Evidence of influenza A infection and risk of transmission between pigs and farmworkers
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Key points
- Interspecies transmission of influenza A virus (IAV) between pigs and people represents a threat to both animal and public health.
- Farmworkers can report to work infected with pandemic H1N1 influenza and can also harbor swine origin influenza virus in their nasal passages temporarily.
- Self-reporting of influenza like illness is not a reliable screening method to detect infected workers

Methods
To better understand the risks of influenza transmission at the farmer-worker-swine interface, a study was conducted during the 2018 and 2019 winter seasons in the Midwestern US. Farmworkers on seven commercial swine breeding herds volunteered to participate. Farmworker sampling consisted of two daily self-collected nasal swabs, twice a week, for a period of 8 weeks. The first nasal swab was collected at the farm in the morning prior to entering the barns and the second collected at the end of the working day. Moreover, farmworkers were asked to complete a short questionnaire each time they collected a nasal swab. The questions gathered information on the participant that may have exhibited ILI (e.g., fever, headache, cough, sneeze, muscular ache), the work activities and the farm area where the worker spent most of the day. Sampling of pigs was performed in the participating farms at the beginning, middle and termination of the farmworker sampling period. All samples collected were tested using rRT-PCR specific for human and swine IAV. A subset of farmworker (n = 30) and swine (n = 20) samples, distributed across farms, was selected for IAV whole genome sequencing. Clade classification for each segment was done using the automated classification tool OctoFLU (Chang et al., 2019) (Zeller et al., 2021).

Results
Of 58 workers providing nasal passage samples during 8-week periods during the 2017/18 and 2018/19 influenza seasons, 33 (57%) tested positive by rRT-PCR at least once. Sixteen (27%) workers tested positive before work and 24 (41%), after work. At the sample level, 58 of 1,785 nasal swabs (3.2%) tested rRT-PCR positive, of which 20 of 898 (2.2%) were collected prior to work, and 38 of 887 (4.3%) after work. Although farmworkers were more likely to test positive at the end of the working day (OR = 1.98, 95% CI 1.14-3.41), there were no influenza-like illness (ILI) symptoms, or other risk indicators, associated with IAV detection before or after reporting to work. Direct whole genome sequencing from samples obtained from worker nasal passages indicated evidence of infection of a worker with pandemic 2009 H1N1 of human-origin IAV (H1-pdm 1A 3.3.2) when reporting to work, and exposure of several workers to a swine-origin IAV (H1-alpha 1A 1.1) circulating in the pigs on the farm where they were employed (Figure 1).

Discussion
We showed evidence that workers can be asymptomatic carriers of swine origin IAV in their nasal passages and confirmed that workers can report to work infected with IAV of human origin that could potentially be transmitted to the pigs. Overall, our results emphasize the need to implement surveillance and transmission preventive protocols at the pig/human interface. Preventing transmission at the pig/people interface will not only benefit public health and prevent zoonotic infections of pandemic potential, but will also help the swine industry to mitigate the economic impact of IAV infections in pigs.

![Figure 1. Clade classifications of the influenza A virus genetic segments from human and swine samples using the OctoFLU platform. Each row is a sample. AM: Samples were collected prior to entering the workplace; PM: Samples were collected after work. pH1: samples subtyped as pandemic-like H1; NT: non-typeable. HA: hemagglutinin; NA: neuraminidase; PB2: polymerase basic 2; PB1: polymerase basic 1; PA: polymerase acid; NP: nucleoprotein; M: matrix; NS: non-structural. Genes segments were classified in different clades and colored as follows: pandemic-like clade (green), H1-alpha clade 1A.1.1 (light blue), H3-2010-human-like clade 3.2010.1 (light green), H3-cluster IV clade 3.1990.4.1 (light brown), live attenuated influenza vaccine clade 1A.2.3-like (blue), N2-2002A and N2-2002B (light yellow), triple reassortant internal gene (TRIG; red), and classical swine (grey). Blank squares are segments from which no sequences were obtained. Number in parenthesis in the sample type column refers to the worker identification.](image-url)