak response, epidemiology and bioinformatics to establish a smaller, portable sequencing laboratory infrastructure based around miniION technology, aimed at producing a deployable, integrated and coherent platform for performing real-time epidemiology of outbreaks from virus genome sequencing. The system has been deployed on a number of occasions, and has demonstrated utility in the field, including for the identification of pathogens in an outbreak. By continuing to develop these packages, we will greatly enhance our capacity to rapidly deploy genomic surveillance into resource-limited environments, allowing us to put viral genomics at the heart of epidemic responses.