



Canadian Food
Inspection Agency

Agence canadienne
d'inspection des aliments

Most recent epidemiology of H5N1-Canada

AnimalHealthCanada



HPAI Workshop
March 29 2023



RDIMS 19016054
SGDDI 19027212



Objective: To provide a summary of the epidemiological knowledge to date on the HPAI H5N1 Event

Outline

1. Introduction of the virus
2. Detection in wild birds
3. Situation in domestic population
4. Phylogenetic and epidemiological analysis

A threat from both sides

Alkie et al. 2022: <https://doi.org/10.1093/ve/veac077>

Atlantic introduction

- Newfoundland-like H5 HPAI
- Dec 2021: Great black-backed gull in NL
- Fully Eurasian lineage
- Then, reassortments with North American lineage

Pacific introduction

- Asian-like H5 HPAI
- Feb 2022: bald eagle in BC
- Genetically related to H5N1 HPAI virus isolated in Hokkaido, Japan, in January 2022


286 IP/295 (97%)

New
incursions:
Dec. 2022
H5N1; Jan
2023 H5N5

9 IP/295 (3%)

5 unavailable
2 pending

Detection in Wildlife



HIGHLY PATHOGENIC AVIAN INFLUENZA - WILDLIFE

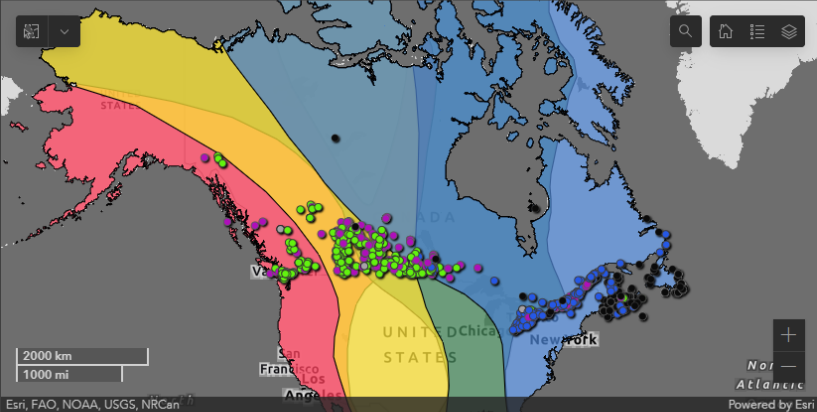
By CFIA NEOC GIS Services

◀ 1 sur 1829 ▶

Most Recent Positive

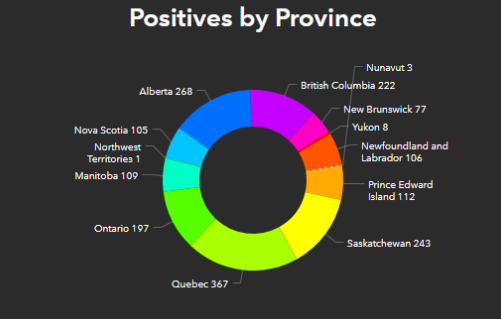
Bird Group	Corvid
Collection_Date	25/02/2023
Common_Name	American Crow
Province	Prince Edward Island
Result	Suspect
Result Authorised Date	28/02/2023
Scientific_Name	Corvus brachyrhynchos
Status	Dead

Dernière mise à jour : il y a 7 minutes



Collecti...	Result_A...	Commo...	Province	Status	Strain	Result	Lineage	Cluster
25/02/2...	28/02/2...	America...	Prince E...	Dead		Suspect		
24/02/2...	28/02/2...	Commo...	Prince E...	Dead		Suspect		
24/02/2...	28/02/2...	Striped ...	Prince E...	Dead		Suspect		
21/02/2...	28/02/2...	Canada ...	Prince E...	Dead		Suspect		
21/02/2...	28/02/2...	Canada ...	Prince E...	Dead		Suspect		
21/02/2...	28/02/2...	Canada ...	Prince E...	Dead		Suspect		


Positives by Province



Alberta	268
British Columbia	222
Nunavut	3
New Brunswick	77
Yukon	8
Newfoundland and Labrador	106
Prince Edward Island	112
Saskatchewan	243
Quebec	367
Ontario	197
Manitoba	109
Northwest Territories	1
Nova Scotia	105

Dernière mise à jour : il y a 7 minutes


Total Number of Positive Samples - Suspect and Confirmed

1829



Highly pathogenic avian influenza (HPAI):
 Suspect: sample positive for avian influenza at a provincial laboratory
 Confirmed: Sampled confirmed as a highly pathogenic avian influenza by CFIA

Dernière mise à jour : il y a 7 minutes

Environment and Climate Change Canada




CANADIAN WILDLIFE HEALTH COOPERATIVE




RÉSEAU CANADIEN POUR LA SANTÉ DE LA FAUNE

Canadian Food Inspection Agency




http://www.cwhc-rcsf.ca/avian_influenza.php


Atlantic Flyway estimate




Mississippi Flyway estimate



Central Flyway estimate



Pacific Flyway estimate



High Path Avian Influenza - Clusters

Gene segments PB2 and NP belonging to North American lineage and gene segments PB1, PA, HA, NA, M and NS belonging to Eurasian lineage

Gene segments PB2 belonging to North American lineage and gene segments PB1, PA, HA, NP, NA, M and NS belonging to Eurasian lineage

Gene segments PB2, NP and NS belonging to North American lineage and gene segments PB1, PA, HA, NA, M belonging to Eurasian lineage

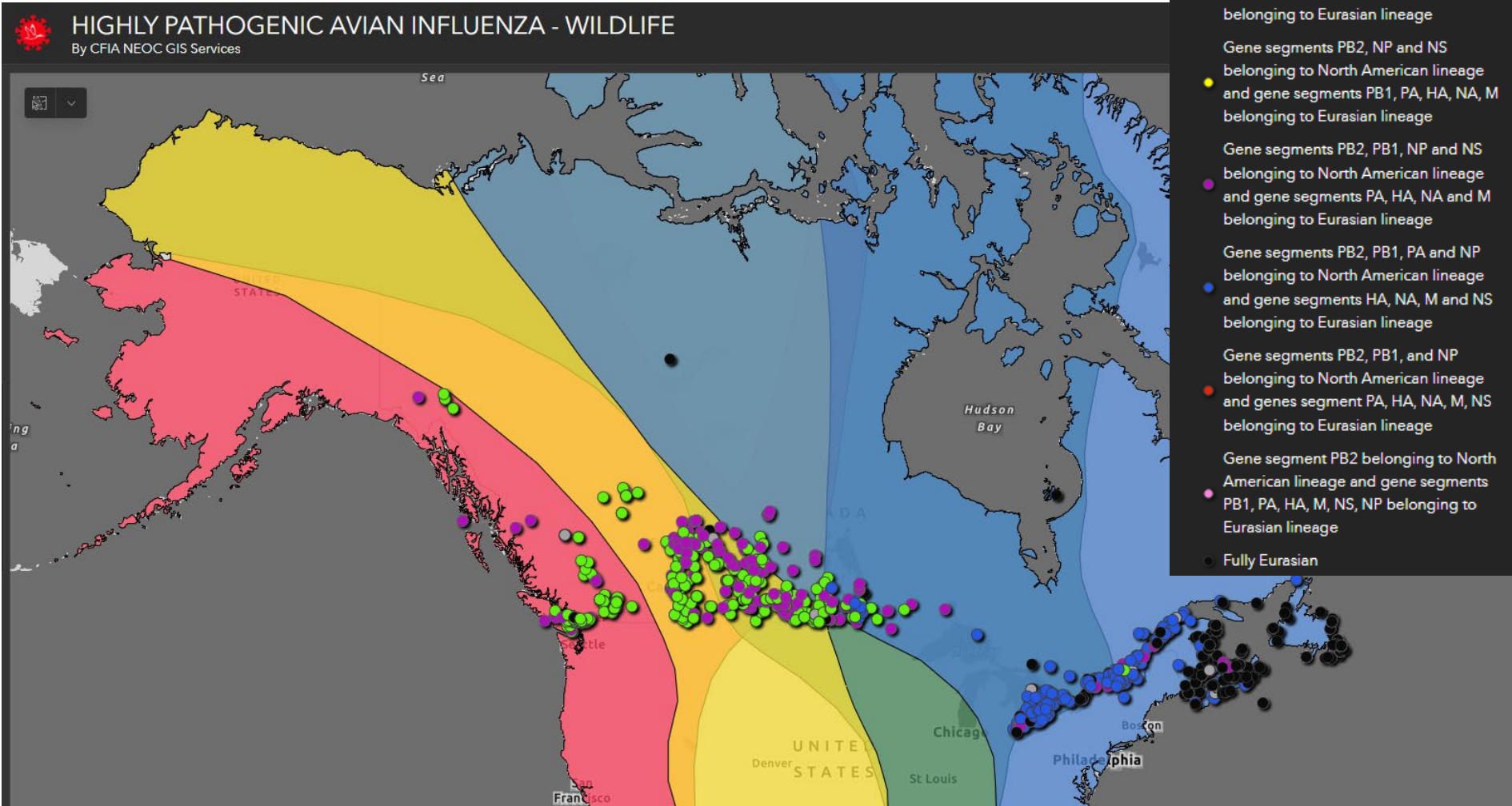
Gene segments PB2, PB1, NP and NS belonging to North American lineage and gene segments PA, HA, NA and M belonging to Eurasian lineage

Gene segments PB2, PB1, PA and NP belonging to North American lineage and gene segments HA, NA, M and NS belonging to Eurasian lineage

Gene segments PB2, PB1, and NP belonging to North American lineage and genes segment PA, HA, NA, M, NS belonging to Eurasian lineage

Gene segment PB2 belonging to North American lineage and gene segments PB1, PA, HA, M, NS, NP belonging to Eurasian lineage

● Fully Eurasian



302 detections in domestic birds

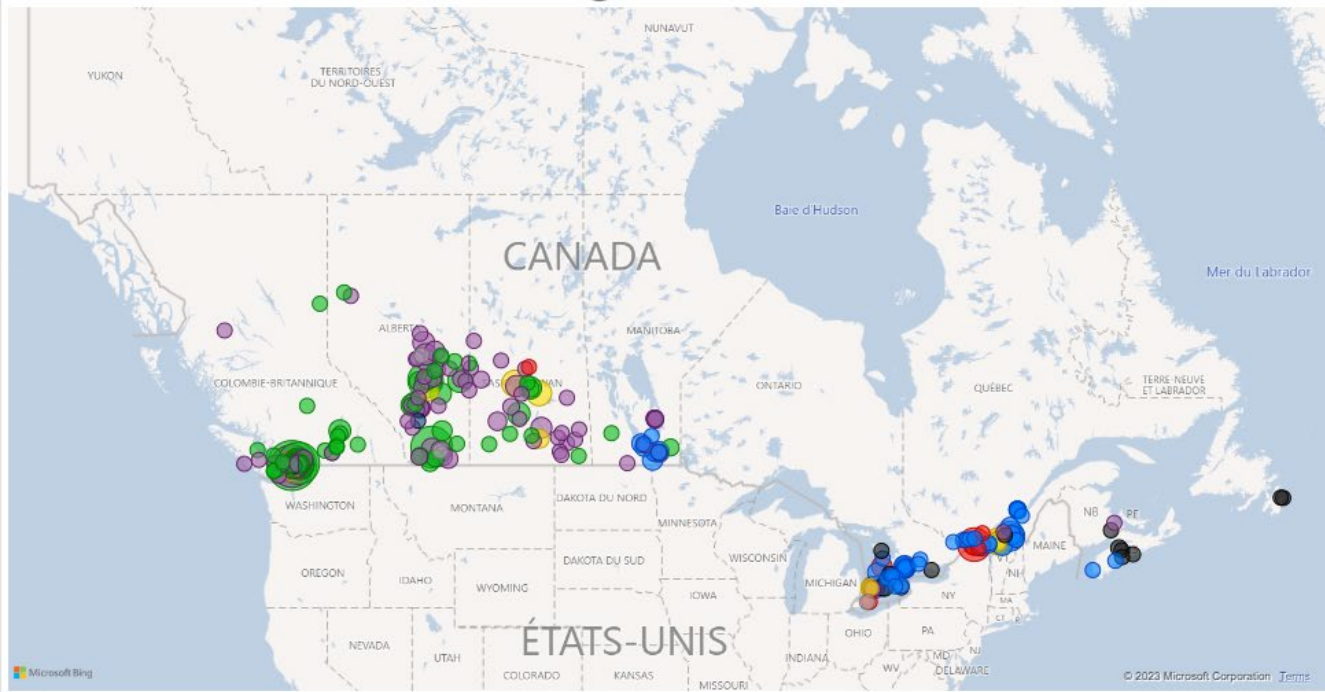
As of March 17, 2023

Geographic Distribution of Wild Birds Clusters matches with the Distribution of Domestic Infected Premises

Province: |
 WOAHA Classification: |
 IP Status: |
 Wave: |
 Cluster: |
 Reference Virus: Reset

Regulation Type: |
 Timeline: |
 Dynamic:

06/12/2021 | 17/03/2023



- Cluster - map**
- (Vide)
 - Fully Eurasian
 - Gene segments PB1 and PA belonging to North American li...
 - Gene segments PB2 and NP belonging to North American li...
 - Gene segments PB2, NP and NS belonging to North Americ...
 - Gene segments PB2, PB1 and NP belonging to North Ameri...
 - Gene segments PB2, PB1, NP and NS belonging to North A...
 - Gene segments PB2, PB1, PA and NP belonging to North A...
 - Gene segments PB2, PB1, PA, NP and NS belonging to Nort...
 - Sample quality insufficient for sequencing to determine gen...

* Date is based on the CFIA Notification Date

Data Last Refreshed: 3/17/2023 9:13:22 AM ET

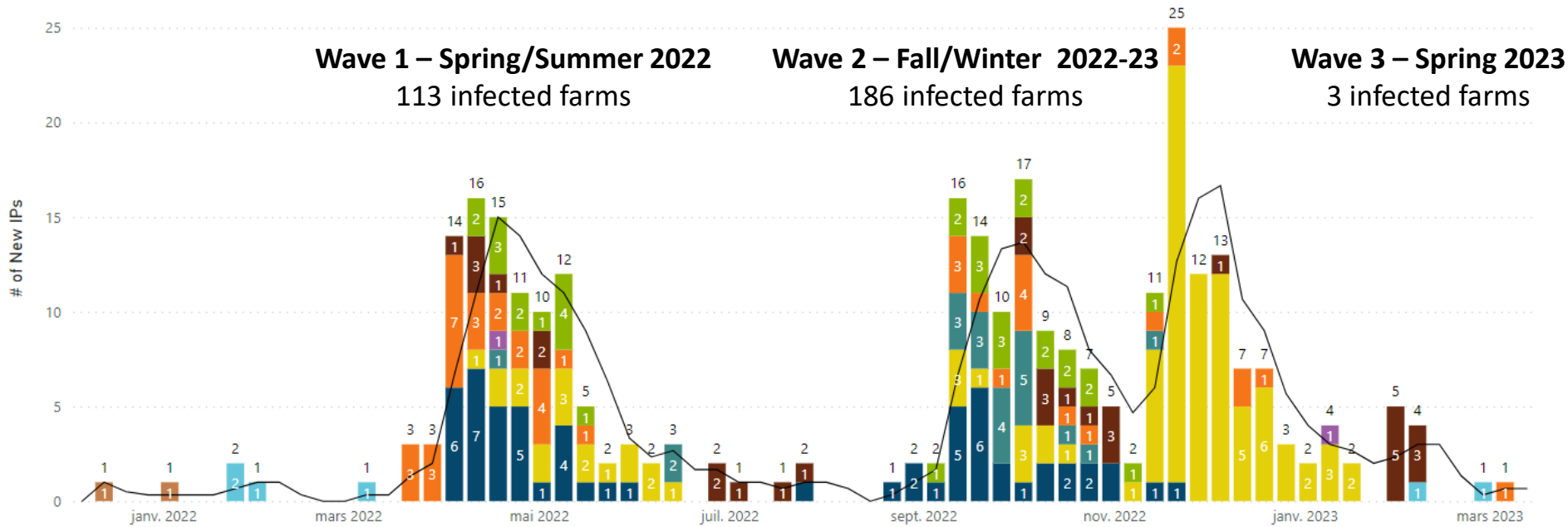
Epidemiologic curve of the HPAI H5N1 Event

(up to March 17, 2023; n=302)

Number of New Infected Premises by Week

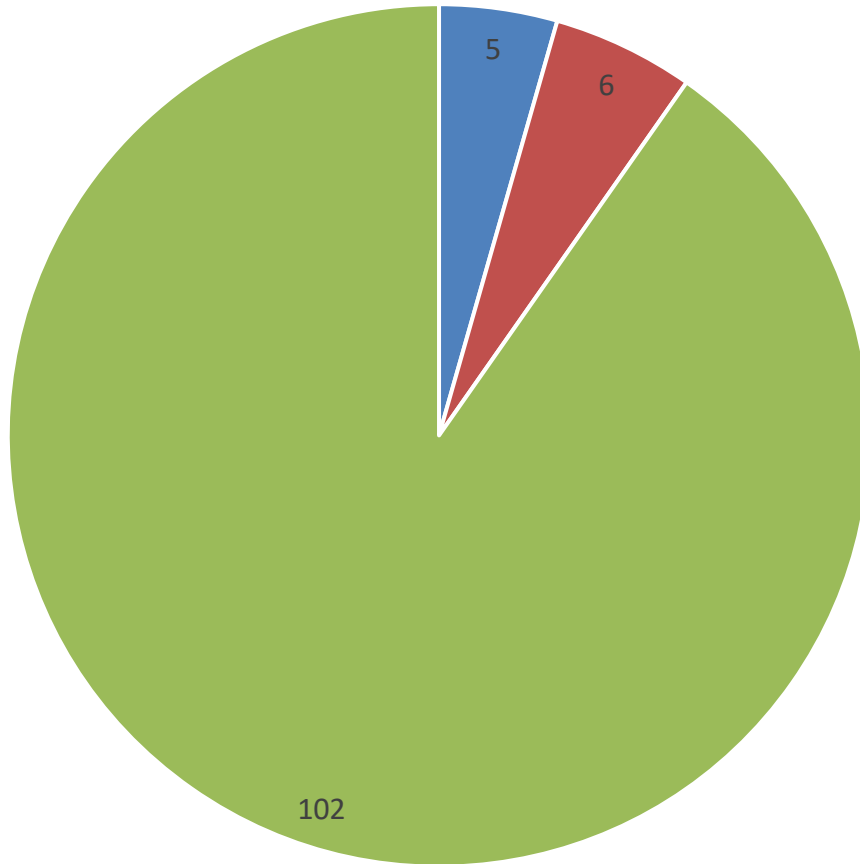
Province: Regulation Type: WOHAI Classification: Date: [Reset Filters](#)

Province: AB BC MB NB NL NS ON QC SK 3-week Moving Average



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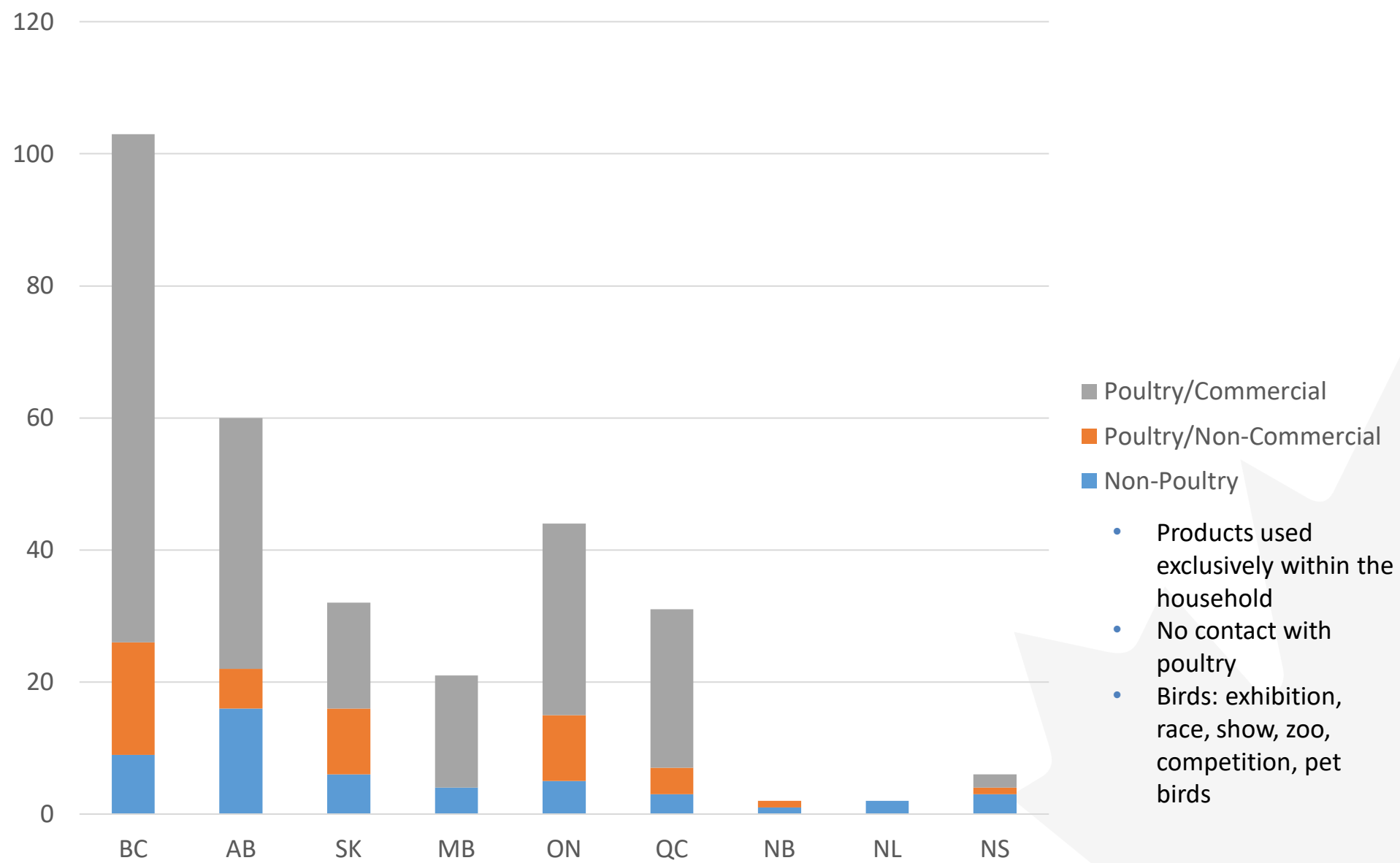
Method of Discovery – first wave (n=113)



- Active-High Risk Contact
- Active-Surveillance
- Passive

Most infected premises (90%) were identified by sick bird calls (passive surveillance)

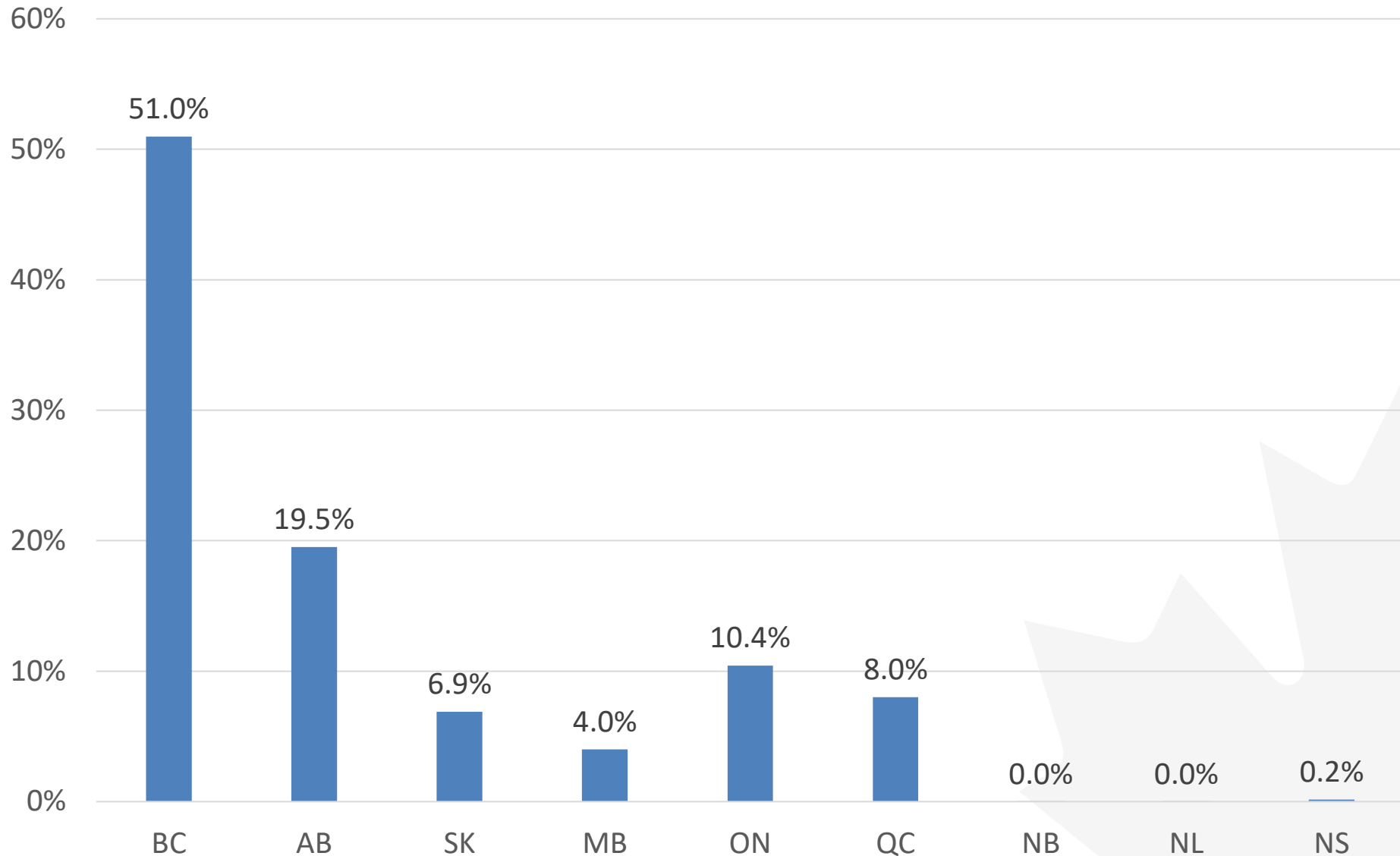
Number of infected premises by province and category



Period - Dec 9 2021 to March 17 2023

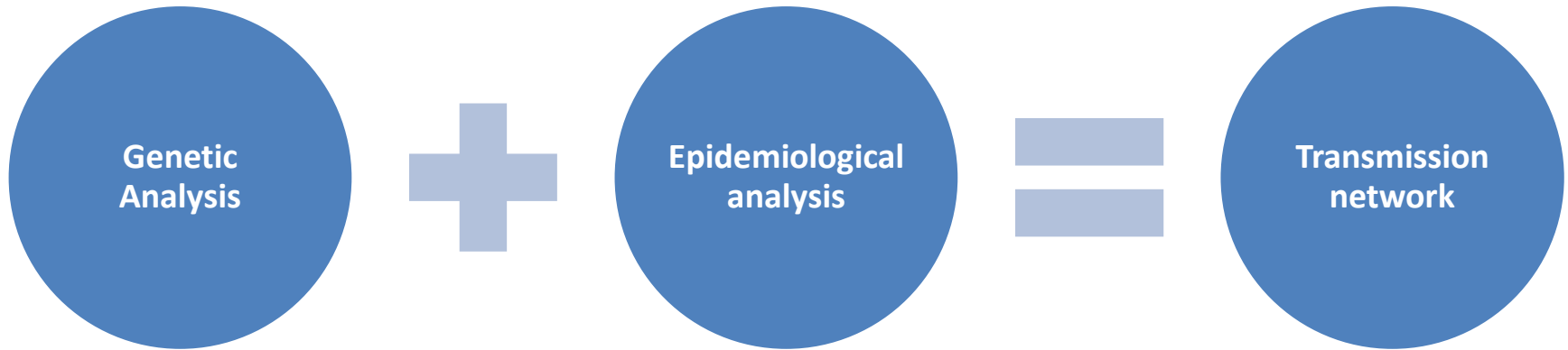
[*WOAH Definitions](#)

Contribution of each province to the total number of birds affected



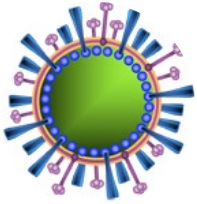
Total Number of Affected Birds > 7.2 million

- Wave 1: >2.1 million
- Wave 2: >5 million



- Analysis of mutations in genome of all positive samples (IPs and wild birds)
- Genetically similar viruses are more likely to share a link
- Review of tracing information collected on each IP
- Establish linkages that make sense from a temporal perspective
- Final transmission network combines results from epi and genetics.

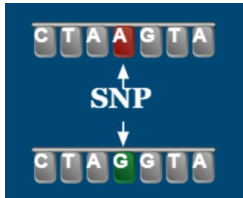
PHYLOGENETIC AND EPIDEMIOLOGICAL ANALYSIS



Genetic analysis - Phylogenetic tree

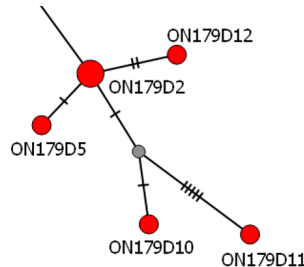
- Avian influenza genome = sequence of **13,500 nucleotides** (letters)

AGCAGAAGCGGAGCGTTTTTC



- Phylogenetic analysis evaluates the differences in the genome (i.e. number of SNP) between virus

- **SNP** (single-nucleotide polymorphism) is a substitution of a single nucleotide at a specific position in the genome

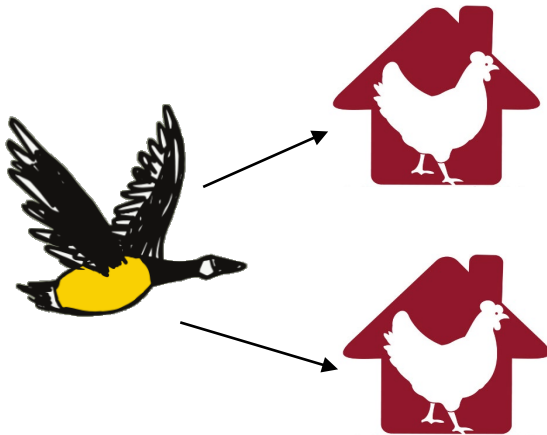


- SNP differences in samples collected on a same farm (generally between 0 to 10 SNP on a same farm; up to 15 SNP on multispecies farm)

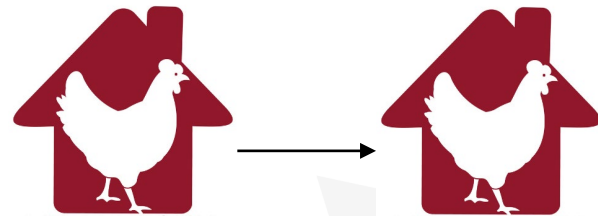
Strains that are phylogenetically closer are more likely to share an epidemiological association

2 options when viruses are genetically similar

Common source

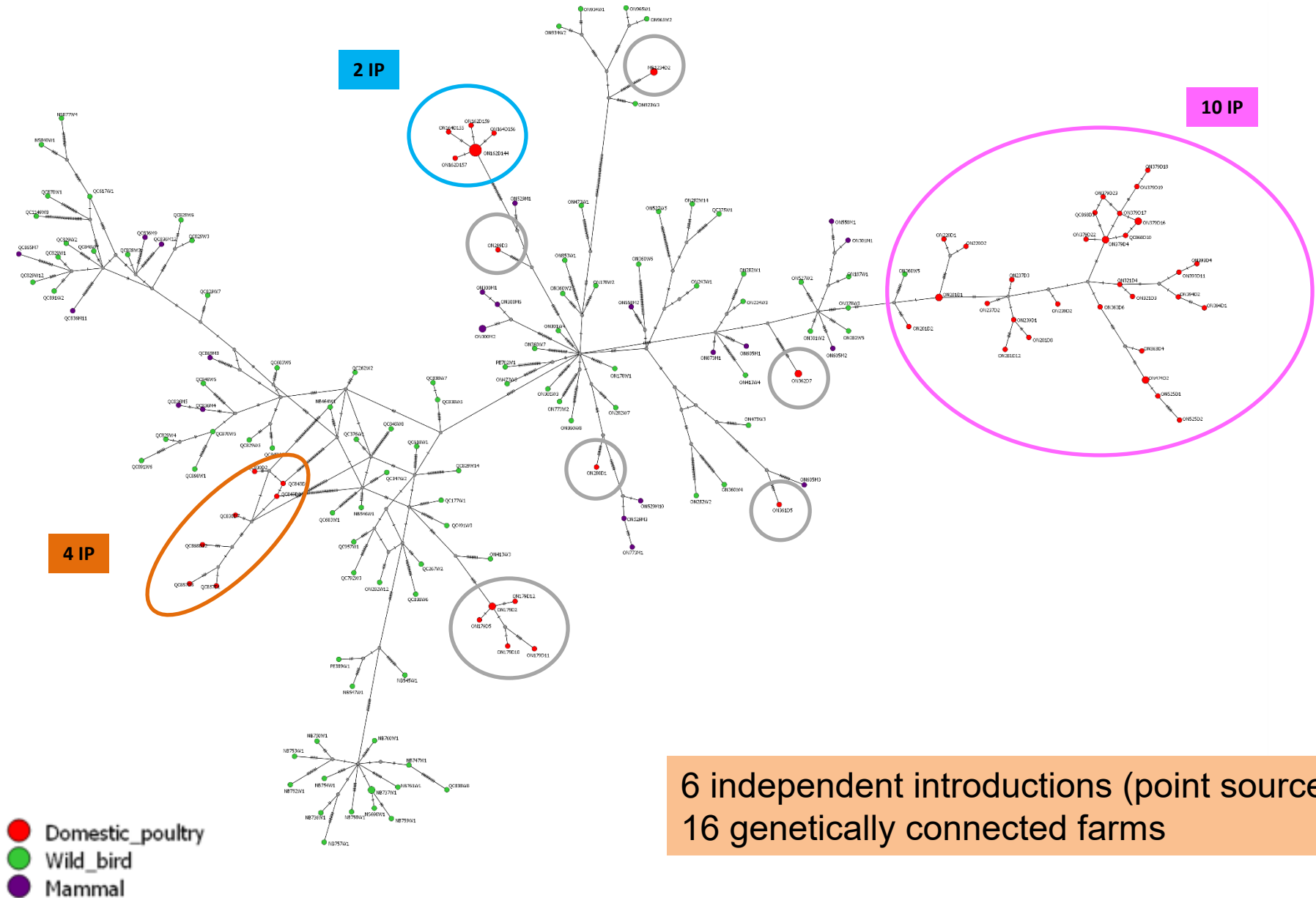


Common vector



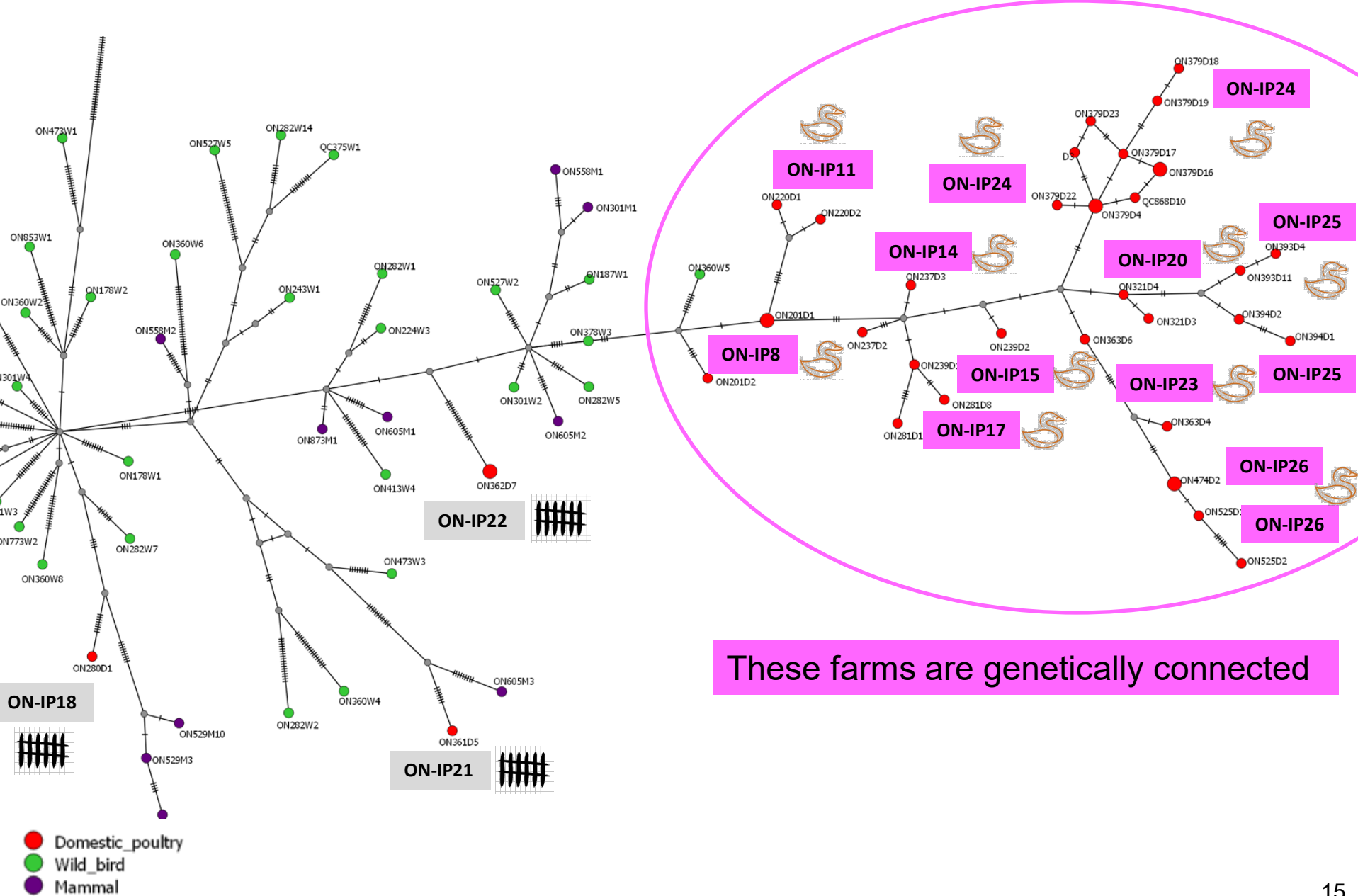
When epi links are found, common vector is more likely

PB2, PB1, PA and NP cluster ON, QC, MB (n=22 IP)

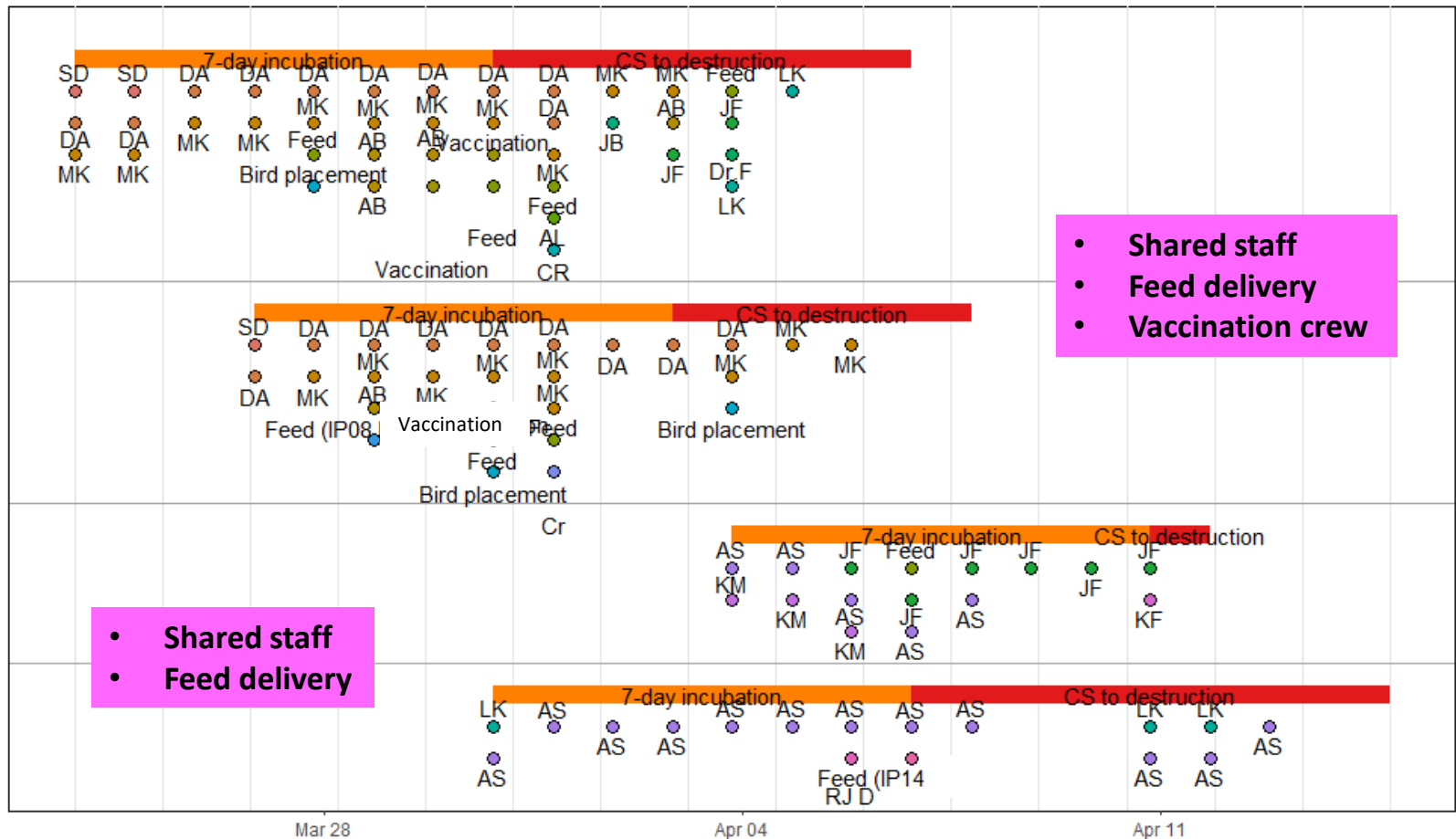


6 independent introductions (point source)
16 genetically connected farms

PB2, PB1, PA and NP cluster ON, QC, MB (n=22 IP)



Epidemiological analysis



ON-IP08

ON-IP11

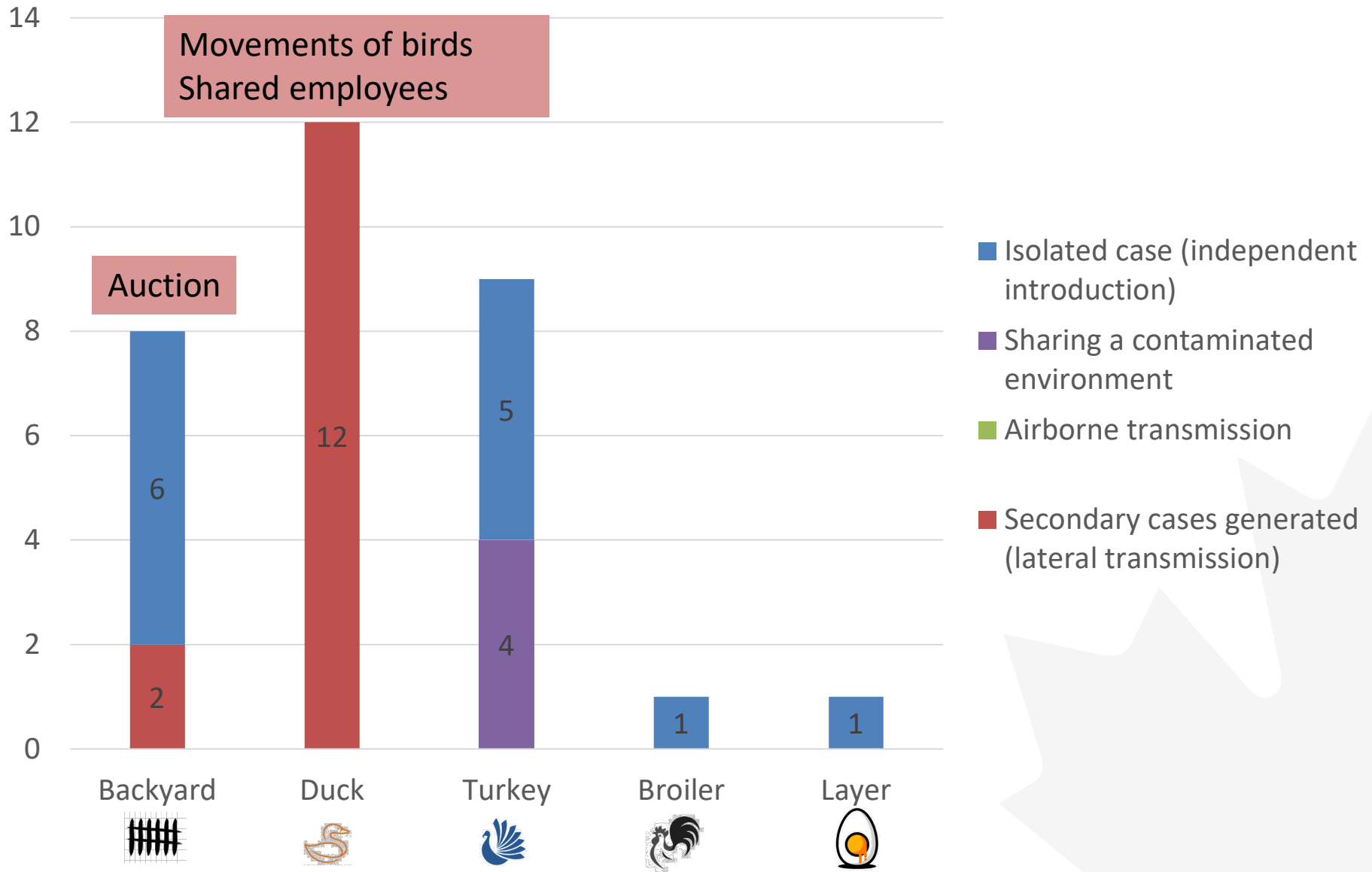
ON-IP14

ON-IP15

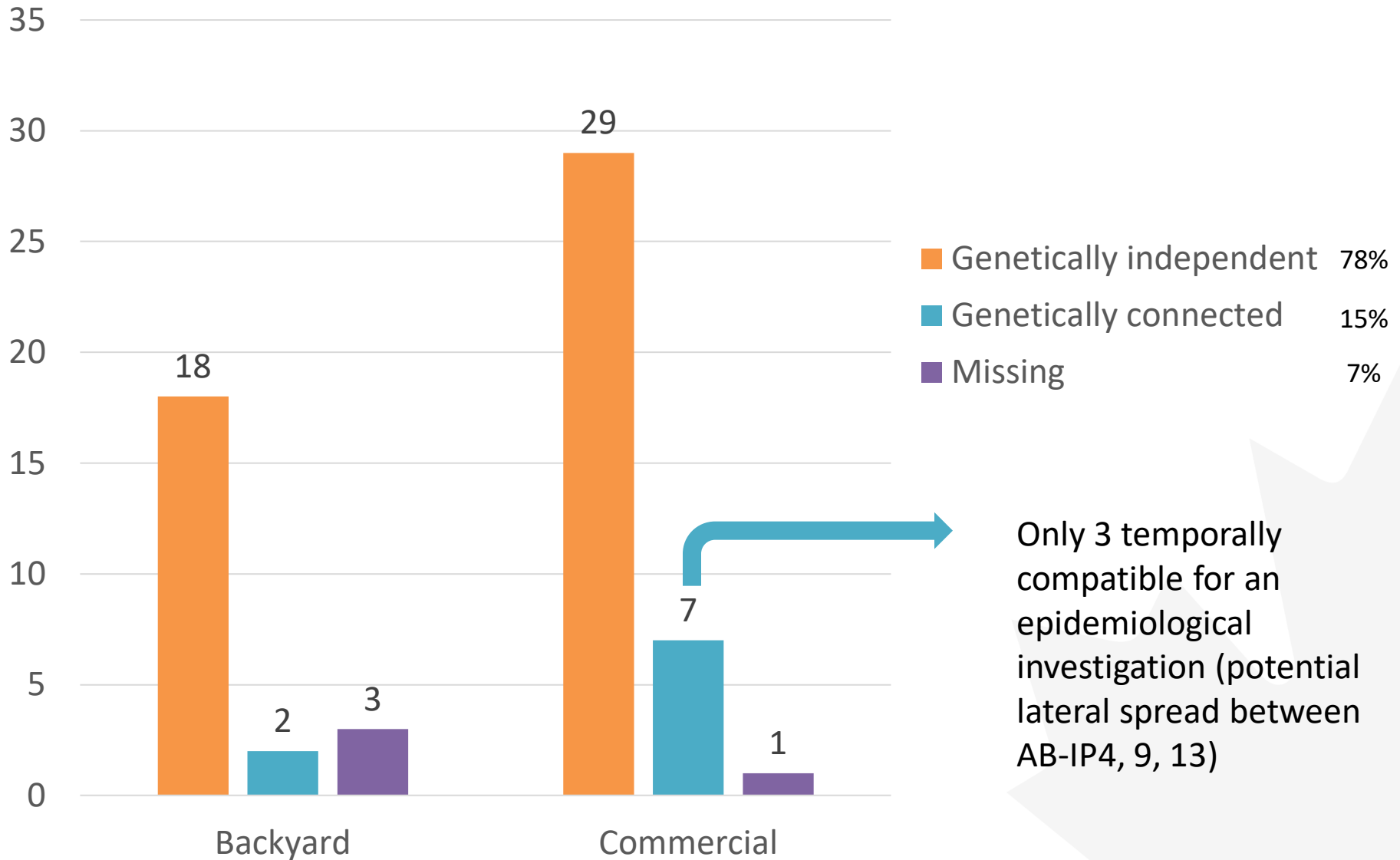
- Shared staff
- Feed delivery
- Vaccination crew

- Shared staff
- Feed delivery


Epidemiological investigations on 31 infected farms in Quebec



Genetic analysis on 60 infected premises in Alberta



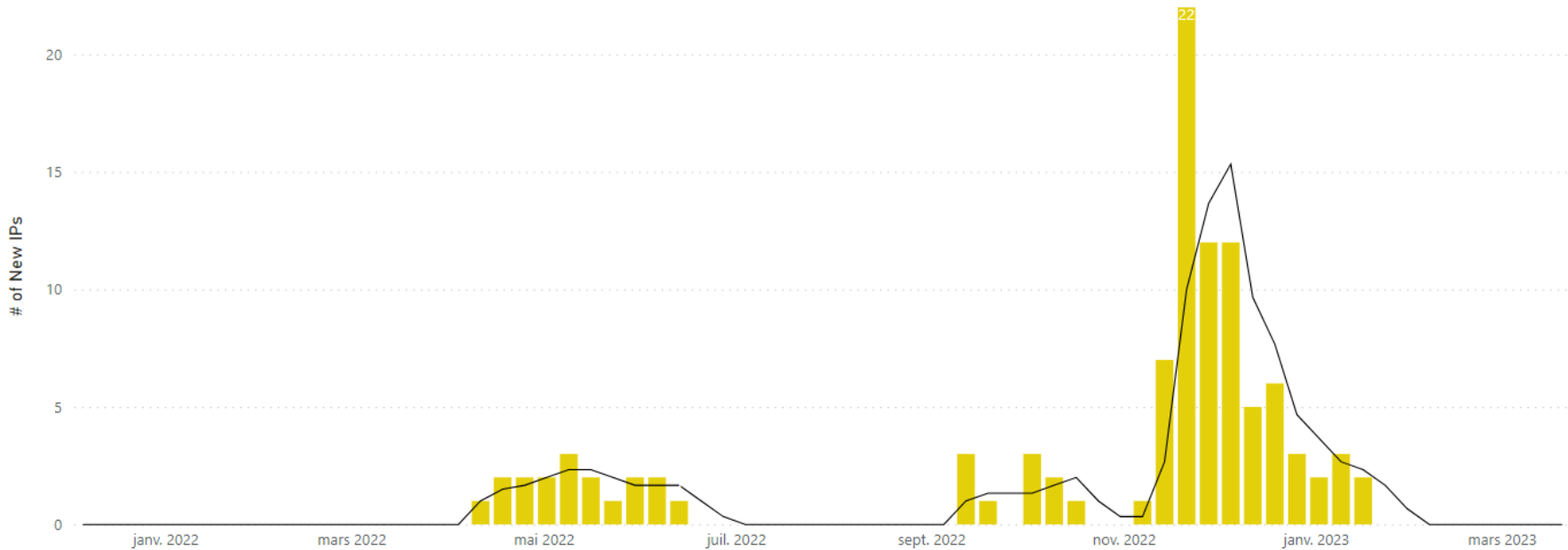
BC situation – 103 IP

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Number of New Infected Premises by Week

Province	Regulation Type	WOAH Classification	Date		Reset Filters
BC	Tout	Tout	06/12/2021	23/03/2023	

Province ● BC ● 3-week Moving Average



* Date is based on CFIA Notification Date

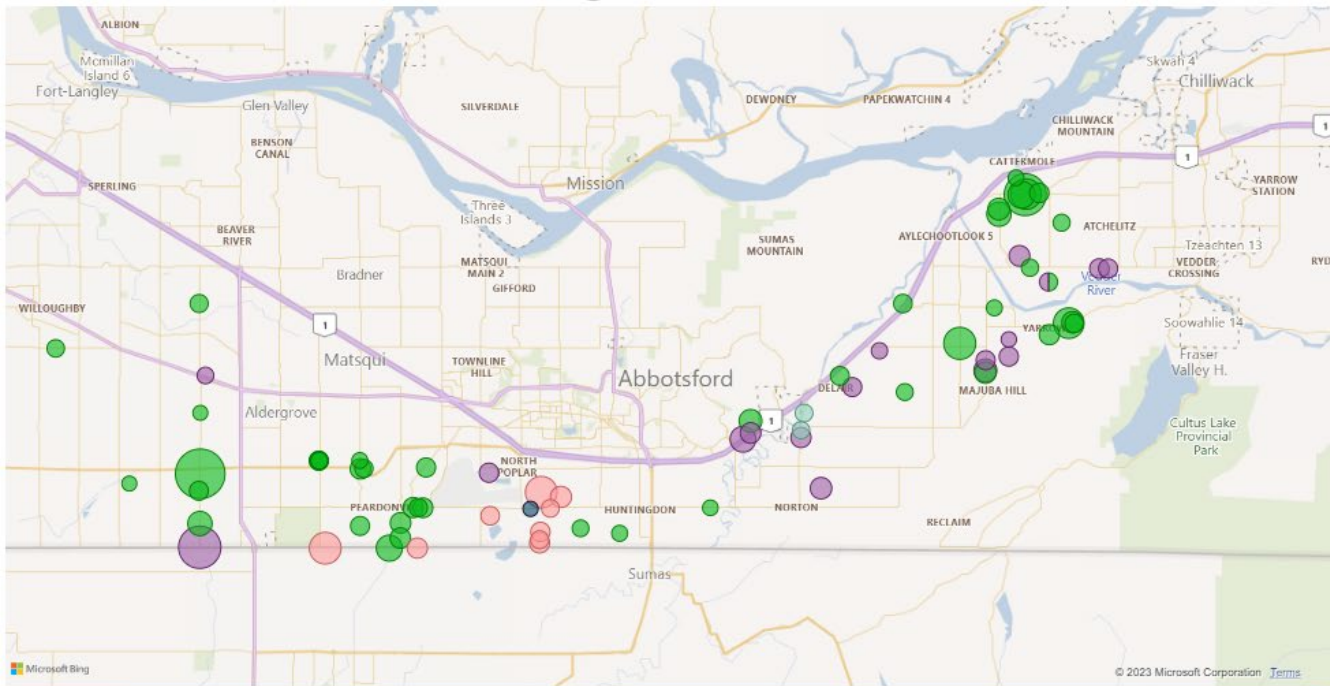
Data Last Refreshed: 3/23/2023 9:13:17 AM ET



BC cases – 4 viral clusters

Province: BC | WOH Classification: Tout | IP Status: Tout | Wave: Tout | Cluster: Tout | Reference Virus: Tout | Reset

Regulation Type: Tout | Timeline: Dynamic | 06/12/2021 | 23/03/2023



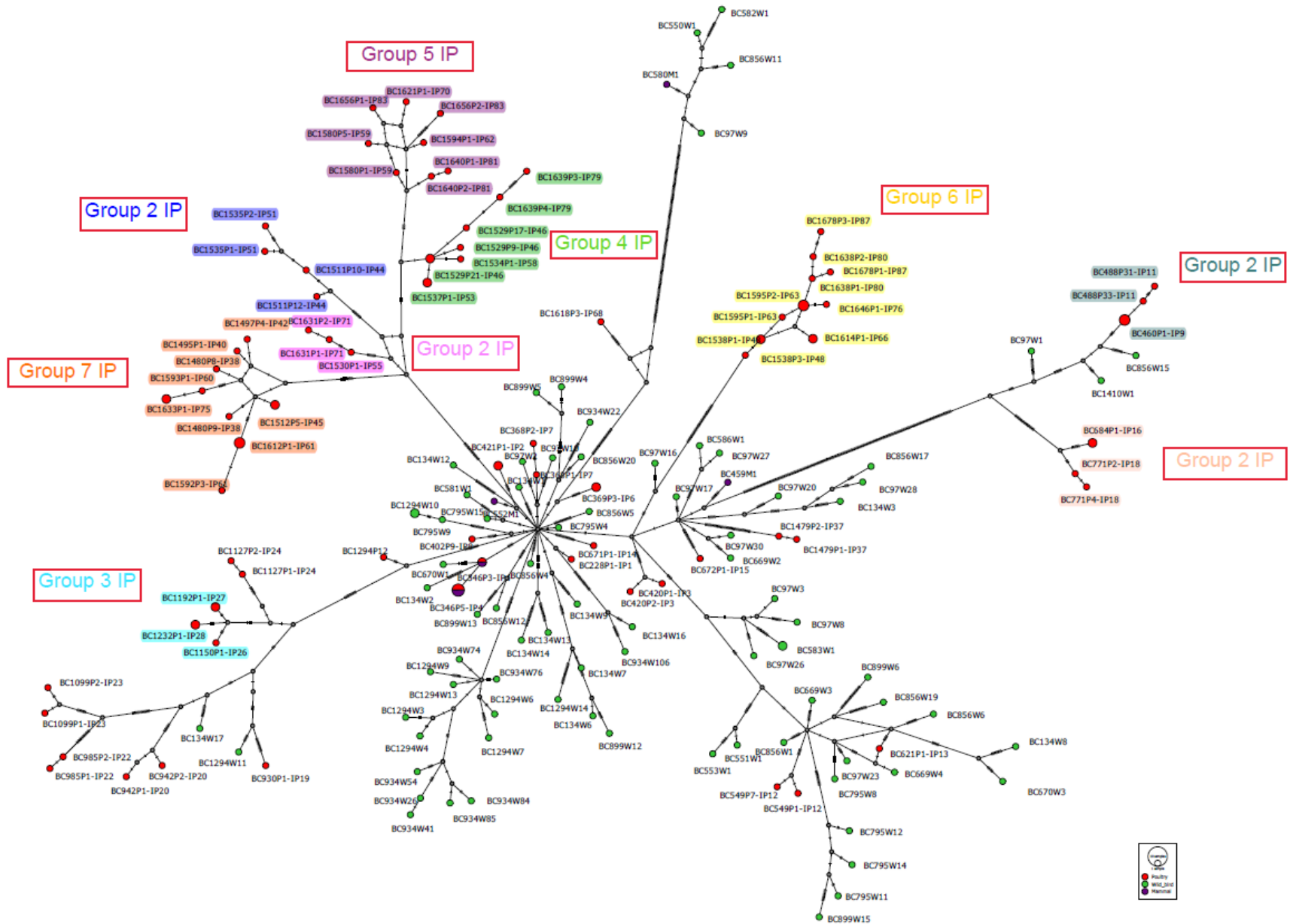
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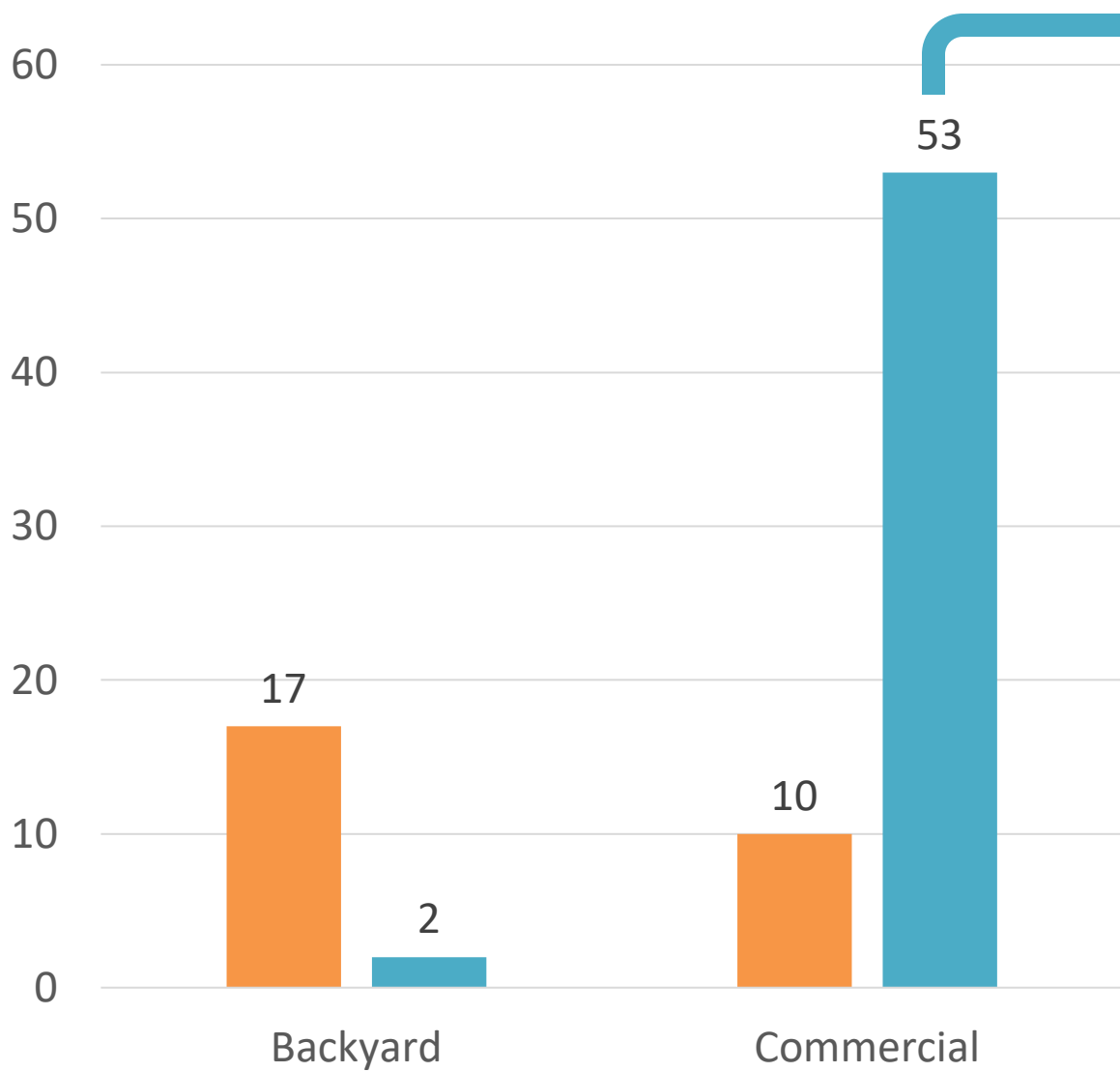


PB2, NP (NA) – 51 farms

18 genetically independent
33 genetically connected: 9 groups



Genetic analysis of BC cases (n=82 IP)



- Common ownership
- Contiguous
- Distance
- Wind
- Tracing:
 - Movement of birds
 - Movement of people/things
 - Likelihood of Spread

■ Genetically independent 33%
■ Genetically connected 67%

Preliminary results

Epi investigation on genetically connected farms		#IP (n=51)
No documented links to other IP (41; 80%)	Potential point source introduction (common contaminated environment)	27
	Potential windborne spread	10
	Potential point source introduction \pm wind	4
Documented links (10; 20%)	Low likelihood of transmission (e.g. feed delivery)	7
	High likelihood of transmission events (e.g. movements of birds or shared personnel)	3

Conclusions

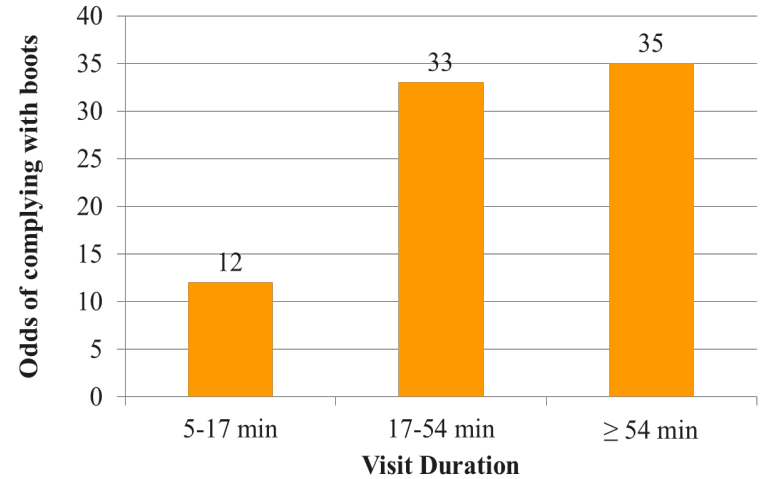
- Lessons learned :
 - Mostly independent introductions of the virus linked to lack of biosecurity (and inappropriate barn entrance design)
 - Lateral spread through regular sharing of employees/equipment (common in integrated companies) and lack of biosecurity
 - Farms with ducks are over represented. Ducks excrete the virus before clinical signs (high contamination level)
 - No evidence of spread from backyard flocks to commercial, and very limited transmission between backyard flocks (auction)
- Unprecedented geographical spread and wild bird species affected and the contamination level of wild birds with HPAI H5N1 across the country is expected to remain high
 - We must all adapt to this new context
 - Interventions to prevent re-occurrences must be tailored to the contamination sources

Biosecurity is the key message

Improve Barn Entrance Design



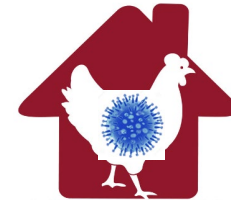
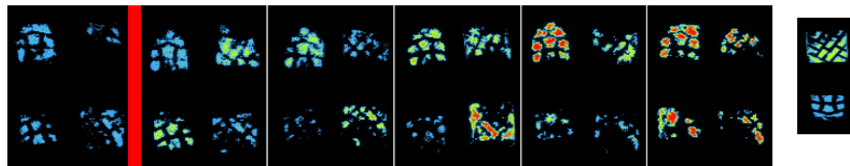
Explain biosecurity to employees



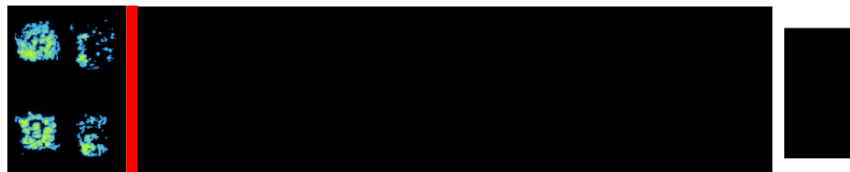
Understand the impact of biosecurity breaches



Not changing boots



Changing boots properly



Biosecurity is the key message

Prevent introduction via shared equipment

C&D equipment stored outside

Control Pests: Wild birds, insects and rodents

- Wild bird deterrent strategies
- Chasing wild birds can increase the likelihood of contaminating tractor and personal shoes, and bringing the virus closer to the barn entrance
- Detection of the H5N1 virus in insects
 - Flies: infective up to 96 hours after exposure, travel generally limited to 3km²
 - Darkling beetles: adult lives from 3 months to 1 year, travels long distance

Article | [Open Access](#) | [Published: 17 June 2021](#)

Efficacy of an automated laser for reducing wild bird visits to the free range area of a poultry farm

[Armin R. W. Elbers](#)  & [José L. Gonzales](#)

Scientific Reports **11**, Article number: 12779 (2021) | [Cite this article](#)

1988 Accesses | 3 Citations | [Metrics](#)





Questions

Biosecurity is a 24/7/365 commitment