

Serological characterization of *Salmonella* spp. infection in finishing pigs from NE Spain

Vico, J.P.

Mainar-Jaime, R.C.*

¹Centro de Investigación y Tecnología Agroalimentaria (CITA) de Aragón. Ctra. Montañana, 930. 50059 Zaragoza, Spain.

*Centro de Investigación y Tecnología Agroalimentaria (CITA) de Aragón. Ctra. Montañana, 930. 50059 Zaragoza, Spain.
e-mail: rcmainar@aragon.es; fax: +34 976 716335

Abstract

The seroprevalence of *Salmonella* spp. in finishing pigs in Aragón (NE of Spain) and the potential factors associated with it were assessed. Serum samples were collected directly from the Regional Diagnostic Laboratory (RDL). Only farms submitting a minimum of 30 serum samples to the RDL were included, i.e. exporting and farrow-to-finish farms, and those in the last stages of the Aujeszky's disease eradication program. Farms were randomly selected and proportionally distributed to the 2008 census. A questionnaire was used to obtain information on selected farms. The HerdCheck ELISA (IDEXX Laboratories) was used for serology. Out of a total of 6,182 sera tested from 217 herds (mean of 28.5 pigs/herd), 2,240 (36.2%) were seropositive when the cutoff used was OD% 20%, and 1,219 (19.7%) at OD% 40%. At least one seropositive animal was found in 91.7% (199) of the herds at OD% 20% and in 71.4% (155) at OD% 40%. The percentage of farms presenting a high within-herd seroprevalence (i.e. >40%) varied from 20% to 40% depending upon the cut-off point used (OD% 40% or 20%). A multivariable random-effect logistic regression showed that seroprevalence (using a cut-off OD% 40%) was significantly lower in winter and positively associated with drinking water sources other than the city supply, higher animal densities, the absence of rodent control programs or all-in/all-out systems, farmers being members of pig health protection associations, and non-solid box separation (i.e. bars or similar). The SaTScan software was used to identify potential clusters of *Salmonella*-infected herds in the area, but no significant clusters were found. Results suggest that *Salmonella* infection is widely spread in the surveyed area and that some of the factors associated with it could be mitigated through overall hygiene and biosecurity measures.