Foodborne zoonoses are a major public health concern. Risk analysis, which underpins international policies on food safety and trade in foodstuffs of animal origin, requires that an assessment be made of the occurrence and severity of human cases for each type of foodstuff. However, the tools currently available for quantifying risks are only capable of estimating the consequences of certain diseases. This article proposes an alternative quantitative approach for prioritising the risk of foodborne zoonoses, based on the creation of a typology of hazards and calculating a risk score. A combination of average hospitalisation and mortality rates is used to quantify the severity of human cases. By calculating the percentage of food-associated cases it is possible to estimate the incidence of cases linked specifically with the foodstuff being assessed. This method is illustrated by applying it to bacterial zoonotic hazards in pork and beef and provides a support tool for veterinary public health decision-makers.

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This paper reviews the evidence for host genetic variation in resistance to infectious diseases for a wide variety of diseases of economic importance in poultry, cattle, pig, sheep and Atlantic salmon. Further, it develops a method of ranking each disease in terms of its overall impact, and combines this ranking with published evidence for host genetic variation and information on the current state of genomic tools in each host species. The outcome is an overall ranking of the amenability of each disease to genomic studies that dissect host genetic variation in resistance. Six disease-based assessment criteria were defined: industry concern, economic impact, public concern, threat to food safety or zoonotic potential, impact on animal welfare and threat to international trade barriers. For each category, a subjective score was assigned to each disease according to the relative strength of evidence, impact, concern or threat posed by that particular disease, and the scores were summed across categories. Evidence for host genetic variation in resistance was determined from available published data, including breed comparison, heritability studies, quantitative trait loci (QTL) studies, evidence of candidate genes with significant effects, data on pathogen sequence and on host gene expression analyses. In total, 16 poultry diseases, 13 cattle diseases, nine pig diseases, 11 sheep diseases and three Atlantic salmon diseases were assessed. The top-ranking diseases or pathogens, i.e. those most amenable to studies dissecting host genetic variation, were *Salmonella* in poultry, bovine mastitis, Marek's disease and coccidiosis, both in poultry. The top-ranking diseases or pathogens in pigs, sheep and Atlantic salmon were *Escherichia coli*, mastitis and infectious pancreatic necrosis, respectively. These rankings summarise the current state of knowledge for each disease and broadly, although not entirely, reflect current international research efforts. They will alter as more information becomes available and as genome tools become more sophisticated for each species. It is suggested that this approach could be used to rank diseases from other perspectives as well, e.g. in terms of disease control strategies.