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An Outbreak of Shigellosis Linked to Imported Basil: The Importance of Standardized Genotyping Tools and Traceability Systems, Norway, October 2011

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BACKGROUND: On 9 October 2011, the Norwegian Institute of Public Health was alerted about an increase in *Shigella sonnei* infections in Troms, northern Norway with identical Multiple-Locus Variable number tandem repeat Analysis (MLVA) profile previously unknown in Norway. Most cases had consumed food provided by one local delicatessen. On 14 October, *S. Sonnei* cases with identical MLVA-profile to those in Troms were reported from Østfold, southern-east Norway. We aimed at identifying the source of the outbreak to prevent further cases.

METHODS: We concurrently performed active case finding of all laboratory confirmed *S. sonnei* infections with the identified MLVA-profile from 1st October in Norway and a cohort study among 50 attendees of a banquet in Troms where food from the delicatessen was served. Trace back investigations of suspected food items were conducted.

RESULTS: Overall, 46 cases were confirmed. Ten of 50 participants in the banquet had symptoms compatible with shigellosis; three of them were laboratory confirmed. Those who ate basil pesto sauce were 2.8 (95%CI 1.3-5.8) times more likely to become a case than those who did not. Patients in Troms and Østfold had consumed basil delivered by the same supplier. The basil, imported from Israel, was withdrawn from the Norwegian market. No further cases were reported. No cases with the outbreak MLVA-profile were reported from other European countries.

CONCLUSIONS: Routine MLVA-typing of all *Shigella* isolates in Norway was paramount to link geographically disparate cases, highlighting the importance of standardized genotyping methods. The rapidly launched epidemiological investigation allowed us to identify the implicated product with wider distribution. The effective trace back investigation helped stopping the outbreak in Norway and led to a European Rapid alert message to prevent further cases.

KEYWORDS: shigellosis, outbreak, genotyping, traceability