Assessment of virus movement across continents: using Northern Pintails as a test

Cooperative Assessment between the USGS, FWS, University of Tokyo, Yamashina Institute

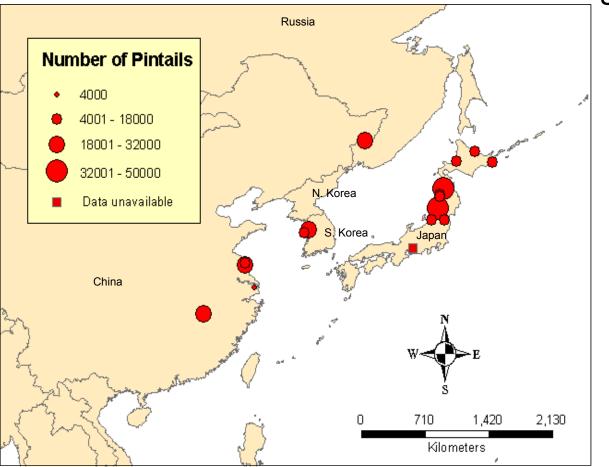


Specific Approaches

- 1. Band Recovery Analyses
- 2. Satellite Telemetry
- 3. Genetic Comparisons of Pintails
- 4. Genetic Comparisons of Viruses.

Why Japan?

- 1. Japan is the major wintering area for pintails in Eastern Asia
- 2. Japan has documented outbreaks of H5N1 that, in at least one case, are thought to have originated in wild birds



Band Recovery Analyses

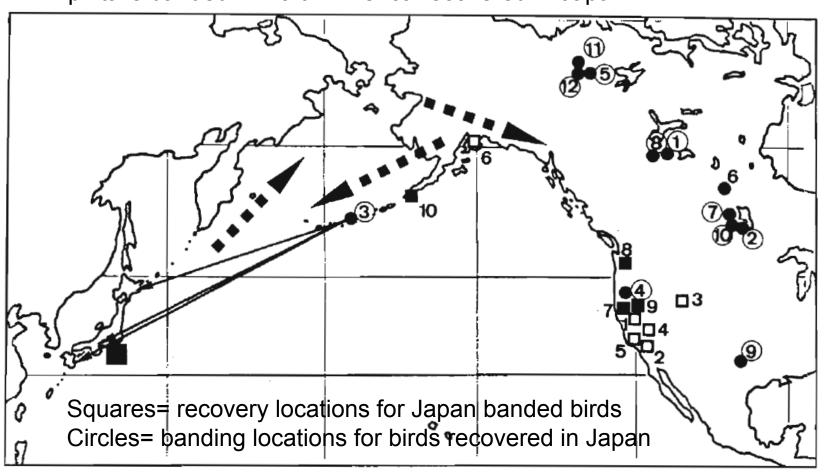
- Yamashina Institute of Ornithology is the functional equivalent of our Bird Banding Laboratory.
- They are not a government agency, basically a NGO
- There is no law governing bird banding within Japan. Anyone can do it, data are not required to be reported.

Intercontinental Band Recoveries

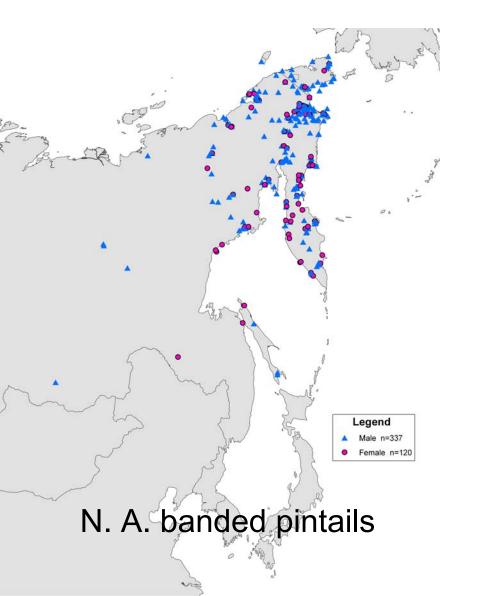
From 1961-2004

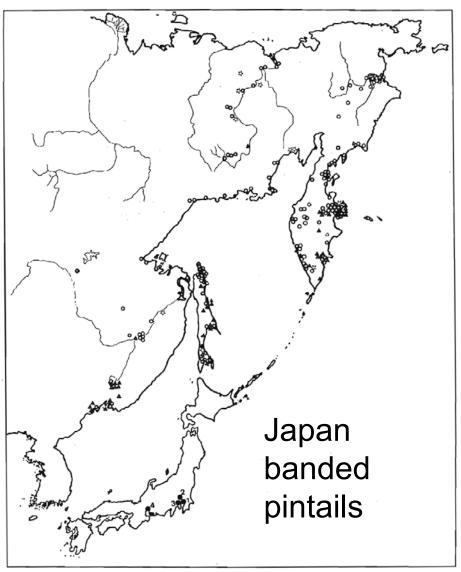
37 pintails banded in Japan recovered in North America

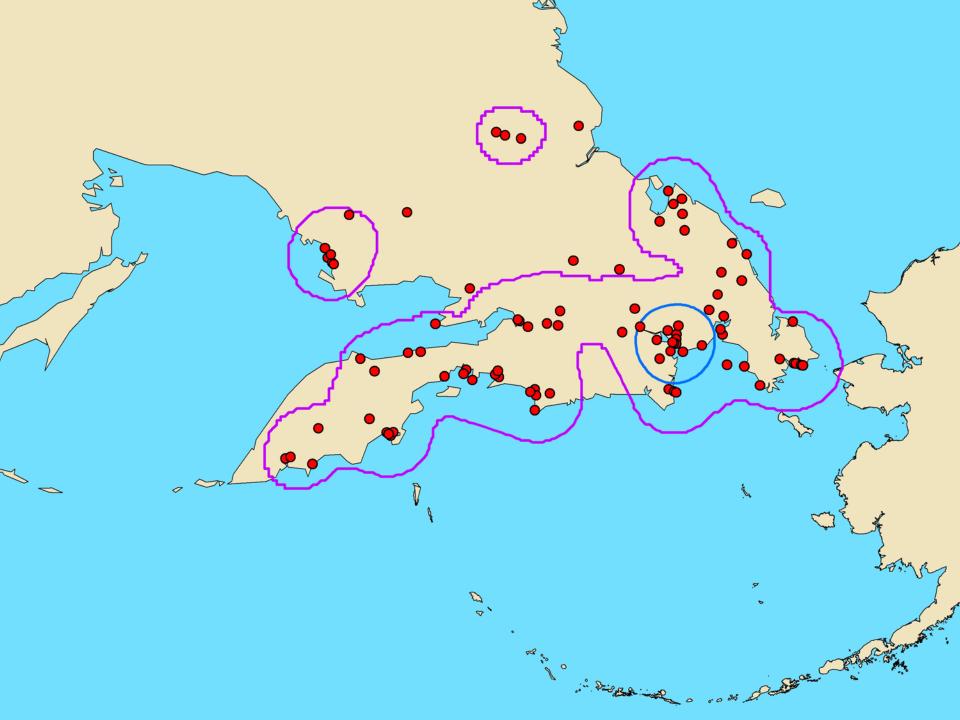
22 pintails banded in North America recovered in Japan



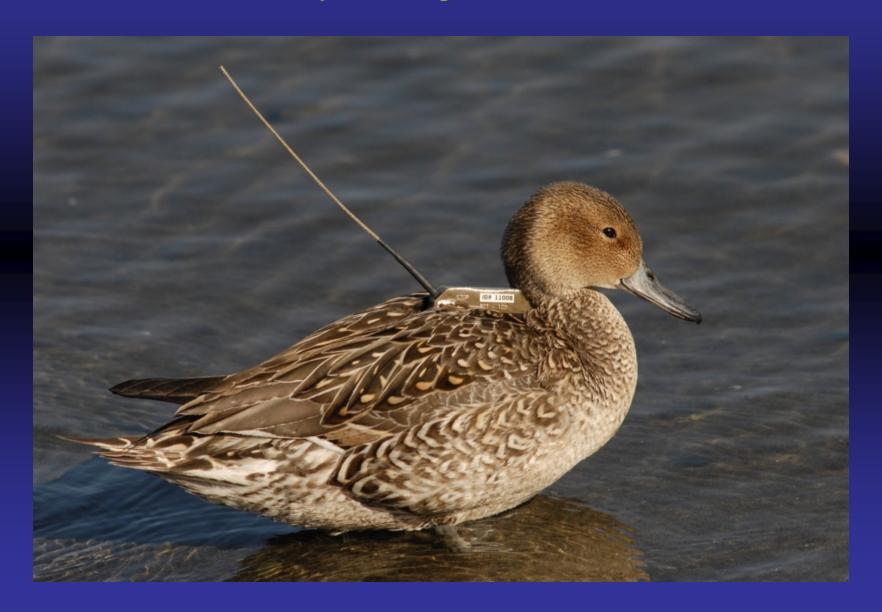
Overlap in recovery locations





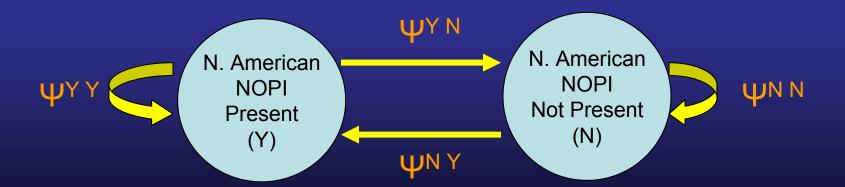


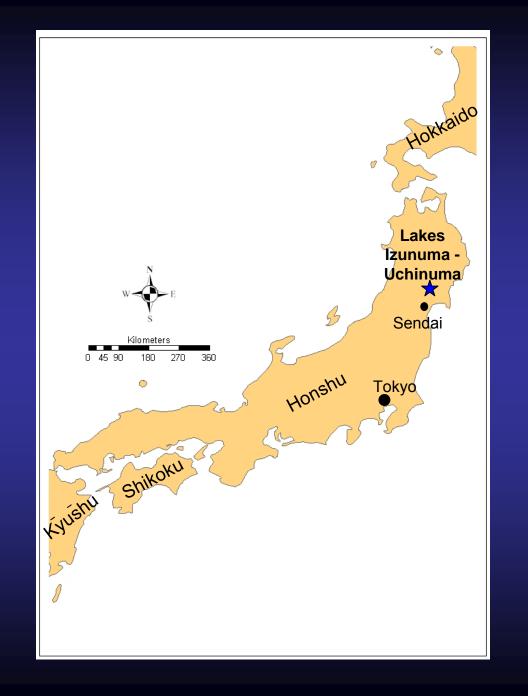
Satellite Telemetry Tracking of Northern Pintails in Asia



Objectives of Satellite Telemetry Study

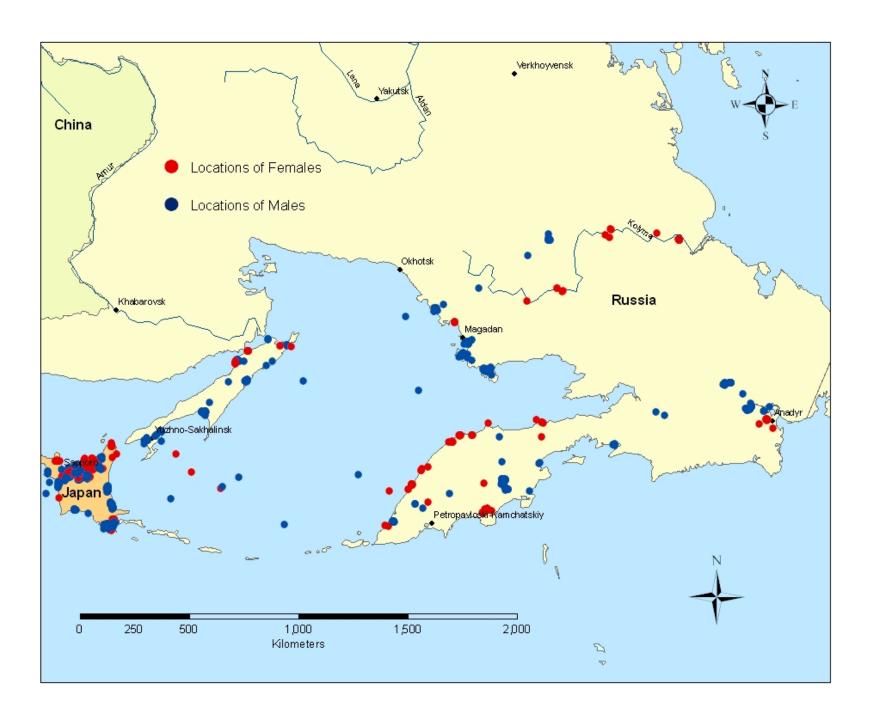
- 1. Evaluate spatial and temporal distribution of Japanese pintails on molting and nesting areas in Russia via satellite telemetry.
- 2. Use multi-strata models to estimate movement of Japanese pintails to areas also likely to be used by North American pintails.











Conclusions

- Evidence that N.A. and East Asian pintails overlap in space and time
 - Occasional direct dispersal between wintering populations.
 - Small proportion of N.A. wintering population is sympatric with Asian population in summer.
 - Satellite telemetry will be used to further define the % time spent in zones of overlap

Evidence of Genetic Exchange

 Ok so now that we have shown that N.A. and Japan wintering pintails overlap in space and time during summer, do they actually have 'contact'?

MtDNA sequence data

- California (n = 60), Japan (n = 53)
- Observed similar levels of diversity in each wintering group
- No evidence for differentiation ($F_{ST} = 0.002$)
- This and other analyses suggest gene flow

Nuclear microsatellite loci

- 8 different loci
- California (n = 138), Japan (n = 60)
- Observed similar levels of genetic diversity in each wintering group
- No evidence for differentiation ($F_{ST} = 0.002$)
- suggests gene flow in agreement with mtDNA

Evidence of Virus Exchange

- To what extent do we find evidence of virus exchange and does it vary by distance?
- Collaborated with USGS Dixon Field Station and California Waterfowl Association to obtain winter virus samples from Pacific Flyway pintails
- Collaborated with USGS National Wildlife Health Center to subtype each virus and sequence all RNA segments

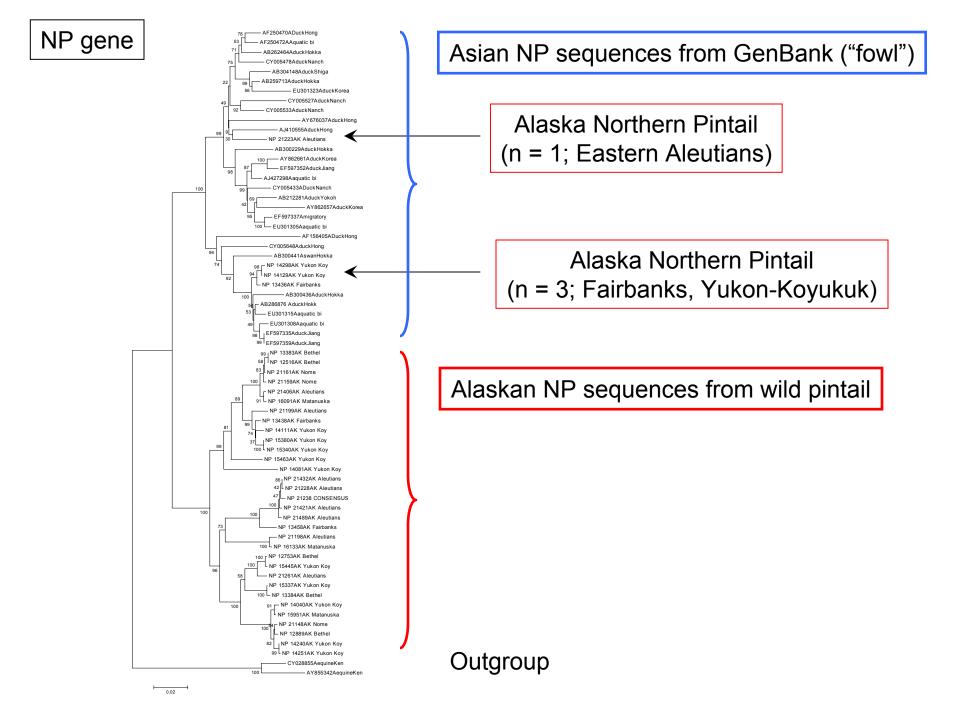
Viral genetic variation: subtyping

```
H1N2
H2N3
H3N1
H3N6
        4
H3N8
        29
H3N9
        1
H4N5
                       83 samples subtyped
H4N6
        11
        5
H5N2
                       24 subtypes observed
H5N9
H6N1
        3
H6N2
H6N4
H7N3
H8N4
H10N2
H10N7
H10N8
        1
        2
H11N2
H11N9
                Green = Rundstadler (1997)
        1
H12N2
                Red = Ito (1995)
H12N5
                Ito found 1 H10N9
H12N8
H12N9
        1
```

Viral genetic variation: sequence data from all 8 RNA segments

Area	N	# putative Eurasian origin*	# putative Eurasian segments (out of 8)
Alaska	38	19 (50%)	1-5 (mode = 1)
California	24	2 (8%)	1-2

^{*}Based on similarity match to sequences available on GenBank



Conclusions

- Evidence that N.A. and East Asian pintails 'exchange' biological material
 - Clear evidence of gene flow amongst populations and viral transfer of some segments
 - Thus, avian species, such as pintails, are a viable mechanism for intercontinental transport of avian influenza viruses via movement and sympatric breeding areas