Title: Whole-genome Sequencing Analyses to Investigate a Nationwide Outbreak of Listeriosis Caused by Ready-to-Eat Processed Meat Products, South Africa, 2017-2018

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Background: In South Africa, between 2017 and 2018, a large and multi-province outbreak of listeriosis, a serious foodborne disease caused by Listeria monocytogenes was traced to ready-to-eat (RTE) processed meat products using epidemiological investigations and whole-genome sequencing (WGS) analyses.

Methods: In addition to standard laboratory techniques, WGS was performed for additional subtyping of the outbreak isolates and to support investigation into the source of the outbreak.

Results: As of 19 June 2018, 1056 cases leading to 214 deaths were reported to the National Institute for Communicable Diseases, South Africa. Multilocus sequence typing (MLST) of 628 clinical isolates using WGS determined that 571/628 (91%) belonged to the L. monocytogenes sequence type 6 (ST6) and the remainder (9%) to 17 other sequence types. Furthermore, WGS-based core genome multilocus sequence typing (cgMLST) analysis using 1748 core genes showed that all ST6 (the outbreak sequence type) clinical isolates belonged to the cgMLST type CT4148. Isolates of the same cgMLST type were found in RTE processed meat products (including a widely consumed product called "polony") and in the processing environment of the manufacturer (0-4 allelic differences), strongly suggesting that the polony and the other RTE products made in this facility is the source of the outbreak.

Conclusions: Popular RTE processed meat products from a single food production facility caused this listeriosis outbreak, which is to date the world's largest. High-throughput sequencing combined with epidemiological and traceback investigation was instrumental in swiftly locating the source of contaminated food, preventing further illnesses and deaths.