Introduction - The first outbreak of infection with pandemic influenza A(H1N1) 2009 virus (H1N1pdm) in a Norwegian swine herd was recorded on 10th of October 2009 (1,2). Until then the Norwegian pig population was considered free of swine influenza (subtypes H1N1 and H3N2) (3). This abstract describes the preliminary results of a retrospective case-control study to investigate human influenza like illness (ILI) as a risk factor for infection of H1N1pdm in Norwegian nucleus and multiplier herds.

Materials and methods - The study population comprised 118 nucleus and multiplier herds. Three herds were excluded on the basis of uncertain infection status at the time of the study. Of the 115 remaining herds, 47 were nucleus herds, and 68 multiplier herds. All herds were tested serologically or by rRT-PCR during the risk period (30th September 2009 until 31st Oct 2010). Information on clinical history of humans and pigs were collected by questionnaire and telephone interview. We calculated the odds ratios (OR) for each risk factor and used one-sided Fisher’s exact test to calculate statistical significance.

Results - Response rate from farmers was 100%. A total of 20 (43%) of the nucleus herds and 28 (41%) of the multiplier herds were classified as positive. Chronological disease data from relevant humans and pigs were available from 14 of the 48 positive herds. Twelve of these reported ILI in humans followed by contact with pigs before the pigs began to show clinical signs of H1N1pdm infection. Extrapolated to the whole study population this gives a probability of 65-99 % (95% confidence interval) of humans being infected before the pigs.

Discussion - The results from this study indicate that ILI in people with pig contact was a significant risk factor for H1N1pdm infection in pigs. During the human influenza season in Norway 2009/2010, nearly all influenza strains that were subtyped were confirmed to be H1N1pdm (4). Furthermore, genome sequencing of the virus from a pig on one farm confirmed it as identical to the virus from a sick farm staff member at the same farm (1). Our findings are supported by other studies that have shown the reverse zoonotic potential of the H1N1pdm (5).

References