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**PREDICT**

## EMERGING DISEASE **INSIGHTS**

Extensive overlap of three SADS-CoV bat hosts within intensive pig farming regions in Asia

In October 2016, a novel coronavirus, swine acute diarrhea syndrome coronavirus (SADS-CoV) was discovered at commercial swine farms in Guangdong Province, China<sup>1</sup>. The death of nearly 25,000 piglets was attributed to infection with SADS-CoV, a virus of likely bat-origin as very closely-related CoVs have been identified in *Rhinolophus* spp. horseshoe bats (*R. affinis*, *R. sinicus*, *R. pusillus*, and *R. rex*) roosting in caves near infected farms.

SADS-CoV threatens commercial pig populations at bat-

pig interfaces where other viral pathogens (e.g. Nipah, Menangle, and Ebola Reston viruses) also have been found. It is therefore critical to identify geographic areas with the greatest potential for bat-pig transmission to mitigate the risk of SADS-CoV and other viral spillover and to prioritize surveillance. Here we use spatial analyses to identify areas of greatest risk of SADS-CoV emergence across China and Southeast Asia by modeling the distribution of key *Rhinolophus* host species and their overlap with commercial pig farms.

### Regions of Greatest Overlap

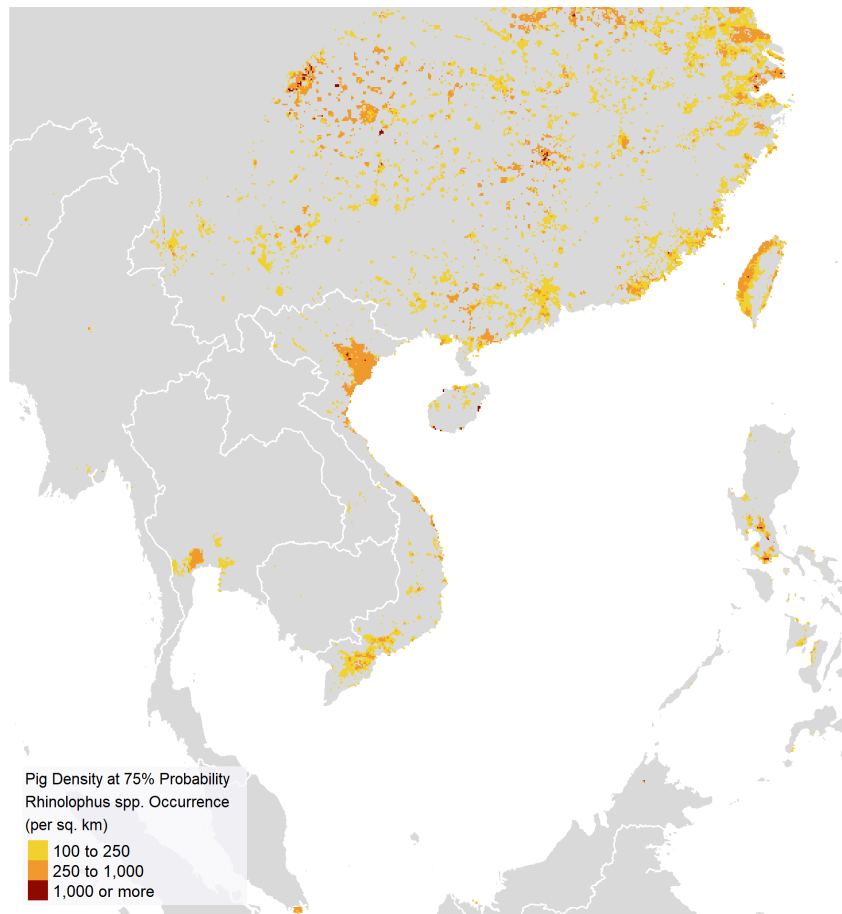
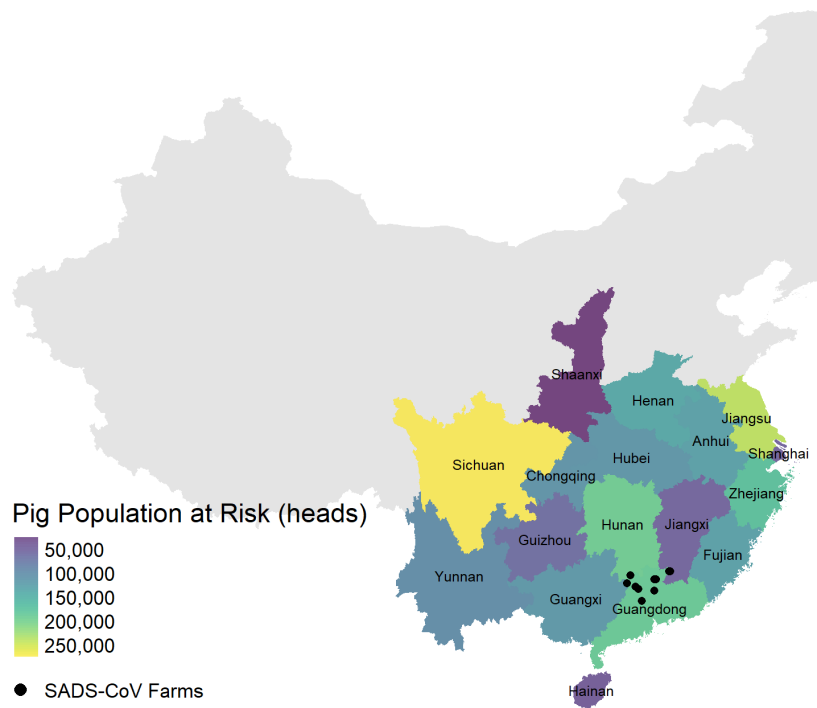
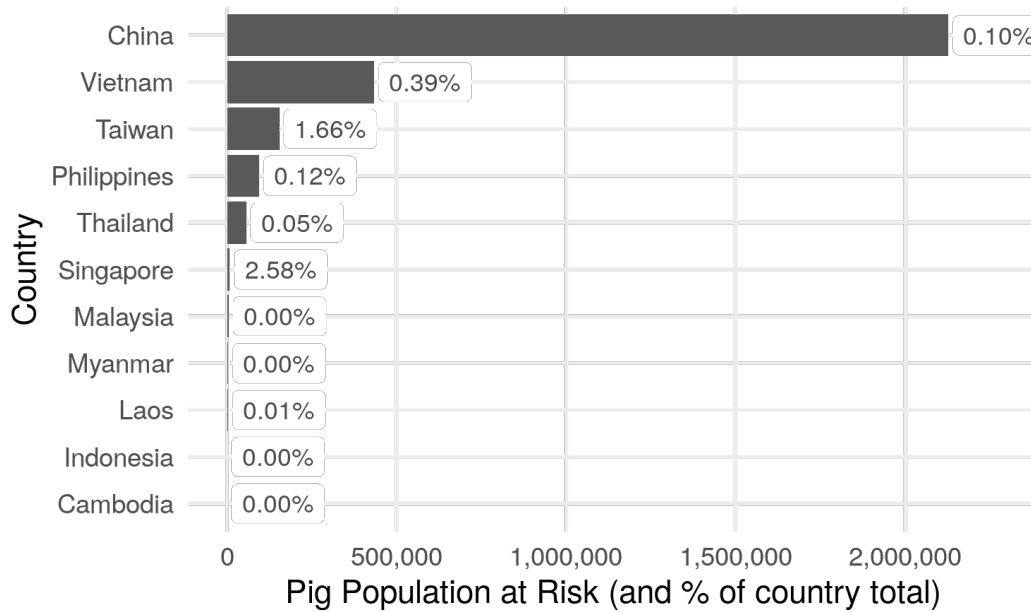


Figure 1: Areas of bat-pig overlap where probability of SADS-CoV *Rhinolophus* spp. reservoir occurrence is high (>75%) and pig densities are indicative of intensive pig farming (>100 pigs per km<sup>2</sup>).

The largest areas of spatial overlap among SADS-CoV host species and pig farms are localized mainly to Southern China (including Taiwan), throughout Vietnam, the Philippines, and Thailand. Compared to other countries, China had the largest area of bat-pig overlap with 330,000 km<sup>2</sup> (3.4% of total country area with a density of >100 pigs per km<sup>2</sup>) and 2,130,000 pigs located within predicted bat distributions. By Chinese province, the largest area of overlap was found in Jiangsu (242,000 pigs over an area 35,200 km<sup>2</sup> amounting to

34.3% of the province's area). Sichuan had the largest pig population at risk: 274,000 pigs over 26,000 km<sup>2</sup> (5.4% of the total area of the province).

**Conclusion:** This analysis uses the best available science to identify key regions where the likelihood of SADS-CoV spillover is highest. It allows better geographic targeting of future research to understand SADS-CoV and interventions to block spillover across the pig-bat interface.

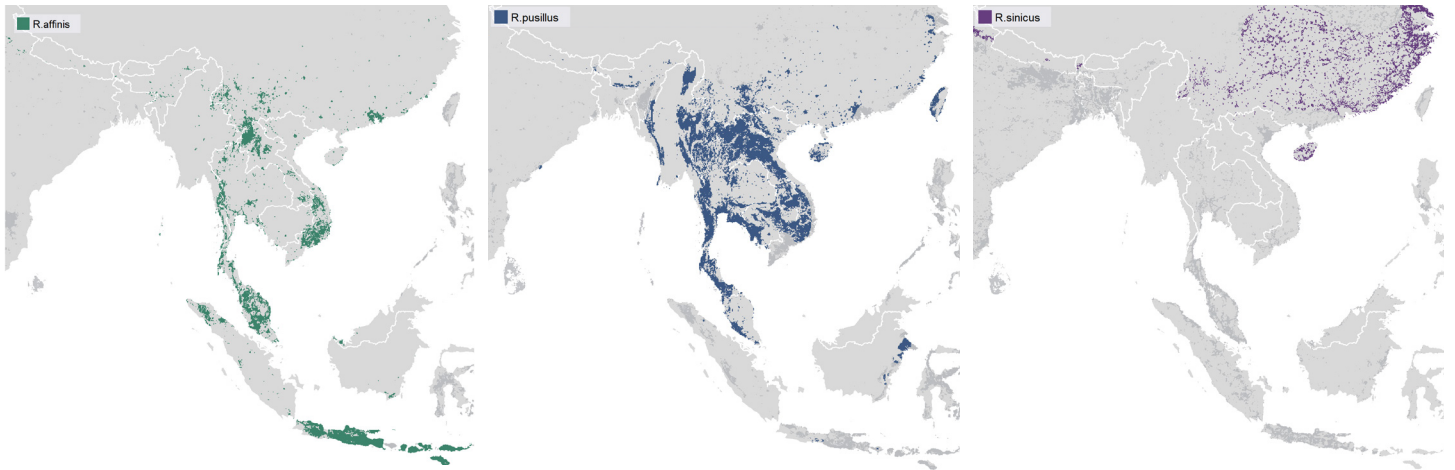


Figures 2-3: Total pig population at risk by country (and percentage of total), and by Chinese province. Pig population at risk is defined by the number of pigs within an area that intersects with predicted bat occurrence. Among China's 2,130,000 pigs in spatial overlap areas, Sichuan and Jiangsu provinces each had over 200,000 pigs in areas of SAD-CoV spillover risk.

## Species Distribution Modeling

The PREDICT-2 Modeling & Analytics team used MaxEnt to create species distribution models for *Rhinolophus affinis*, *R. pusillus*, and *R. sinicus*, potential hosts implicated in the initial SADS-CoV spillover event. There were insufficient occurrence records to model the species distribution for *R. rex*, the fourth bat species in which SADS-CoV was previously detected<sup>1</sup>. Occurrence records for each host species were derived from

PREDICT-1, PREDICT-2, and NIAID 1R01AI110964 data, and the Global Biodiversity Information Facility (GBIF). Fourteen bioclimatic variables from BIOCLIM, land cover type, karst landscapes, night time lights, and human population density were inputs for the model. Predictive accuracy was high for the best-fitting models, with mean AUC values of 0.82 (*R. affinis*), 0.80 (*R. pusillus*), and 0.72 (*R. sinicus*).



Figures 4-6: Species distribution models of *R. affinis*, *R. pusillus*, and *R. sinicus* projected to IUCN species range extents (colored), and predicted distributions outside of IUCN range in grey. These bat species distribution models were used to map bat-pig overlap in Figure 1.

### References:

1. Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, et al. Fatal acute diarrhoea syndrome caused by an HKU-2 related coronavirus of bat origin. *Nature*. 2018; 556(7700):255-258. doi: 10.1038/s41586-018-0010-9.
2. Proosdij ASJ, Sosef MSM, Wieringa JJ, Raes N. Minimum required number of specimen records to develop accurate species distribution models. *Ecography*. 2015; 39(6):542-552. doi: 10.1111/ecog.01509.
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