



GAINS II South America
The Neotropical Waterbird Census Database

Mapping hotspots of Avian Influenza potential spread in South America

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1. Introduction

The objective of this report is to document the development of spatial models to identify hotspots of Avian Influenza potential spread in South America, based on the Neotropical Waterbird Census (NWC) data on 29 selected species, and their map visualizations for summer and winter austral seasons.

2. Source Data

Species Database

Wetlands International Argentina provided an MS Excel spreadsheet containing data from the Neotropical Waterbird Census (NWC) on the occurrence and abundance of the following species selected for their high risk potential (Table 1).

Table 1. GAINS II South America's Species List, Risk Scorings and Species Code.

<i>Species</i>	<i>Scoring</i>	<i>Species Code</i>
<i>Anas cyanoptera</i>	2	ANACY
<i>Anas flavirostris flavirostris</i>	3	ANAFI
<i>Anas georgica spinicauda</i>	3	ANAGE
<i>Anas platalea</i>	2	ANAPA
<i>Anas sibilatrix</i>	2	ANASI
<i>Anas versicolor</i>	2	ANAVE
<i>Calidris bairdii</i>	2	CALBA
<i>Calidris fuscicollis</i>	4	CALFU
<i>Calidris melanotos</i>	3	CALME
<i>Callonetta leucophrys</i>	2	CALLE
<i>Charadrius falklandicus</i>	2	CHAFA

<i>Species</i>	<i>Scoring</i>	<i>Species Code</i>
<i>Chloephaga picta</i>	4	CHLPI
<i>Chloephaga poliocephala</i>	4	CHLPO
<i>Dendrocygna autumnalis</i>	3	DENAU
<i>Dendrocygna bicolor</i>	3	DENBI
<i>Dendrocygna viduata</i>	4	DENVI
<i>Heteronetta atricapilla</i>	2	HETAT
<i>Larus cirrocephalus</i>	3	LARCI
<i>Larus maculipennis</i>	4	LARMC
<i>Limosa haemastica</i>	2	LIMHA
<i>Micropalama himantopus</i>	2	MICHI
<i>Netta peposaca</i>	4	NETPE
<i>Pluvialis dominica</i>	4	PLUDO
<i>Rynchops niger</i>	2	RYNNI
<i>Steganopus tricolor</i>	2	PHATR
<i>Sterna trudeaui</i>	2	STETR
<i>Tringa flavipes</i>	3	TRIFL
<i>Tringa melanoleuca</i>	2	TRIME
<i>Tryngites subruficollis</i>	3	TRYSU

We used Delany *et al.* (2006) criteria to score each species, based on the fact that behavioural and ecological factors are important determinants for the acquisition and transmission of the Highly Pathogenic Avian Influenza (HPAI) virus. Based on these authors, we considered the following factors:

- Habitat use during migration and wintering, *as birds may also be indirectly infected through the environment. It can be expected that indirect infection takes place relatively easily in fresh-water habitats.*
- Gregariousness during migration and wintering, *as epidemiological principles suggest that species which are highly gregarious are more likely to become infected with HPAI, since close contact between birds may result in the virus being more readily passed from bird to bird within flocks.*
- Degree of mixing with other species during migration and wintering, *as waterbirds which readily mix with others species are thought to be more likely to become infected with HPAI, since contact between species may result in transmission of the viral infection.*

Attribute information of the Selected Species Database is described in Table 2. Records were grouped into austral winter (June, July and August) and summer months (December, January, February, and March) to code for corresponding season, creating a field to hold this information and allow record extraction. The following criteria were used to exclude records from the original dataset:

- a. Missing information on geographical location.
- b. Sites outside South America mainland buffer (e.g.: Galapagos, Easter Is.).
- c. Observations outside chosen months.

Table 2. Attributes of GAINS II South America’s Selected Species Database used in this study.

FIELD NAME	DESCRIPTION
PAIS	Country
REGION	Región
NOMBRE SITIO	Site Name
CODIGO SITIO	Site Code / Identifier
Latitud	WGS84 Latitude in decimal degrees
Longitud	WGS84 Longitude in decimal degrees
FECHA	Count date
ESPECIE	Species Code
CONTEO	Abundance as number of individuals

Base Maps

South American Countries shapefile format geographic database was based on ESRI (2000), modified to include detailed coastlines and missing islands.

Site location data was compiled from the full NWC database (all species) as a point shapefile format geographic database.

3. Avian Influenza Potential Spread Indicators

Spatial Model Geographic Framework and species data summary

We used a regular grid of polygons with 0.5 degree cell size covering the whole study area. Polygon vector format was preferred to ease spatial and attribute calculations. Cell size was chosen based on a similar work done by Cummins et al. for Southern Africa (2008), taking into account that there are many areas void of census data and many wetlands are complex in shape and large, having several census sites. This size has as advantage that indicators can be combined or aggregated into large analysis units.

Polygon cells were assigned an arbitrary numeric identification (Cell ID). Using a point to polygon spatial join, each NWC site was assigned its corresponding Cell ID.

NWC selected species MS Excel spreadsheet together with NWC sites with Cell ID attributes were imported to an MS Access database, to allow data management for indicator calculations. Species data were joined to Cell IDs based on common NWC site Code with the resulting attribute structure shown in Table 3. Records were selected into Winter and Summer seasons. Calculations for each indicator were done separately for each season. Once each indicator was calculated for each Cell Id, data was exported to be linked in the mapping software.

Table 3. Attributes of MSAccess master table used in this study.

FIELD	DESCRIPTION
Cell ID	Polygon Grid Cell numeric identifier
Site Code	Site Code / Identifier
Season	Code for summer or winter season
Species	Species Code
Abundance	Abundance as number of individuals

Species Richness

For each season, Cell Ids were cross-tabulated by species occurrence (**Occ**) using the count operator on the abundance field. Species total occurrence was converted to 0/1 to indicate absence/ presence and was summed across species by Cell ID to obtain Cell Total Species Richness:

$$R_{season}(i) = \sum_{j=1}^{Rmax} (Occ_{ji})$$

Where

R (*i*) is Total species richness in cell *i*

Rmax is Maximum species richness observed for the season

Occ is species *j* presence registered in the cell *i* for the season

Maximum Abundance

For each season, Cell Ids were cross-tabulated by species maximum abundance (**Max Ab**), using the maximum operator on the abundance field. This reflects the maximum size registered for any single observation of a single species in a given cell. As some species may be occur in all sites within a cell, while others may be rare or occasional, we calculated an occurrence factor (**OccFact**) to correct for this unevenness. We calculated the combined maximum abundance expected for all selected species (**MxAb**) according to the following formula:

$$MxAb_{season}(i) = \sum_{j=1}^R (Max Ab_{ji} * OccFact_{ji})$$

Where

MxAb is the combined total corrected maximum abundance of the selected species in cell *i*

R is species richness for the season

Max Ab_{ji} is the maximum abundance registered for species *j* in cell *i*

OccFact_{ji} is the proportion of species *j* occurrences (**Occ**) to the total number of visits recorded in cell *i* (**SiteOcc**), calculated as

$$OccFact_{season}(i) = \sum_{j=1}^R (Occ_{ji}/SiteOcc_i)$$

Avian Influenza Susceptibility (Combined Variables)

For each cell, we calculated a susceptibility index (**SI**) by including the species risk score (Table 1) in the Maximum Abundance indicator formula as follows:

$$SI_{season}(i) = \sum_{j=1}^R (Max Ab_{ji} * OccFact_{ji} * RiskScore_j)$$

Conceptually, this indicator represents the expected number or frequency of encounters to waterbird species with potential to spread avian influenza.

4. Maps

Six maps were generated using ArcMap 9.2, depicting the indexes previously described (Table 4).

Table 4. Names of the Files that were used to produce the Figures.

File	Figure No.	Figure Name
WinterRichness92.mxd	1	Winter Species Richness
SummerRichness92.mxd	2	Summer Species Richness
WinterMaxAbund92.mxd	3	Winter Maximum Abundance
SummerMaxAbund92.mxd	4	Summer Maximum Abundance
Wintersucept92.mxd	5	Winter Avian Influenza Susceptibility
Summerrsucept92.mxd	6	Summer Avian Influenza Susceptibility

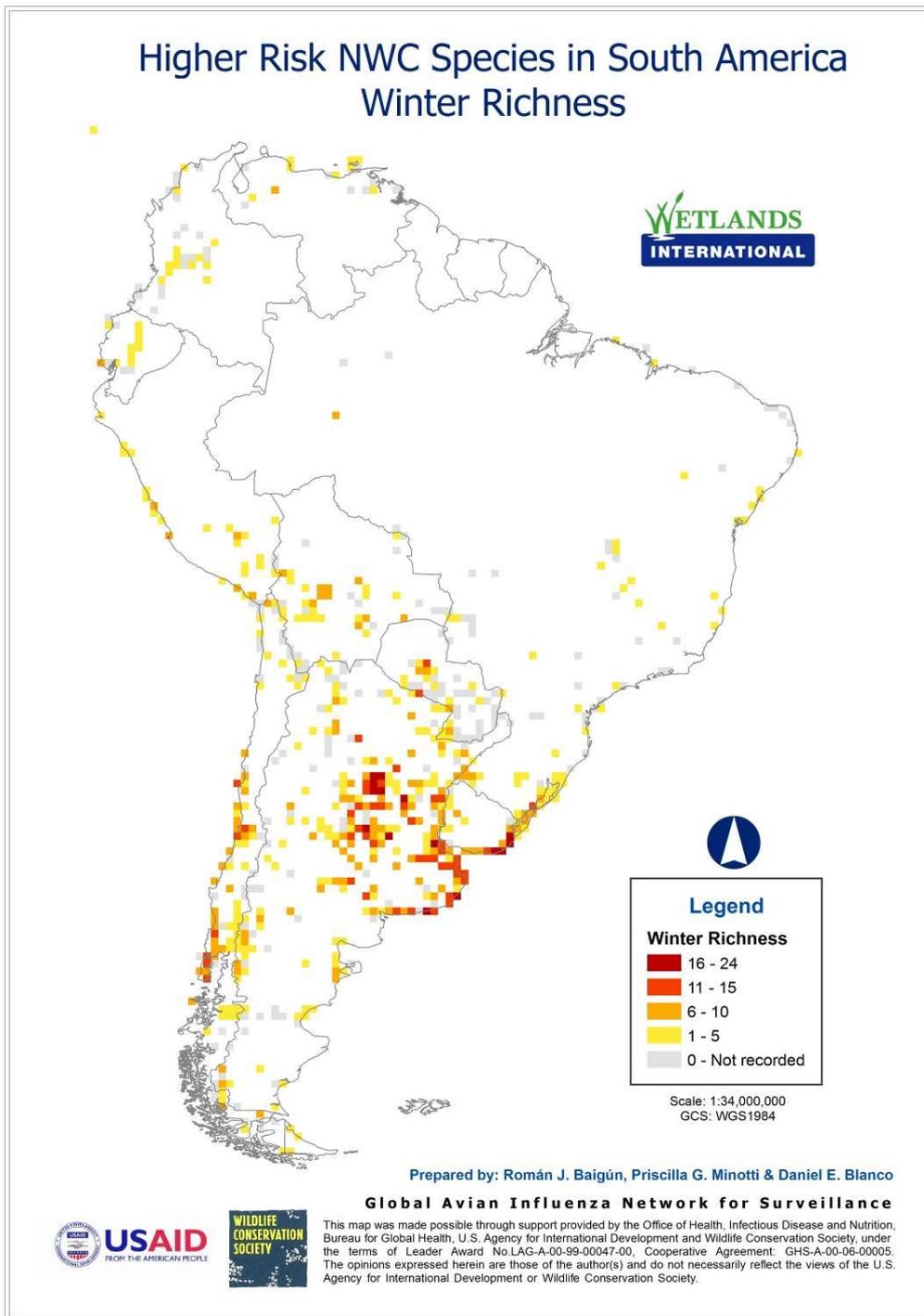


Figure 1. Winter species richness of selected higher risk species in South America.

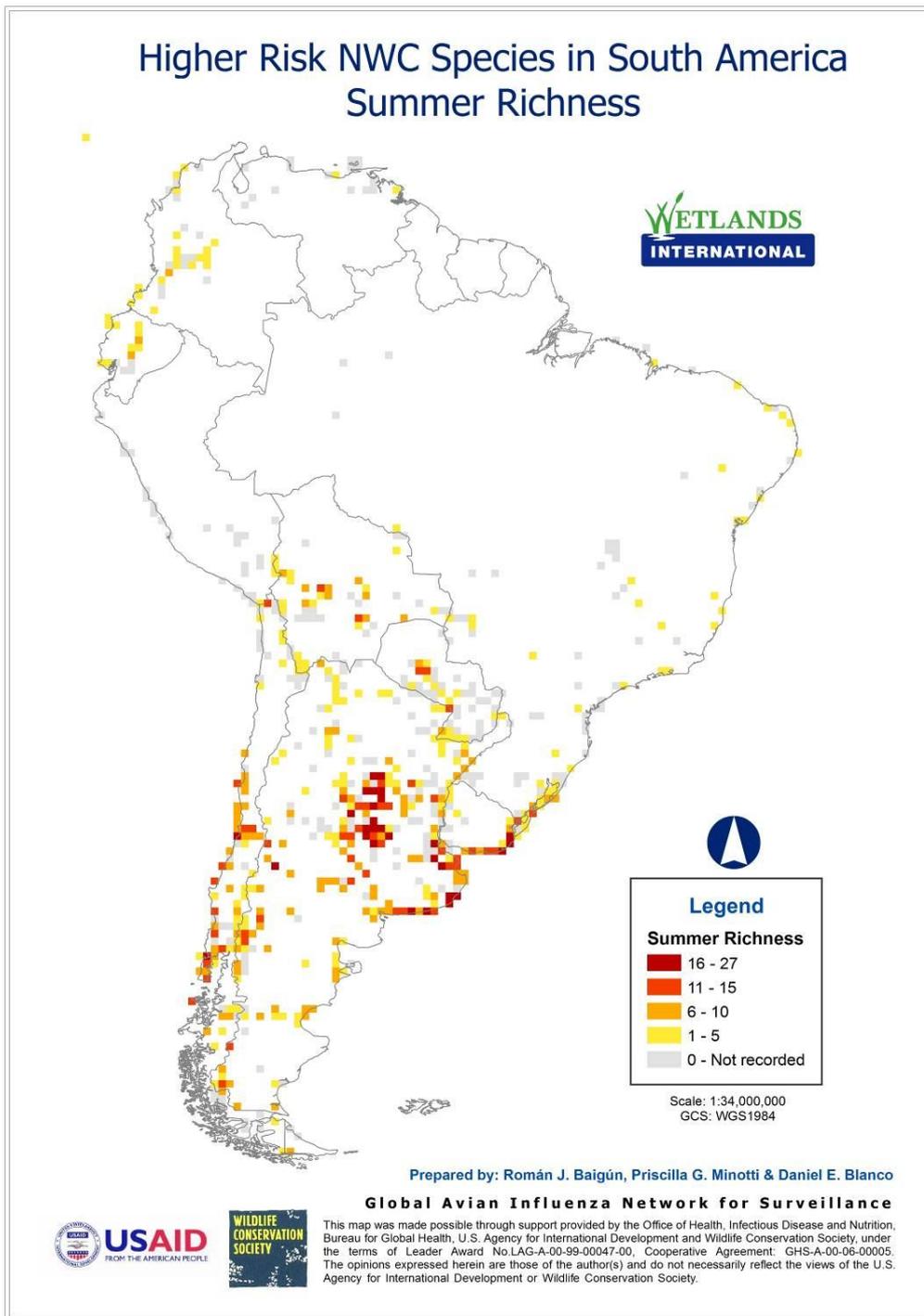


Figure 2. Summer species richness of selected higher risk species in South America.

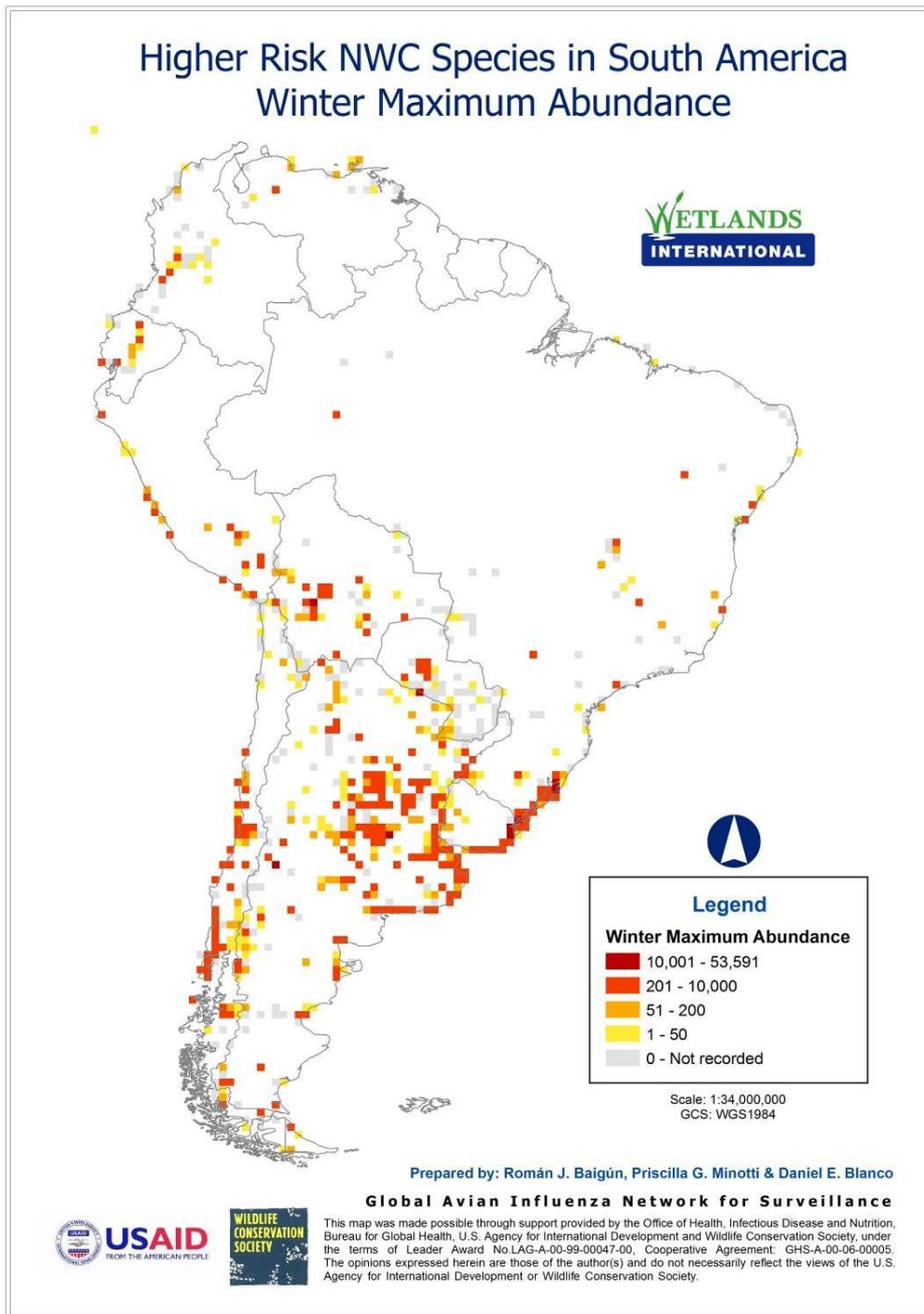


Figure 3. Winter maximum abundance of selected higher risk species in South America.

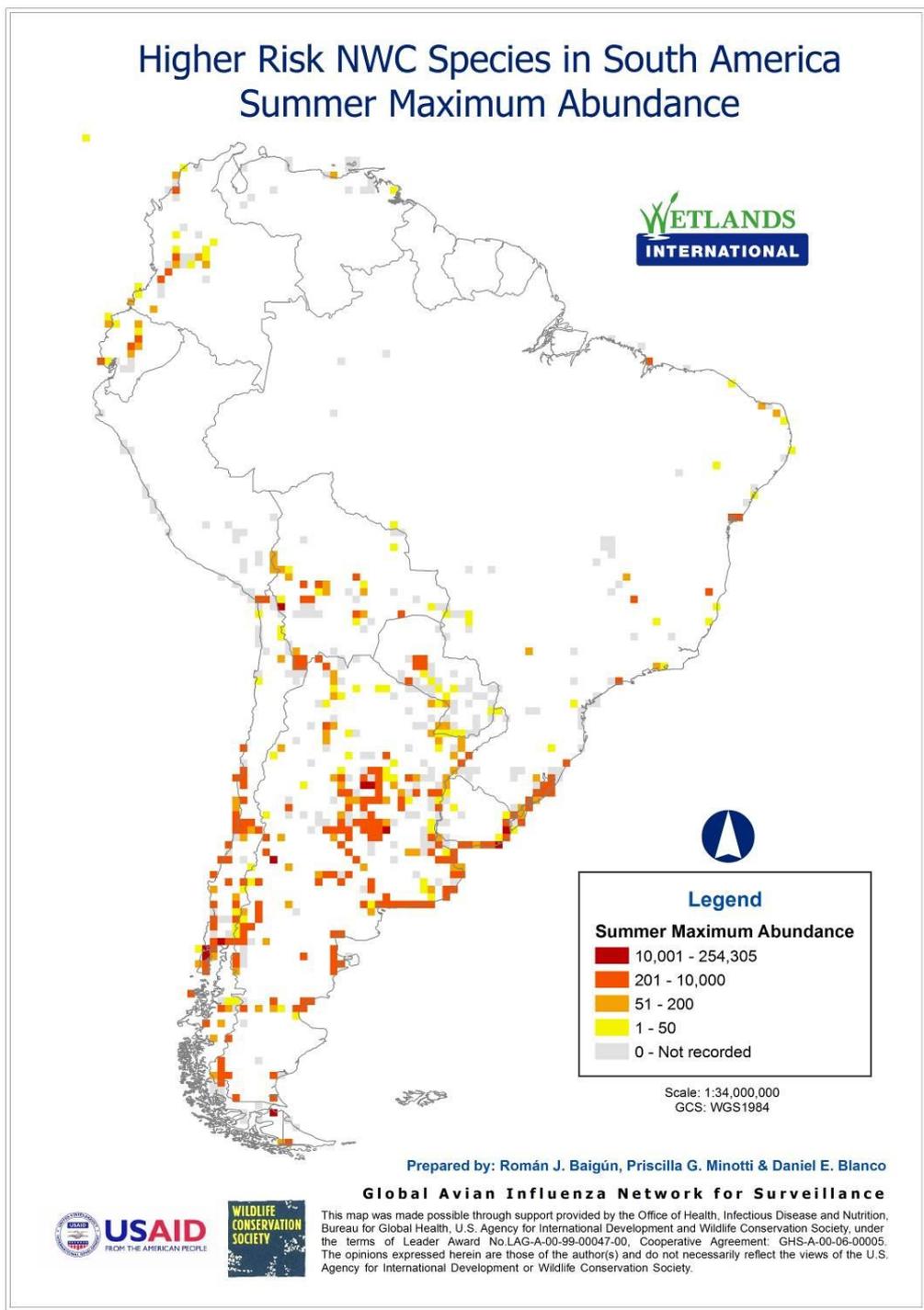


Figure 4. Summer maximum abundance of selected higher risk species in South America.

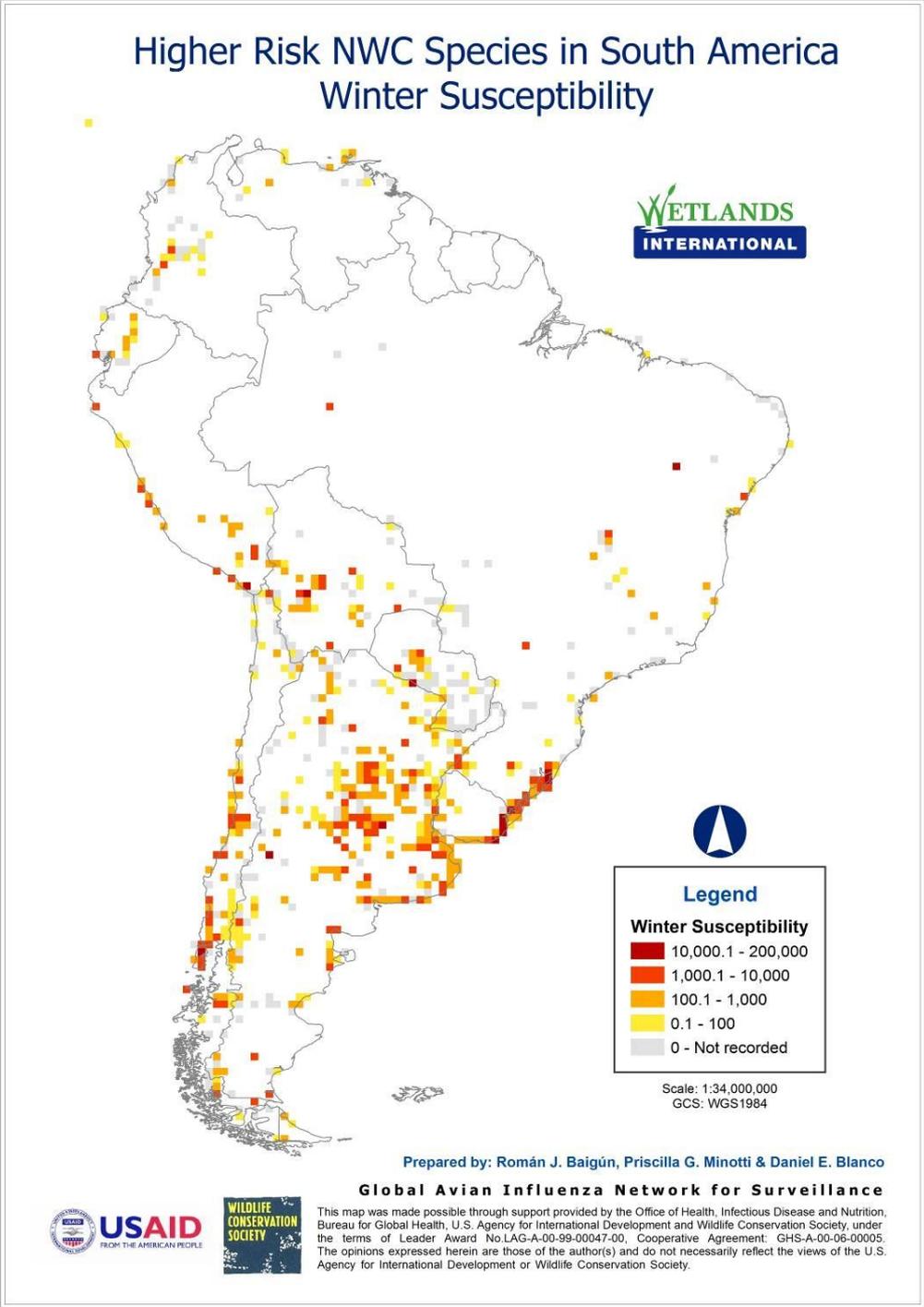
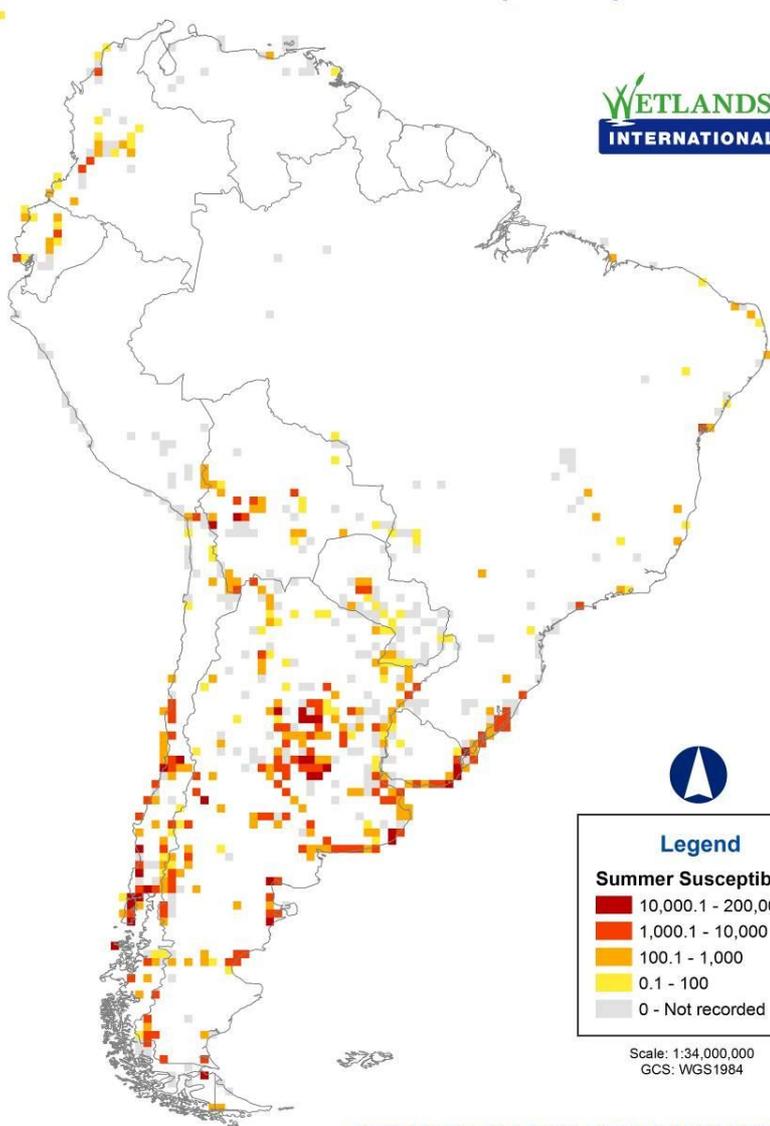


Figure 5. Winter Avian Influenza Susceptibility (Combined Variables) of selected higher risk species in South America.

Higher Risk NWC Species in South America Summer Susceptibility



WETLANDS
INTERNATIONAL



Legend

Summer Susceptibility

10,000.1 - 200,000
1,000.1 - 10,000
100.1 - 1,000
0.1 - 100
0 - Not recorded

Scale: 1:34,000,000
GCS: WGS1984

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Global Avian Influenza Network for Surveillance



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Figure 6. Summer Avian Influenza Susceptibility (Combined Variables) of selected higher risk species in South America.

5. References

- Cumming, G. S., P. A. R. Hockey, L. W. Bruinzeel, and M. A. Du Plessis 2008. Wild bird movements and avian influenza risk mapping in southern Africa. *Ecology and Society* 13(2): 26. [online] URL: <http://www.ecologyandsociety.org/vol13/iss2/art26/>
- Delany S., J. Veen, and J. Clark (Eds.) 2006 .Urgent preliminary assessment of ornithological data relevant to the spread of Avian Influenza in Europe. Report to the European Commission. Wetlands International - EURING.