Public Health burden of exposure to microbes and parasites originating from pigs and pork

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Abstract

The production and consumption of pork still is an important source of human illness. Quantifying the burden of illness requires the integration of data from a wide variety of sources. First, relevant hazards need to be identified, based on sources such as outbreaks of human illness, and the occurrence of pathogens in pigs, pork and pork products. Then, the incidence of disease due to these pathogens in the population must be assessed. Reported cases only reflect a minor part of all illness and there are different approaches to estimating underreporting factors. The health impact of different pathogens varies widely in severity, duration and associated fatalities. Summary measures of population health, in particular the Disability Adjusted Life Years, are increasingly used to integrate all health effects into one metric. Most pathogens of interest do not only occur in pigs, but also in other food animals or other sources. Hence, the proportion of cases that is attributable to the pig reservoir or to pork consumption needs to be established as a next step. This presentation will summarize results from different national and EU-wide studies on the burden of illness due to pigs and pork, with a focus on non-typhoidal Salmonella spp. and Toxoplasma gondii. The WHO Foodborne Disease Burden Epidemiology Reference Group (FERG) aims to assemble, appraise and report on the current, the projected as well as the averted burden of foodborne disease estimates at a global level. Several reviews have already been published, including a review on the global public health significance of Taenia solium. It is increasingly recognized that humans are not only exposed to pathogens originating from the pig reservoir by handling or consumption of meat, but also by direct contact with live animals or by indirect environmental transmission. In some cases, such as MRSA, direct contact appears to be the dominant source of exposure, whereas for other pathogens (e.g. Campylobacter), the pathways are much more complex.