

From national to international – challenges in cross-border multi-country, multi-vehicle foodborne outbreak investigations

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This issue of *Eurosurveillance* features two articles by Horvath et al. and Scavia et al. reporting the findings of the investigations of an unusual increase in *Salmonella* Goldcoast infections in Hungary and Italy respectively, in 2009 [1,2]. The increase in notified cases started around June and July in both countries. While the magnitude remained limited, it persisted over a period of several weeks and therefore, in early October, Hungary reported this increase to the European Epidemic Intelligence Information System for food- and water-borne diseases in the European Union (EU) [3], to check if other EU/European Economic Area (EEA) Member States had experienced a similar increase. In response to this, within four weeks, five countries: Denmark, Italy, Norway, Spain, and United Kingdom, reported recently diagnosed laboratory-confirmed *S. Goldcoast* cases possibly linked to the cases in Hungary [4].

S. Goldcoast is a rare serovar, with between 150 and 200 cases reported annually in the EU/EEA from 2007 to 2010, excluding 2009 (unpublished data). In 2009, 314 cases were reported, representing a significant increase compared to the background level in the years 2007 to 2010.

The investigations reported in this issue concluded that a contamination of meat had probably occurred along the pork production chain, had persisted over several months and resulted in multiple vehicles derived from the pork production chain causing an unusually high number of sporadic and clustered cases.

The two articles highlight challenges in the investigation of potential cross-border multi-country outbreaks where multiple contaminated vehicles originating from the similar type of food production chain may serve as a source of infection of sporadic cases and may cause point source outbreaks at local, regional or national level. Firstly, such outbreaks do not usually result in a large number of cases accumulated over a limited time period and associated with a single vehicle. Therefore, the delay in the recognition of a potential common origin impairs the ability to investigate timely

and precisely the food items consumed during the incubation period of the cases. Secondly, as the contamination may involve several products, pork meat containing products in the outbreaks described in this issue of *Eurosurveillance*, epidemiological investigations may remain inconclusive. In such instances investigating household outbreaks can be of high value. Even though often small and limited, household outbreaks may reveal a common exposure to pork meat or a single vehicle in a family cluster and family clusters may indicate the presence of contaminated raw food of animal origin on the retail market. It is noteworthy that both outbreaks described reported the involvement of homemade products from pork meat. Households have been reported as the most important setting for *Salmonella* outbreaks; 55.6% of notified *Salmonella* foodborne outbreaks with strong evidence (n=341) occurred in single households in 2010 [5].

The high similarity of the molecular typing results from samples of animal, food and human origin in the Italian investigation further strengthened the evidence supporting the origin of the contamination in the pork production chain. The high genetic homology based on pulsed-field gel electrophoresis (PFGE) analysis between the Hungarian and Italian outbreak profiles allowed linking the increase in the number of cases in the two countries to a probable common source of contamination. In addition, the simultaneous occurrence of the increase as well as the strong suspicion of pork containing products as a source of infection in both countries, further strengthened this hypothesis. The timely epidemiological and microbiological investigation along the food chain was however not possible and was largely hampered by the difficulty in tracing back the meat used in salami production.

The two *S. Goldcoast* outbreaks stress the importance of collaboration between public health and veterinary authorities and the need to share samples and data from human, animal, food and feed across sectors when investigating such complex outbreaks. In addition, it is crucial to ensure the comparability of

molecular typing methods used in both sectors so that a microbiological link between human and food/animal samples, which should be confirmed through an epidemiological link, can be ascertained in a timely manner. The limitations of the epidemiological investigation in a context of sporadic cases and small clusters prevent establishing firm evidence of an association with a particular vehicle. In such situations, the concordance of molecular and epidemiological evidence pointing towards a source of contamination is crucial.

Similarly, linking cases and clusters that occur at the same time in several countries allows the coordination of investigations through the use of standard questionnaires adapted to cultural differences and the sharing of results. This in turn may increase the statistical power of the investigation by enrolling more cases in the analytical studies. However, the sharing of information among countries only after an alert from a single country, does not allow for early recognition of a similar pattern occurring simultaneously in several Member States. This is why the European Centre for Disease Prevention and Control (ECDC) has started, together with EU/EEA countries, a pilot project for molecular-typing-based surveillance. The aim of this project is to enable immediate sharing of molecular typing information for *Salmonella* serovars, Shiga toxin/verocytotoxin –producing *Escherichia coli* and *Listeria monocytogenes* to allow early recognition of such patterns through regular analysis of molecular typing profiles [6]. This will ensure that even small multi-country outbreaks will be recognised early on in the future, and permit timely investigation of potential sources and vehicles of infection and implementation of control measures. The establishment of similar type data collection in the food sector will further enhance the possibilities to timely control the spread of food-borne pathogens.

Conflict of interest

None declared.

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