

# **The Temporal, Spatial and Evolutionary Dynamics of Ebola Virus in West Africa**

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The 2014-2015 Ebola virus outbreak in Guinea, Sierra Leone and Liberia has resulted in nearly 30,000 known cases, caused at least 11,000 deaths and, at time of writing, is still on-going, with a few residual chains of transmission in Guinea and Sierra Leone. Here we discuss how sequencing of complete viral genomes can help characterise an outbreak in the initial stages, infer the primary drivers of spatial spread during the peak of the epidemic. We will also discuss the possibility and reality of 'real-time' molecular epidemiology where viral genomes are generated within days of a sample being collected and how this can help inform the difficult process of breaking the final chains of transmission.