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Detection and management of highly pathogenic avian influenza A/H5N1 clade 2.3.2.1c virus in poultry in Cameroon, 2016–2017**Abel Wade**

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In May 2016, highly pathogenic avian influenza virus (HPAIV) of the subtype A/H5N1 was detected in Cameroon in an industrial poultry farm at Mvog-Betsi, Yaounde (Centre region), with a recorded sudden increase of deaths among chickens, and an overall mortality rate of 75%. The virus spread further and caused new outbreaks in some parts of the country. In total, 21 outbreaks were confirmed from May 2016 to March 2017 (six in the Centre, six in the West, eight in the South and one in the Adamaoua regions). This resulted in an estimated total loss of 138,252 birds (44,451 deaths due to infection and 93,801 stamped out). Only domestic birds (chicken, ducks and geese) were affected in farms as well as in poultry markets. The outbreaks occurred in three waves, the first from May to

June 2016, the second in September 2016 and the last wave in March 2017. A multi-sectorial management were used to control the outbreaks. The topology of the phylogeny based on the haemagglutinin gene segment indicated that the causative H5N1 viruses fall within the genetic clade 2.3.2.1c, sharing a same group with the A/H5N1 viruses collected in Niger in 2015 and 2016. More importantly, the gene constellation of four representative viruses showed evidence of H5N1/H9N2 intra-clade reassortment. Additional epidemiological and genetic data from affected countries in West Africa are needed to better trace the origin, spread and evolution of A/H5N1 in Cameroon.

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