

# Understanding the role of the environment in the spread and variability of Avian Influenza proves useful to mitigating risk

PRESENTER:

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**BACKGROUND:** Avian Influenza virus (AIV) is not only a major concern for domestic poultry but also severely affects wild bird health and populations across the United States. Waterfowl are the primary reservoir for AIV, therefore understanding the viral ecology and prevalence of AIV within waterfowl populations and their respective habitats is essential towards mitigating risk. Through this ongoing research, modified PCR and sequencing of wetland water, sediment, and wild waterfowl swabs is used to gauge AIV prevalence and ecology within biotic and abiotic reservoirs. Sediment, wetland water, and live waterfowl swabs showed high prevalence in the summer of 2021 (winter of 2022/2023 results pending). These results indicate that environmental sampling is a feasible way to monitor AIV presence and/or absence.

## STUDY AREA

### Focused in the Sacramento Valley

- Two separate hydrological basins
  - Sacramento Basin (Sacramento NWR Complex)
  - Butte Basin (Gray Lodge SWA, Butte Basin SWA)
- 5 high use and 5 low use wetland areas
  - Use level determined by NexRad technology, along with observed bird counts

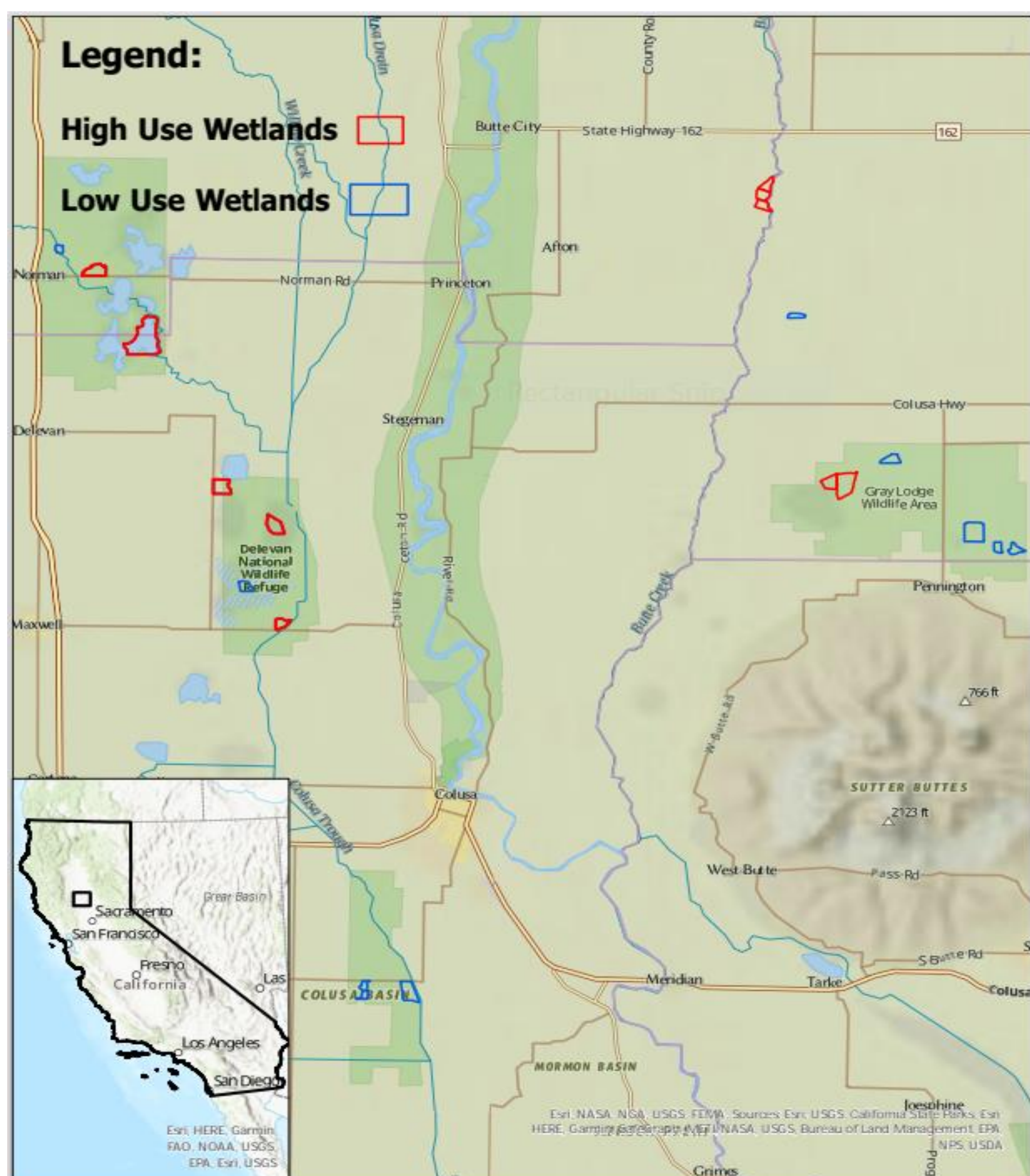


Figure 1. Sampling area highlighting high- and low-use selected wetland areas.

# Prevalence and Viral Ecology of Avian Influenza in Wetlands of High Versus Low Waterfowl Use in the Central Valley of California

## Wetland Water Samples

- Of the 94 water samples tested thus far, 33 contained reads matching Avian Influenza (35.11%)
- When comparing low use wetlands to high use wetlands, a visible trend can be observed (higher viral load in high use wetlands)

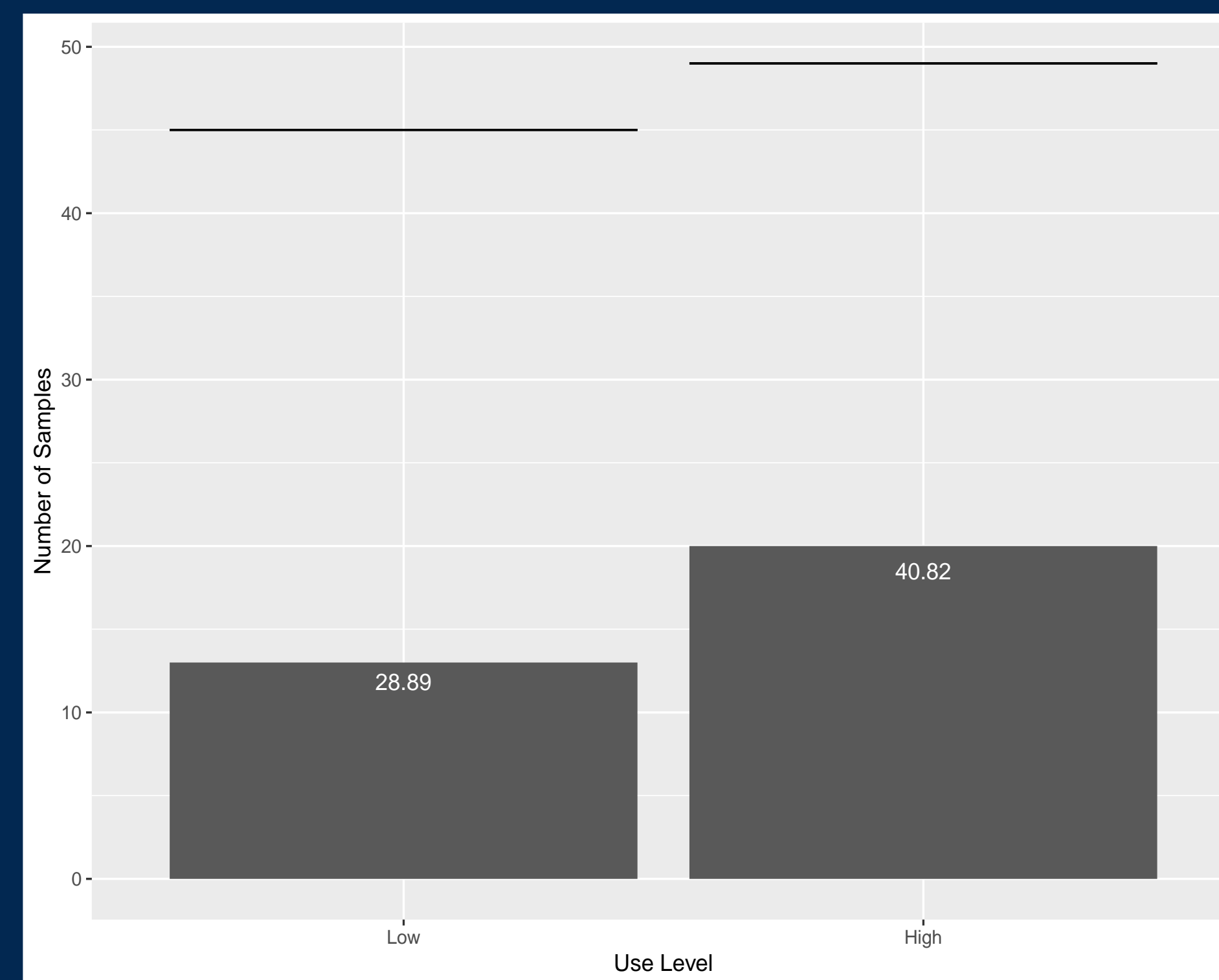


Figure 4. AIV prevalence in wetland water samples

## Wetland Sediment Samples

- Of the 94 sediment samples tested thus far, 80 contained reads matching Avian Influenza (85.11%)
- When comparing low use wetlands to high use wetlands, a visible trend can be observed (higher viral load in high use wetlands)

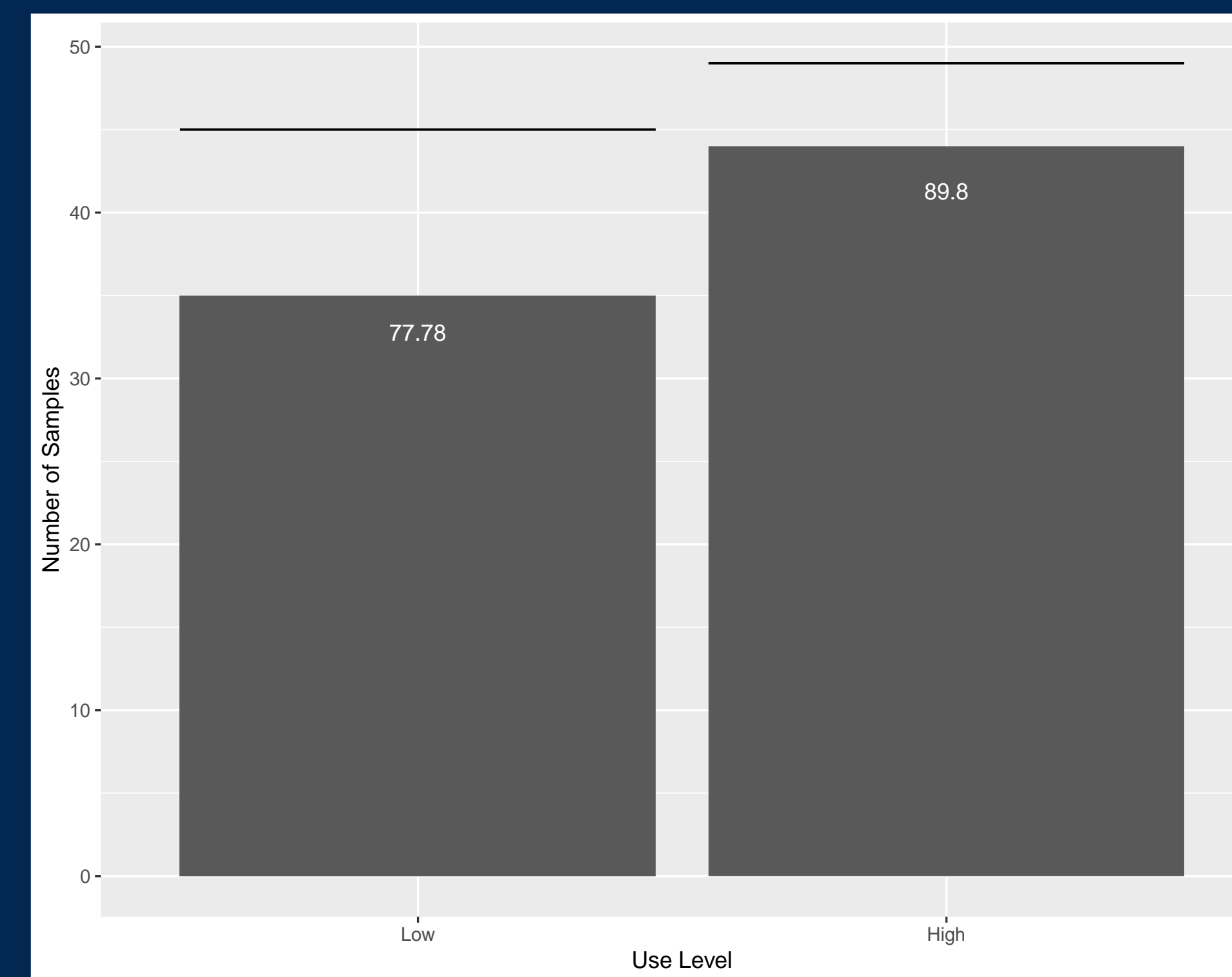


Figure 5. AIV prevalence in wetland sediment samples

With these preliminary results, we have been able to show that testing the environment, especially within the habitats of wild waterfowl, is a feasible way to show AIV presence and/or absence. Thus far, sediment seems to prove the most sensitive, often times with samples yielding a full 8 segments of the AIV genome. While at times in both forms of environmental samples incomplete genomes were found, these methods still locate AIV in a vast area, and show presence of the virus shed and transmitted by waterfowl. In the future, these methods and data could be useful to gauge viral load within wild bird populations, as well as warn poultry producers of a need for heightened biosecurity.

Sampling Period	Basin	Filtered Water Samples	Surface Water Samples	Soil Samples	Avian Swabs
Summer 2021	Sacramento Basin	50	10	50	182
	Butte Basin	50	10	50	--
Winter 2022	Sacramento Basin	50	10	50	80
	Butte Basin	50	10	50	80
Winter 2023	Sacramento Basin	50	10	50	80
	Butte Basin	50	10	50	80

Table 1. Breakdown of samples gathered per sampling period, in each individual basin.

## OUR WORK

### Live Bird Swabs

- Of 96 tested bird swabs (oropharyngeal and cloacal) collected in Summer of 2021, 47 have contained reads matching Avian Influenza (48.96% prevalence rate).
- 8 different low-path subtypes identified across 3 species of waterfowl, 2 of which identified as H7 (potential to turn Highly Pathogenic in poultry)

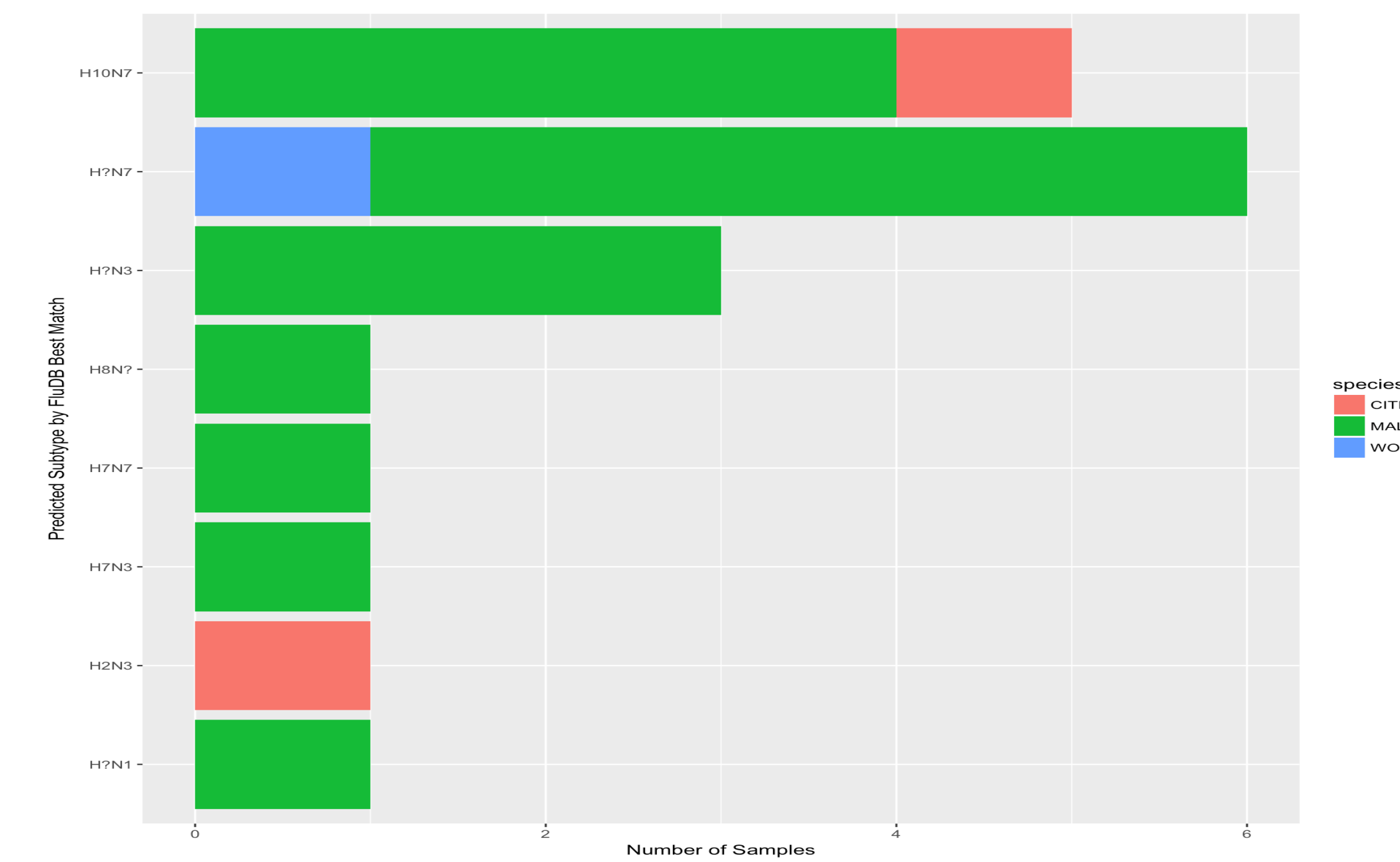


Figure 2. AIV genotypes identified in live bird swabs across 3 tested duck species

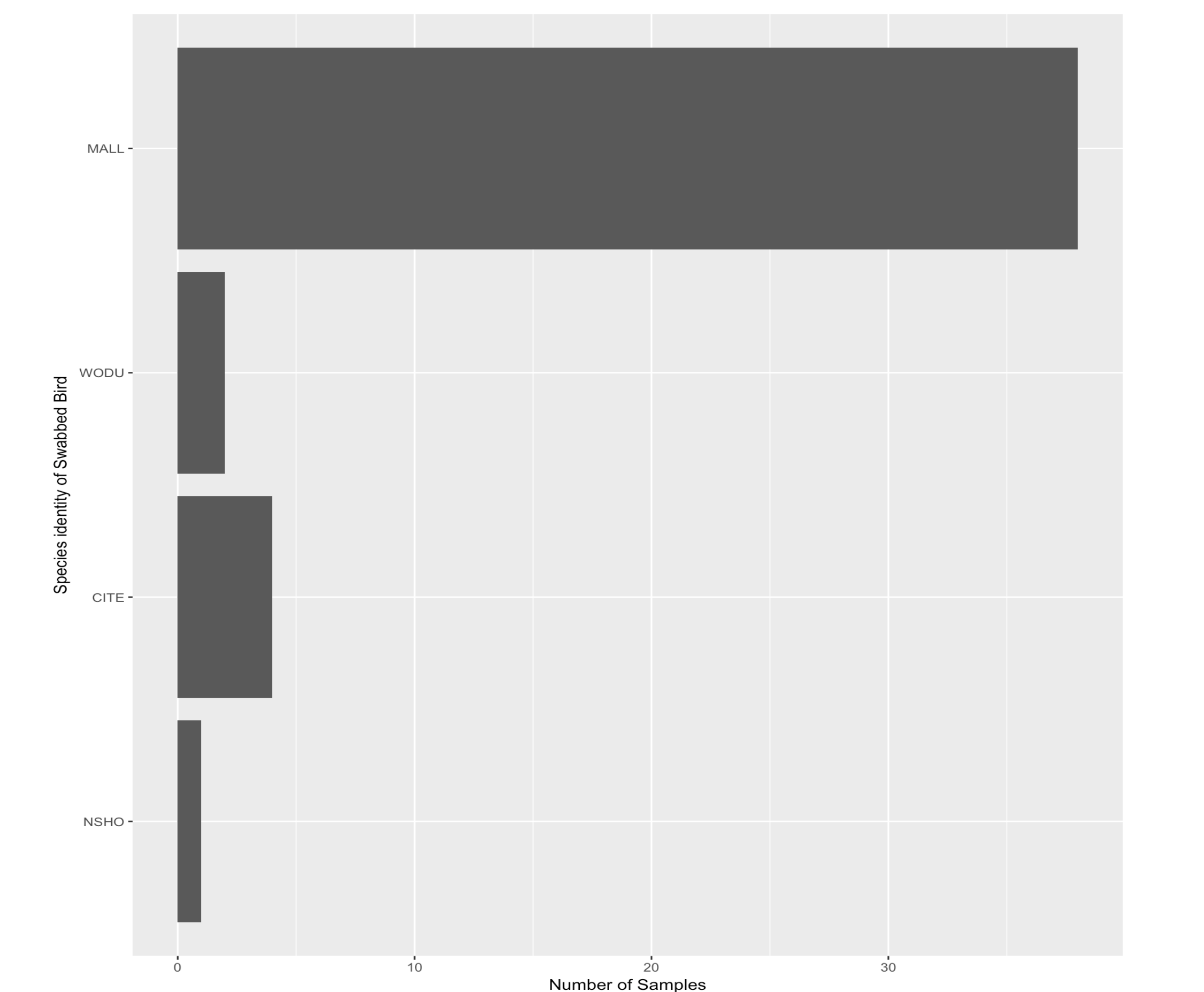


Figure 3. AIV abundance per species swabbed

With these samples, we subjected RNA post-extraction to Influenza-A whole-segment amplification using multi-segment RT-PCR, which uses primers complimentary to genome segment packaging regions conserved across all Influenza-A viruses (including AIV). This procedure, when compared to others used previously, utilize much more sensitive reading methods. Thus, by identifying all Influenza-A viral segments within each sample (environmental or within live birds) and then filtering down to AIV segments, we are able to identify much more virus than we would have using previous methods.



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