

factors for NTS infection. Controlling *Salmonella* Virchow infections is a public health priority.

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0827

### Rotavirus cases among Rotarix vaccinated children below five years during the 2018 outbreak in the Kingdom of Eswatini



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**Background:** A large outbreak of diarrhoeal disease in children under 5 years was reported in four surveillance sentinel sites Mbabane Government Hospital, Raleigh Fitkin Memorial Hospital, Hlathikhulu Government Hospital and Good Shepherd Hospital. Rapid increase of number diarrhoeal cases, were reported from week 34 to 41 (August to October 2018). Approximately 1,535 children presented with acute diarrhea, vomiting and dehydration.

**Methods and materials:** Diarrhoeal stool samples were routinely collected for surveillance from children less than 5 years of age to determine the etiology of the diarrhoea. A total of 139 stool samples were tested for rotavirus using enzyme immunoassay kit, Molecular characterization using polyacrylamide gel electrophoresis, semi nested reverse-transcription polymerase chain reaction, sequencing and phylogenetic analysis. Rotavirus negative stool samples were further tested for bacteria and parasites using molecular diagnostic assays.

**Results:** The rotavirus positive samples were positive for group A rotavirus with a prevalence of (117/211) 53% with the age groups mostly affected being: <12 months = (68/117) 58.1%, 3–24 months = 23.9% (28/117) and >24 months = 16.2% (19/117). The PAGE patterns observed were long RNA migration pattern. The G3P[8] 59/75 (78.6%) rotavirus strain were mainly associated with the outbreak. Phylogenetic analysis of the partial length VP4 P[8] associated G3 clustered together with other P[8] strains detected in Africa and distantly related to vaccine strains (Rotarix™ and RotaTeq™). Pathogens that were observed in Eswatini were *Shigella*/Enteroinvasive *E. coli* 18% (11/61) was frequently detected followed by *Campylobacter jejuni/coli* 13% (8/61) and *Giardia lamblia* 13% (8/61).

**Conclusion:** Majority of the children affected by the rotavirus received vaccination and the rotavirus genotype G3P[8] was the major cause of these outbreak. It also important to note that the G3P[8] that was circulating was the wild type stains not related to the vaccine strains. As evident from the Maximum likelihood phylogenetic tree generated, G3P[8] study strains clustered in different lineages as compared to the vaccine strains (Rotarix™ and RotaTeq™). Further studies on whole genome sequence analysis are required to determine the evolutionary relationship among the strains and surveillance of rotavirus among the infants should be continued while increasing the rotavirus vaccine coverage and add a booster dose to increase protection.

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0828

### Detection and genetic characterization of avian influenza A (H5N6) virus clade 2.3.4.4 in isolates from house crow and poultry in Bangladesh, 2017



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**Background:** Bangladesh has experienced repeated house crow (*Corvus splendens*) mortality events due to highly pathogenic avian influenza (HPAI) viruses since 2011. We investigated one such event in Dhaka in 2017 to detect and molecularly characterize the virus in crows and poultry from nearby live poultry markets (LPMs).

**Methods and materials:** We collected cloacal and oropharyngeal swab samples from dead and moribund crows ( $N=166$ ) and environmental samples ( $N=149$ ) from 19 nearby LPMs. Samples were tested by qRT-PCR for influenza A (M gene) and H5/H7/H9/N1/N6. H5 positive samples were inoculated into embryonated eggs for virus culture. We performed conventional RT-PCR and Sanger sequencing of the isolated viruses and used MEGA7 for phylogenetic analysis.

**Results:** 91.6% ( $n=152$ ; 95% Confidence Interval (CI): 86.3–95.3) of crows were positive with influenza A/H5 including 77.6% for H5N1 ( $n=118$ ), 2% for H5N6 ( $n=3$ ) and 20.4% H5Nx ( $n=31$ ). Of the 149 LPM samples, 46.3% ( $n=69$ ; 95%CI: 38.1–54.7) were positive for influenza A/H5 among which 85.5% for H5N1, 5.8% for H5N6 and 9% for H5Nx. We successfully isolated 2 H5N6; 1 from chicken and 1 from crow. Here we describe molecular characteristics of H5N6 only. Phylogeny of the HA gene showed 99.0% nucleotide similarity with the H5N8 virus belonging to clade 2.3.4.4B, isolated from Muscovy duck in Congo, 2017. NA gene showed 98.4% similarity with that of H4N6, isolated from duck in Mongolia, 2015. The PB1 and PA gene had high nucleotide identity, 98.0% and 99.0% respectively, with an H3N1 isolated from duck in Bangladesh, 2017. NP, M and NS genes of the two H5N6 isolates are closely related to H5N8. The isolates were identified as HPAIV based on multiple basic amino acids at the HA proteolytic cleavage site. Molecular markers in the HA protein suggested predicted binding to human receptor  $\alpha_2,6$  linkage and increased pandemic potential.

**Conclusion:** This investigation detected and characterized a novel H5N6 reassortant in wild birds for the first time and highlighted the potential for the exchange of HPAI between poultry and wild birds. Continued surveillance of both poultry and wild birds is

needed for early detection of novel viral introductions, to trace the transmission route and to reduce public health risks.

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0829

### Measles outbreak investigation in Kambia District, Sierra Leone-2018



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**Background:** Measles, an acute highly infectious viral disease, remains one of the leading causes of childhood morbidity and mortality worldwide. Despite the availability of safe and effective vaccines, measles cases have been reported in Sierra Leone. On 29 October 2018, the Kambia district health management team was notified of a suspected measles outbreak. On 1 November 2019, we investigated the outbreak to confirm the diagnosis, assess the magnitude, identify potential risk factors, and institute control measures.

**Methods and materials:** We defined a suspected case as any person with fever and maculopapular rash in Kambia district from 1st October 2018 and a probable case as any suspected case with epidemiologic link to a laboratory confirmed case. We reviewed medical records, interviewed parents, patients and collected blood samples for measles confirmation. We collected patients' demographic, clinical and exposure history. We conducted active case search and needs assessment for measles reactive mass vaccination in the community. We conducted social mobilization and risk communication.

**Results:** A total of 91 cases (14 laboratory-confirmed and 77 probable cases) with no deaths reported. The overall Attack Rate (AR) was 24.2/100,000 persons, with the highest AR (119.6/100,000 persons) among the 6–11 months age group. The median age was 24.5 months (range 4–348), and 48 (56%) were females. Four out of seven chiefdoms were affected and Gibnleh-Dixon chiefdom was the most affected (AR = 274.9/100,000). The first four detected cases had travel history to the neighboring Republic of Guinea, where there was a confirmed measles outbreak, and three of the four affected villages are close to the border. The district administrative vaccination coverage was 87%, however, of the total 84 eligible cases, only two had vaccination cards.

**Conclusion:** A measles outbreak was confirmed in Kambia district which shares a border with Guinea. The importation of measles cases in a susceptible community might have contributed to the spread of measles in the affected chiefdoms. A reactive mass vaccination targeting children aged six months to 15 years was conducted and achieved coverage of 100.8%.

We recommended strengthening routine immunization through increased outreach vaccination sessions to communities, supplementary vaccination and to strengthen cross border surveillance and response framework.

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0830

### Epidemiology of measles in a security compromised setting: A retrospective analysis of surveillance data in Borno State Nigeria, 2007–2017



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**Background:** Measles is a vaccine preventable viral disease, causing significant morbidity and mortality in children under five. Nigeria has the highest burden of measles globally with most of her cases occurring in the Northern region. Since 2007, Borno State has been the epi-center of insurgency affecting measles elimination efforts in the State.

**Methods and materials:** We conducted a retrospective analysis of confirmed measles cases reported through the measles case-based integrated Disease Surveillance and Response (IDSR) for January 2007 to October 2017. We descriptively characterized the cases, determined the trend and predicted expected number of measles cases in the succeeding five years using time series analysis.

**Results:** A total of 688 laboratory confirmed cases of measles was reviewed, 366 (53.2%) of whom were males. Children aged 1–4 years 386 (56.1%) and Bayo Local Government Area (LGA) 73 (10.6%) were most affected. Measles cases were reported in all the years and in all the 22 LGAs. The year 2007 had the highest number of cases 124 (18.0%) followed by the year 2016, 117 (17.0%). Cases peak in January and February each year. However, we observed a shifting trend with onset of new cases during the rainy season. The incidence of new cases ranged from 2.5/100,000 in Gwoza LGA to 92.4/100,000 in Bayo LGA. Half of the LGAs had an incidence of above 15.6/100,000. Time series analysis showed a reduction in measles cases by 2.9% over the ten years and time accounts for only 1% in the variation of measles cases.

**Conclusion:** Measles burden is high in Borno state affecting mostly children aged 1–4 years. Cases were reported both in dry and wet seasons. New cases were reported in both secure and insecure LGAs with poorer reporting from security compromised LGAs. Time is not seen to be a major contributor to the trend of measles cases thus suggesting other drivers. We recommend improved routine immunization and strengthening of measles surveillance system especially in security compromised LGAs in Borno State in order to achieve the global measles elimination target.

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