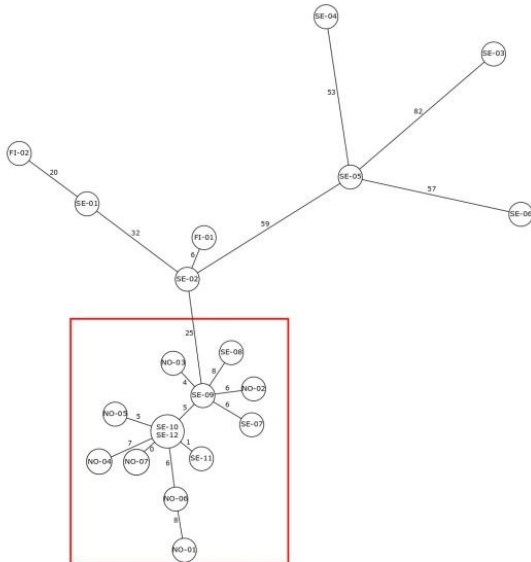


Whole genome sequencing reveals cluster of resistant bacterium in returning travelers

12 July 2018

Figure 2. Minimum spanning tree of *Klebsiella pneumoniae* ST392 isolates from Sweden, Norway and Finland, 2014–2018



Minimum spanning tree showing the *Klebsiella pneumoniae* ST392 isolates from 2015–2018 analysed using SNPs (Public Health Agency of Sweden). 86% of the genome could be included in the analysis. The red box indicates the current outbreak cluster including the 13 Swedish and Norwegian cases. Isolates SE03-05 (top right) are epidemiologically unrelated control isolates of *K. pneumoniae* ST392.

All cases were associated with hospital admissions in Gran Canaria, Spain. Bacterial isolates showed tight clustering when analysed by whole genome sequencing, suggesting a common place of acquisition. Credit: ECDC

Thirteen patients with OXA-48-producing *Klebsiella pneumoniae* ST392 have been reported by Sweden and Norway between January and April 2018—all returning travellers with prior hospital admission in Gran Canaria, Spain. Whole genome sequencing showed tight clustering between the bacterial isolates from the cases.

According to ECDC's risk assessment published today, the risk for individual travellers to acquire OXA-48-producing *K. pneumoniae* ST392 of the Gran Canaria cluster without healthcare contact is very low.

However, if carriers of the bacteria are admitted to a [hospital](#) in their country of origin, there is a high

risk for further transmission and outbreaks if carriage is not detected and if adequate infection prevention and control measures are not in place.

Whole genome sequencing analysis indicates a common place of acquisition for the cases. Given the large number of tourists visiting Gran Canaria, one hospital may become the source of spread to other European countries when [patients](#) are transferred from one country to another, making this cluster a cross-border threat, states the report.

In 2016, more than 15 million citizens from the European Union and European Economic Area (EU/EEA), mainly from Spain, the UK and Germany, travelled to the Canary Islands according to International Air Transport Association.

OXA-48-producing *K. pneumoniae* is a resistant bacterium typically acquired in healthcare settings. Hospitalisation abroad and cross-border transfer of patients are well known modes of introduction of carbapenemase-producing Enterobacteriaceae (CPE), including OXA-48-producing *K. pneumoniae* ST392, into countries with lower prevalence.

The report suggests that hospitals in EU/EEA countries should consider taking, at [hospital admission](#), a detailed history of all travels and hospitalisations of the patient.

All patients who are directly transferred or were hospitalised in a foreign country 12 months prior to hospital admission may be considered for screening, regardless of the CPE prevalence at place of hospitalisation.

Provided by European Centre for Disease Prevention and Control (ECDC)

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