



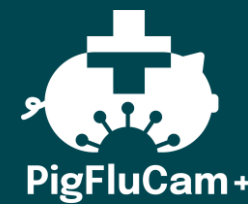
# Understanding zoonotic and pandemic risk in relation to swine production systems in Cambodia

Hannah Holt

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# Background

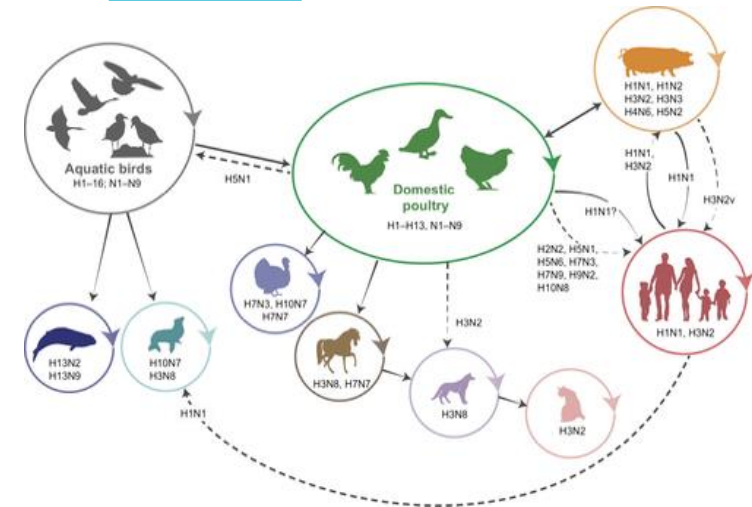


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- Pigs play a key role in pandemic influenza emergence
- Limited knowledge on ecology and evolution of influenza viruses in pigs
- In Cambodia:
  - Fertile conditions for interspecies transmission and virus reassortment
  - Livestock sector undergoing rapid change
  - No routine/systematic surveillance for influenza among swine
  - No influenza virus sequence data from swine

Joseph U, Su YF, Vijaykrishna D, Smith GJD (2017) The ecology and adaptive evolution of influenza A interspecies transmission. *Influenza and Other Respiratory Viruses* 11, 74–84. doi: [10.1111/irv.12412](https://doi.org/10.1111/irv.12412)



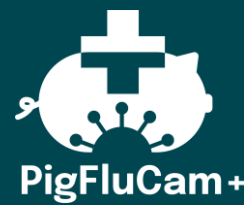
## AGRICULTURE

### African swine fever wipes out Asia's backyard pig farmers

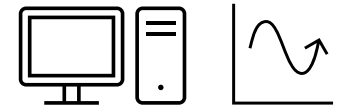
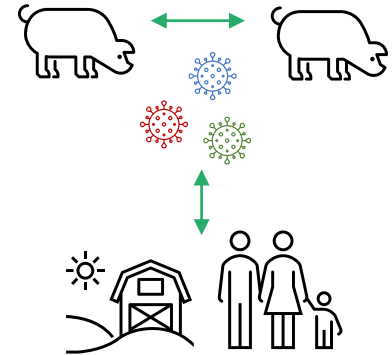
Outbreak forcing a shift to commercial operations with biosecurity resources

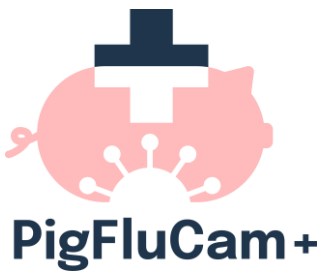


# Objectives



1. Characterise the live pig trading network in Cambodia
  - a. Describe the epidemiology and diversity of swine influenza in pig systems
  - b. Investigate how anticipated changes may influence influenza transmission risk among pigs/pig farms
2. Identify how rates of zoonotic influenza transmission vary across demographic and occupational groups
3. Develop models of influenza transmission dynamics at the swine-human interface, to inform strategies for early detection and reduction of zoonotic and pandemic risk
4. Enhance capacity for One Health research, surveillance, and collaboration

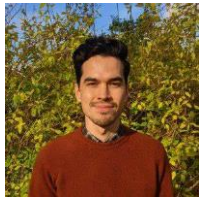
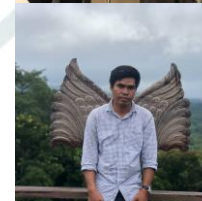




University of Health Sciences (Public Health Institute)

Livestock Development for Community Livelihood (Cambodian NGO)

General Directorate of Animal Health & Production (Government)



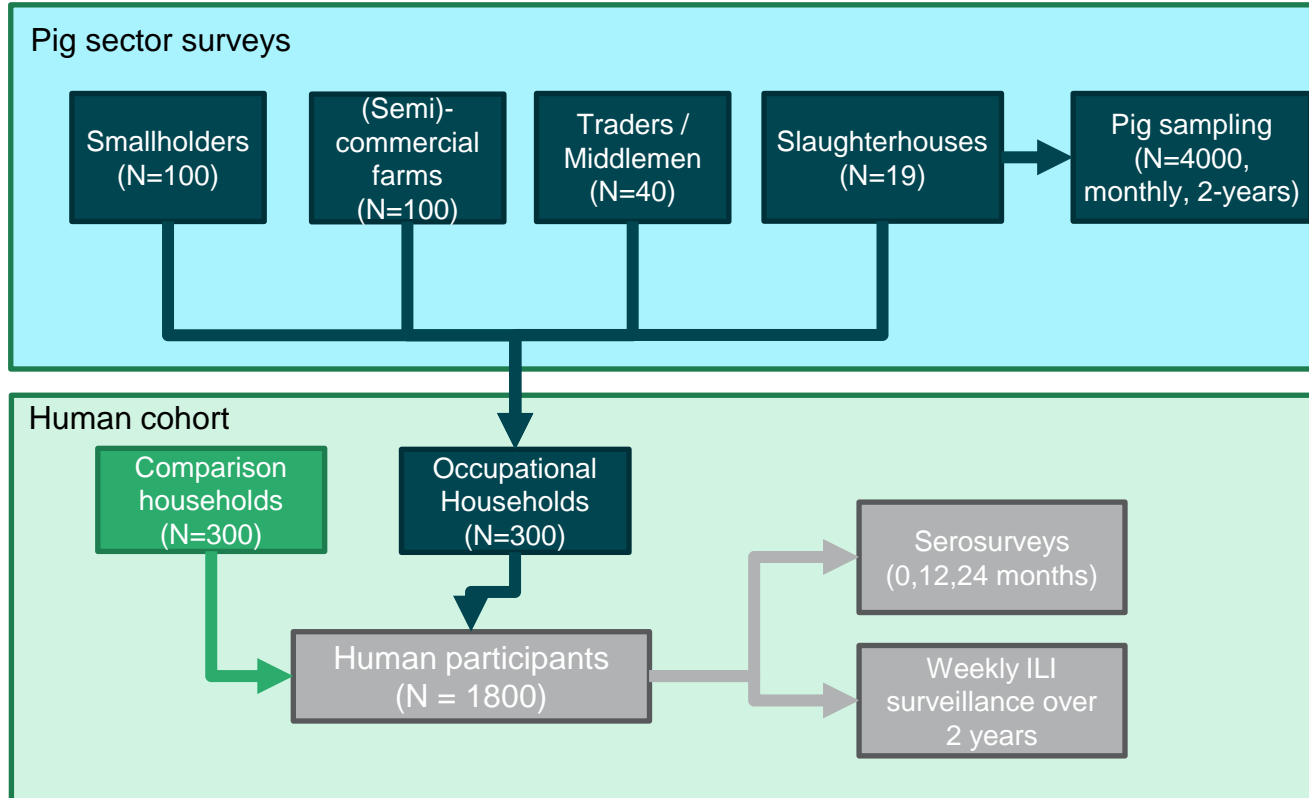
**Funder**

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# Epidemiological surveys



- Interviews with actors in the pig network (demographics, management and trade)
- Sampling of pigs at slaughterhouses
- Non-invasive sampling in pig farms
- Serological surveillance of influenza in human cohort

# Questionnaires – pig network

	1. Producers (Smallholders, boar service, farms)	2. Exchangers (Middlemen, traders, butchers)	3. Slaughter houses
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Alter	Recall period	6 months	14 days	7 days
	Pig trade (inc. boar hire)	<b>Actor;</b> Location; Company affiliation; <b>Pigs traded;</b> # and types; Trade frequency; Relationship; Contact details		
Ego	GPS	✓	x	✓
	Demographics	✓	✓	✓
	Management	✓	✓	✓
	Pig health	✓	✓	✓
	Longitudinal	x	✓	✓

▼ **B. Pig Trading/Exchange and other contacts**

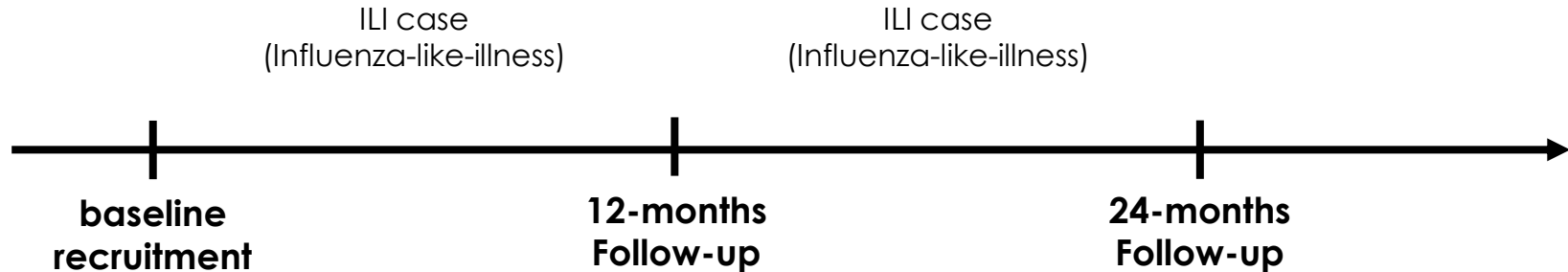
**B1. Do you keep records of the farm's purchases and sales of pigs?**  
*If they do ask if you can take pictures of the records*

Yes  
 No  
 Unsure

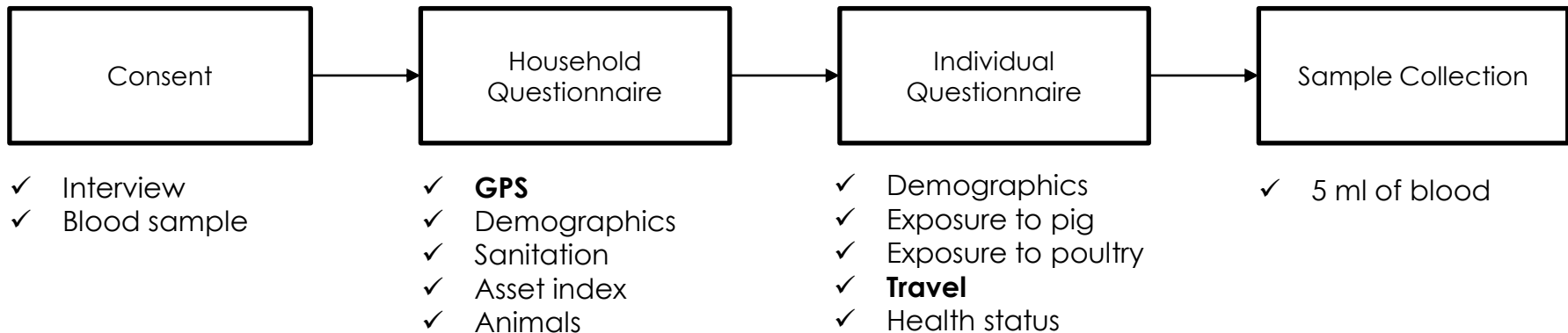
**B2. In the past 6 months, have you purchased (or otherwise acquired) any LIVE pigs?**

Yes  
 No  
 Unsure

# Human cohort surveys



## Study procedures



# Pig production landscape



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Smallholders (N = 173)



Boar Service Providers (N = 19)

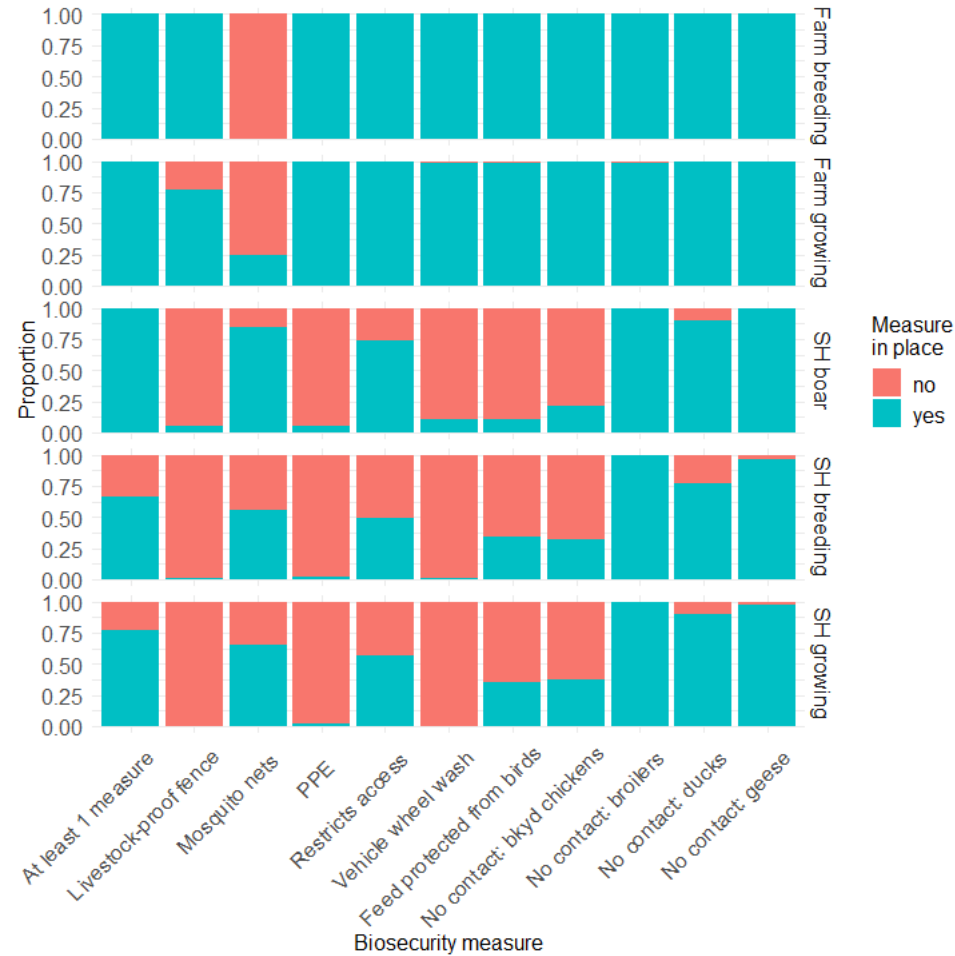


Commercial farms (N = 91)

Breeding farms

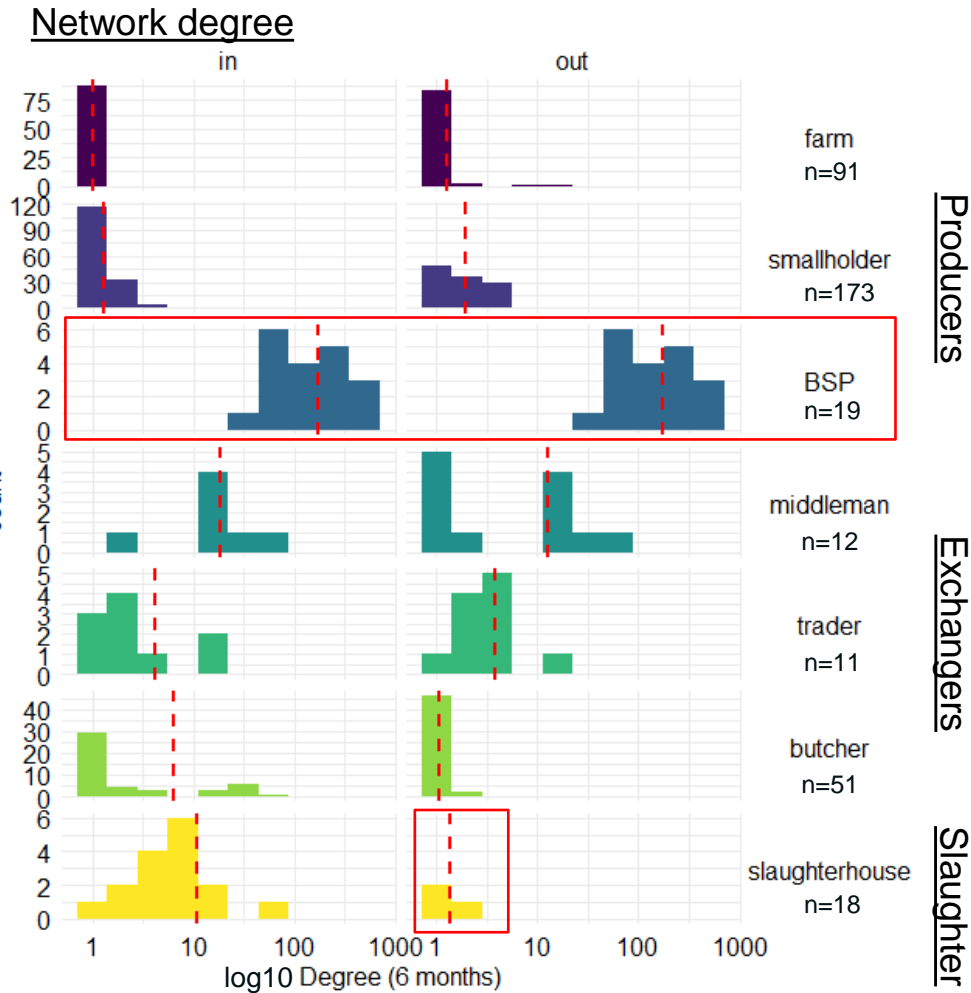


Growing farms





# Pig network

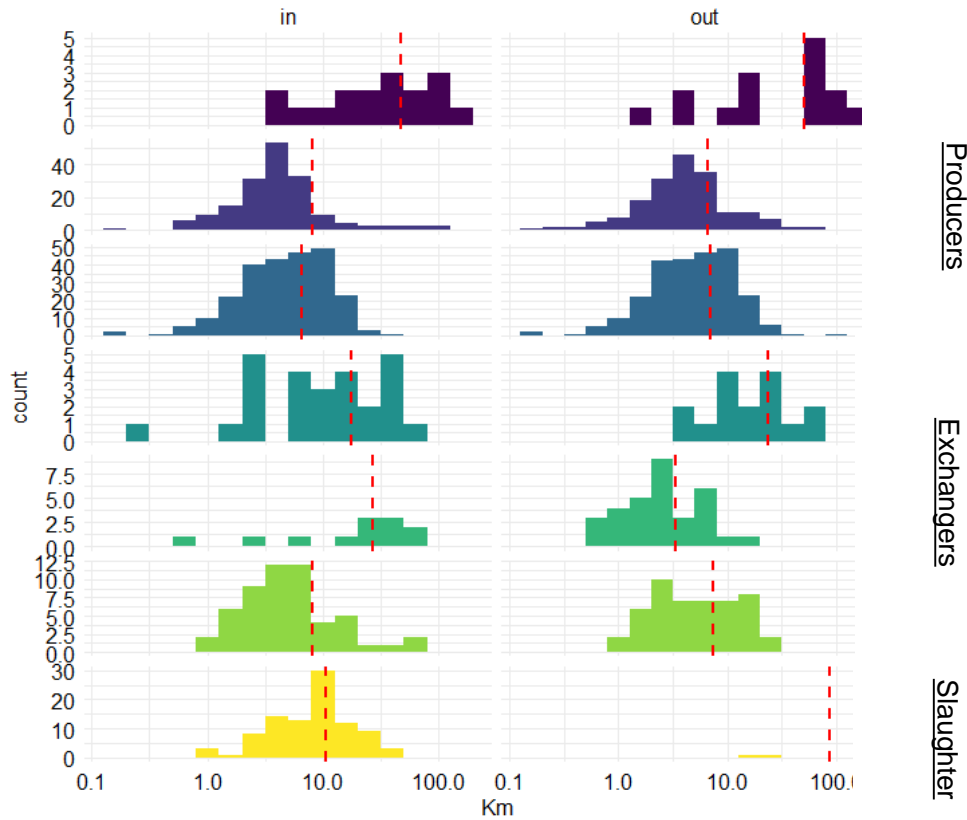


- Most actors have few suppliers and repeat transactions
- Some outward flow from slaughterhouses
- Boar service providers: hubs



Tornimbene and Drew (2012)

# Trade distances



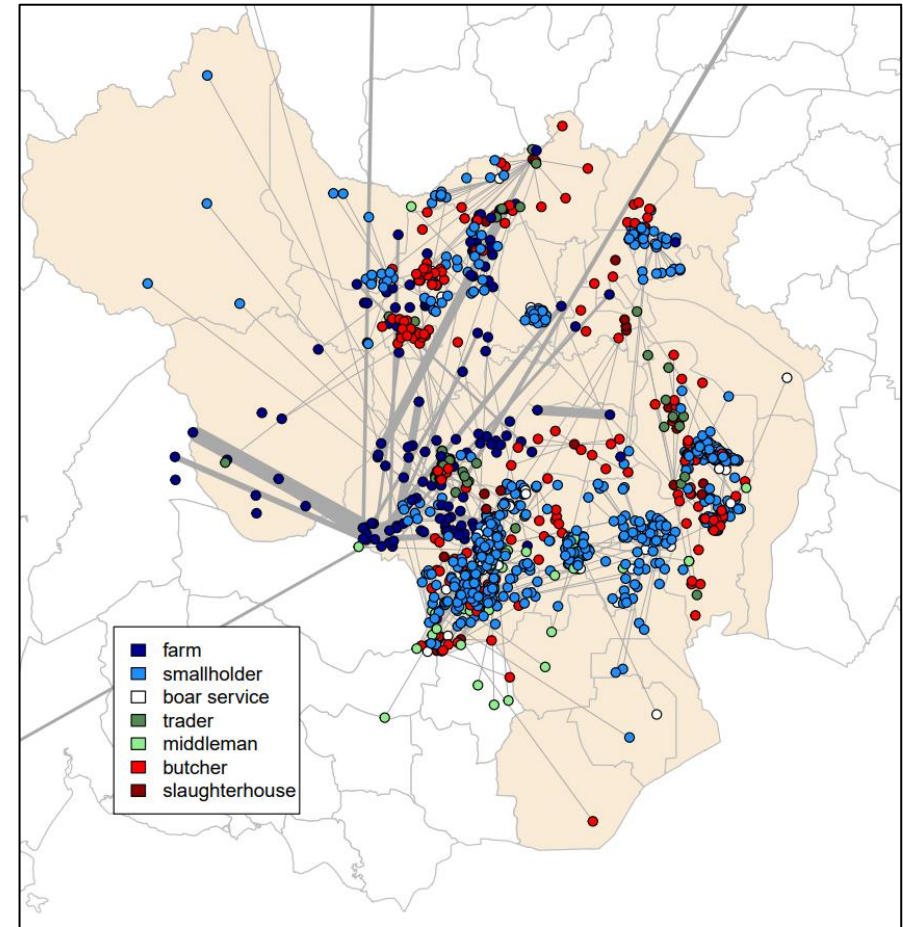
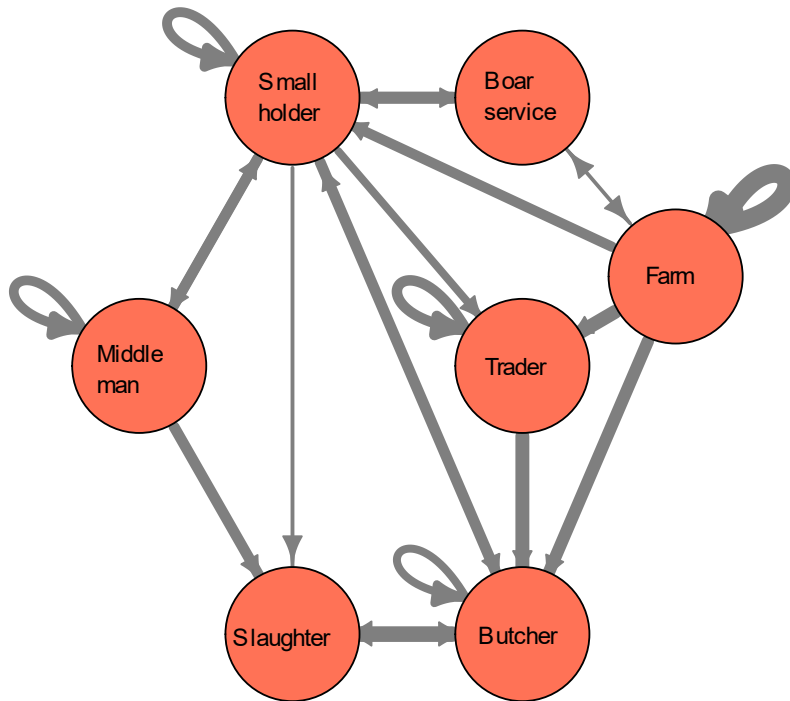
- Most trades occurred at short distances
- Exchangers facilitate longer trades
- Farms commonly trade at larger distances



# Pig network



All pig types

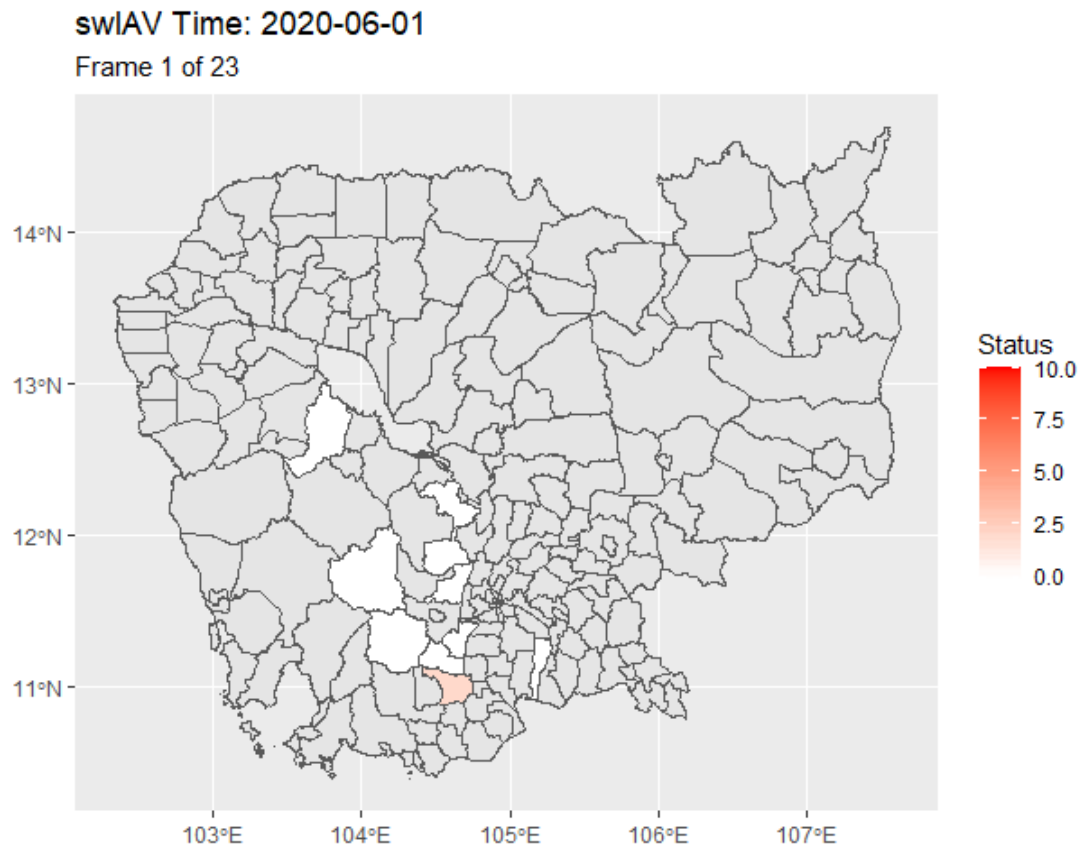


(Locations jittered within district/commune)

- **Next step:** simulate complete network using *exponential random graph models*

# Pig slaughterhouse surveillance

- Samples collected from ~4000 pigs at slaughterhouse
- 2% PCR positive for influenza A M-gene / 34% seropositive by ELISA
- Smallholders had 0.15 (95% CI: 0.02 to 0.81) odds of testing positive



# Influenza surveillance in pigs

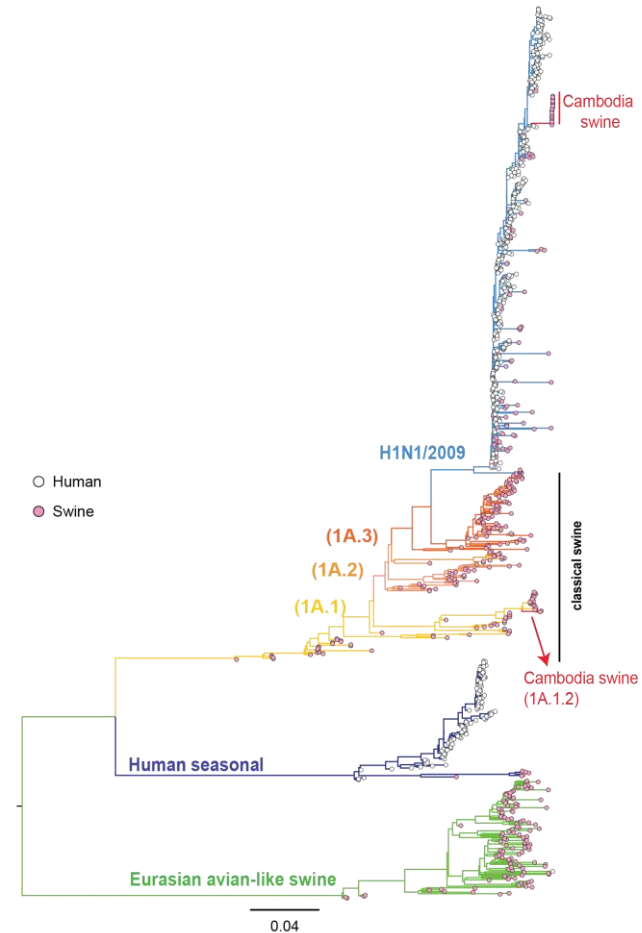


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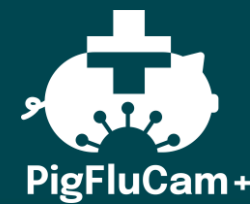
- NGS sequencing yielded 29 complete genomes
- Majority of the viruses belong to human H1N1 pandemic virus. Eight human H3 sequences were also detected.
- Phylogenetic analysis ongoing.
- Next step: Luminex assays using antigens developed from the sequence data and test all pig and human sera

a) H1-HA





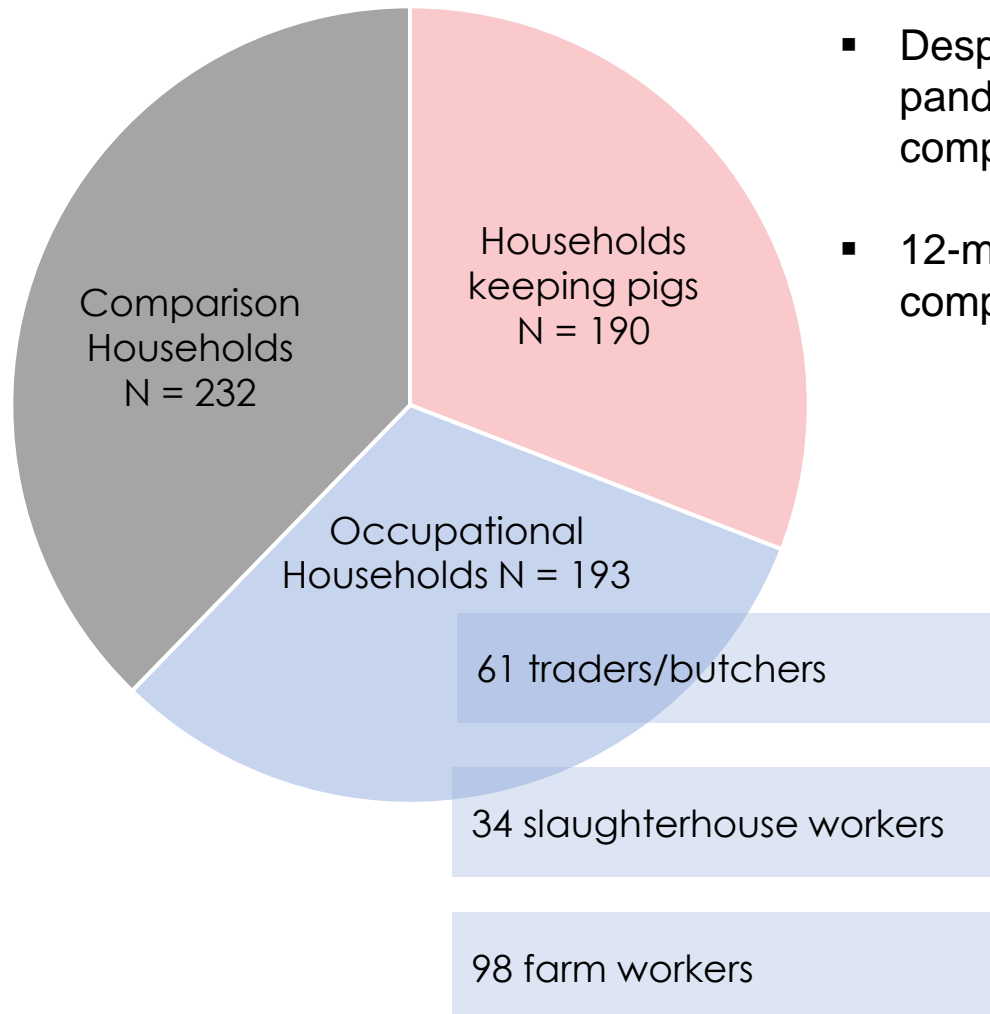
# Human cohort survey



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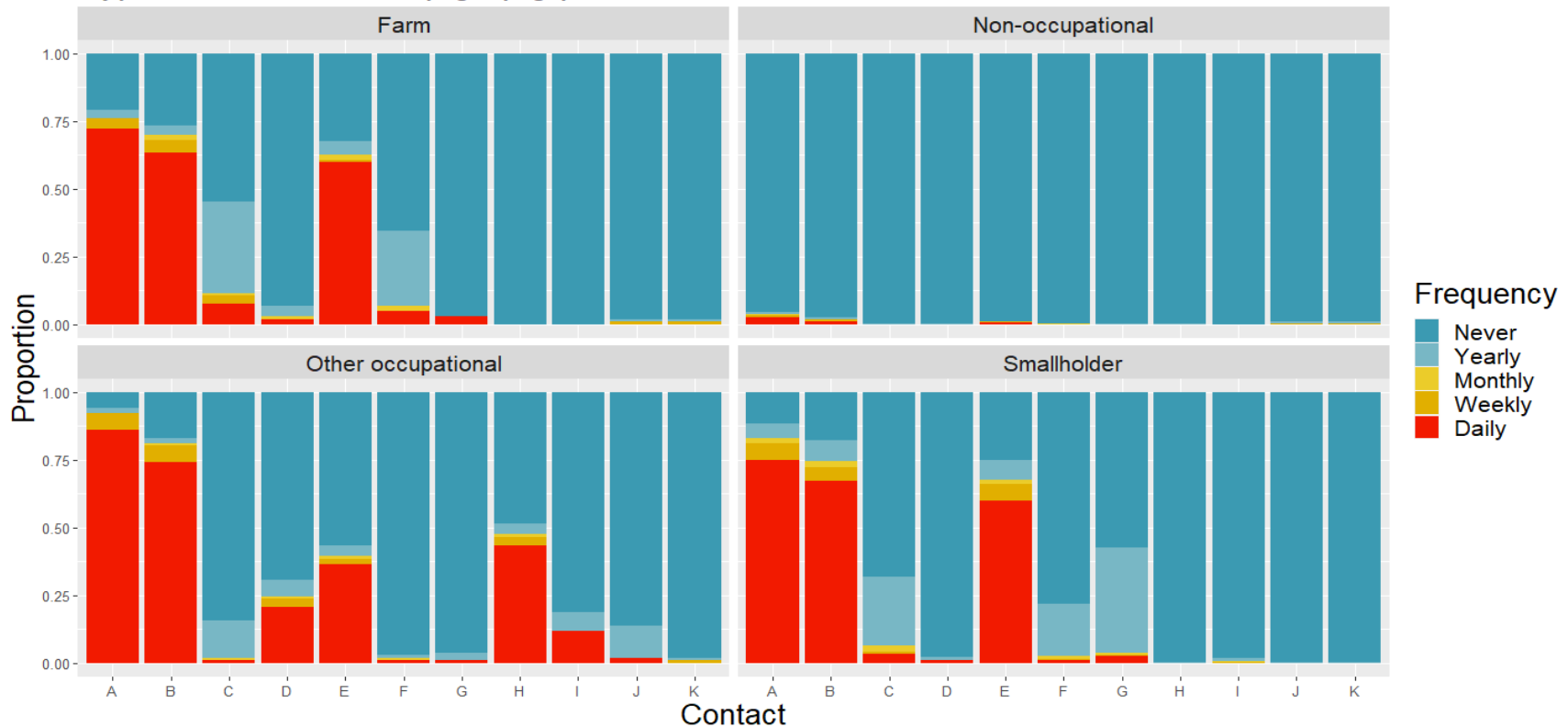
## Households Recruited N = 615



- Despite significant delays due to COVID-19 pandemic, baseline recruitment has been completed
- 12-month follow-up surveys have been completed in 417 (67.8%) of households

# Pig contacts

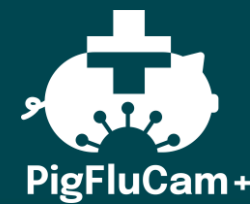
## Types of contact with pigs/pig products



*Frequency of pig contacts of individuals recruited according to type of household.*

*A = Occupation involves pig, B = Touch live pigs, C = Touch sick pigs, D = Transport pigs, E = Clean pen, F = Treat pigs, G = Farrowing, H = Slaughter, I = Process Carcass, J = Handle offal, K = Eat raw pork.*

# One Health Network & Training



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- Post-graduate students (1 PhD student, 3 LSHTM MSc students, 2 UHS MSc students)
- **Training workshops:**
  - Field biosafety and biosecurity (with ACIAR – P Selleck)
  - Field epidemiology
  - **Spatio-Temporal** analysis (with RVC – G. Fournie & D. Pfeiffer)
  - Qualitative interview methods
- One Health online training course (LSHTM Open Study online platform)
- Statistical analysis with R (starting tomorrow)

