Cassava mosaic disease (CMD), caused by begomoviruses (family Geminiviridae), is a major constraint to cassava (Manihot esculenta) production in Africa (Fargette et al., 1993). CMD-associated begomoviruses in the African cassava mosaic virus (ACMV) or East African cassava mosaic virus (EACMV) clusters (Bull et al., 2006). To determine the suspected begomoviruses associated with CMD symptoms, leaf samples were collected from five symptomatic cassava plants in Cameroon, and from three symptomatic plants in Togo in August 2014 (Table 1). Total DNA was isolated as described by Shepherd et al. (2008). Circular, single-stranded DNA was enriched by rolling circle amplification (RCA). The RCA products were pooled by country of origin and sequenced using the Illumina HiSeq 2500 next-generation sequencing (NGS) platform. Sequence reads were assembled into full-length viral sequences (c. 2.7 kb) using SeqManNGen software v.3 (DNASTAR Inc., Madison, WI) and submitted to BLASTn analysis. In addition to the ACMV DNA-A and B components as expected, the DNA-A and B components of Soybean chlorotic blotch virus (SbCBV) (Olufemi et al., 2010) and West African Asystasia virus 1 (WAAV1) (Wyant et al., 2015) were also identified. For SbCBV, sequence identities ranged from 97-99% and 95-96% for the DNA-A and B components, respectively, whereas for WAAV1, sequence identities ranged from 92-95% and 93-96% for the DNA-A and B components, respectively. The DNA sequences for each cloned amplicon were determined by Sanger sequencing. Amongst the five samples collected from Cameroon, three were infected only with ACMV, one was infected with SbCBV and WAAV1, and one was infected with ACMV, SbCBV and WAAV1. The three Togolese samples were all infected with ACMV and one was also infected with SbCMV. BLASTn analysis of the CP and BV1 genes indicated that they shared 99-100% sequence identity with the NGS-determined sequences. To our knowledge, this is the first report of SbCBV and WAAV1 isolated from symptomatic cassava. The isolates shared a close phylogenetic relatedness with previously described SbCBV and WAAV1 isolates, respectively (Fig. 1). This indicated that cassava-associated isolates are strains or isolates of SbCBV and WAAV1 based on the guidelines of the ICTV Geminiviridae Study Group for strain and species demarcation (Brown et al., 2015). The grouping of EACMV, SbCBV, WAAV1, and Madagascar Asystasia virus (MAAV) together in a separate clade (Fig. 1), suggests that they have probably evolved from a common ancestor, despite perhaps recent adaptation to host plants representing different plant families. Whether symptoms caused by SbCBV and WAAV1 are masked by the presence of ACMV in cassava remains to be determined. Giving the small number of samples analysed, further work is required to understand the contribution of these two viruses in cassava mosaic disease epidemiology in Africa.

Acknowledgements
This research was partly funded by National Science Foundation award number IOS-1212576. Walter Leke was supported by the Fulbright Foundation.

References