LES VIRUS INFLUENZA H17 :
LE RESERVOIR CHAUVE-SOURIS

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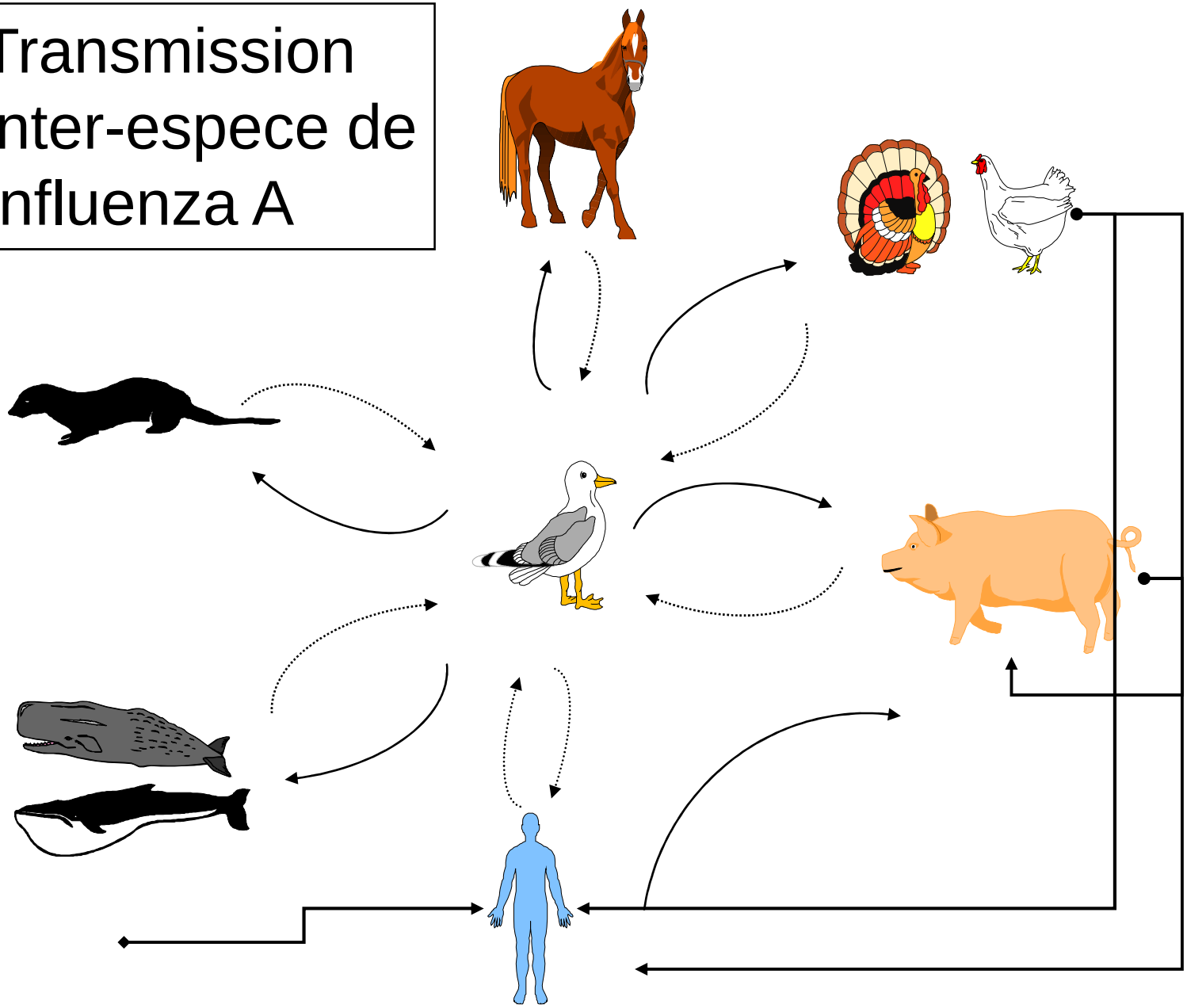
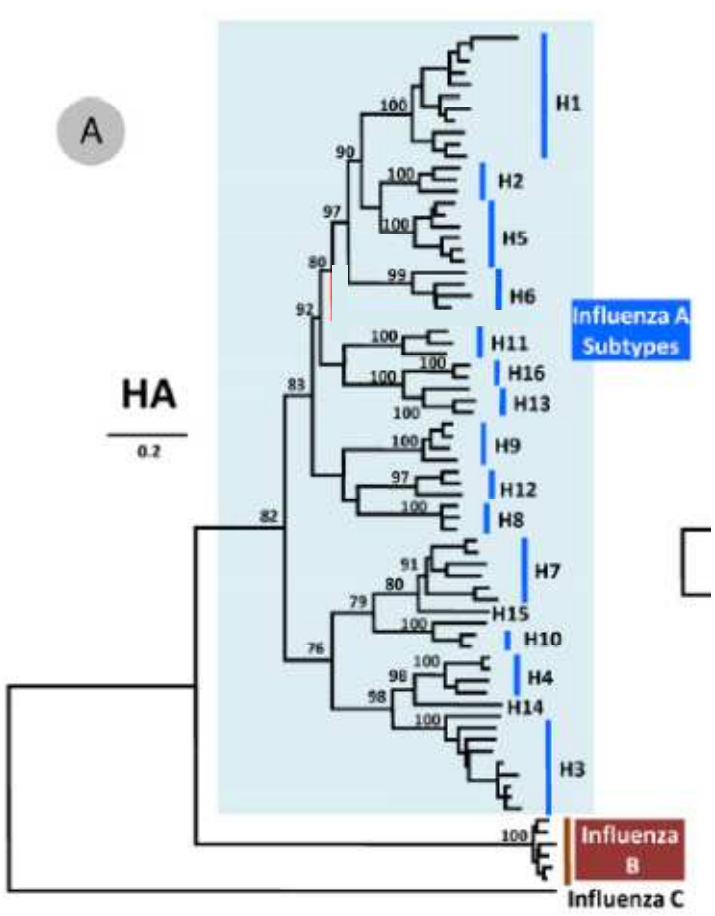
H1				
H2				
H3				
H4				
H5				
H6				
H7				
H8				
H9				
H10				
H11				
H12				
H13				
H14				
H15				
H16				

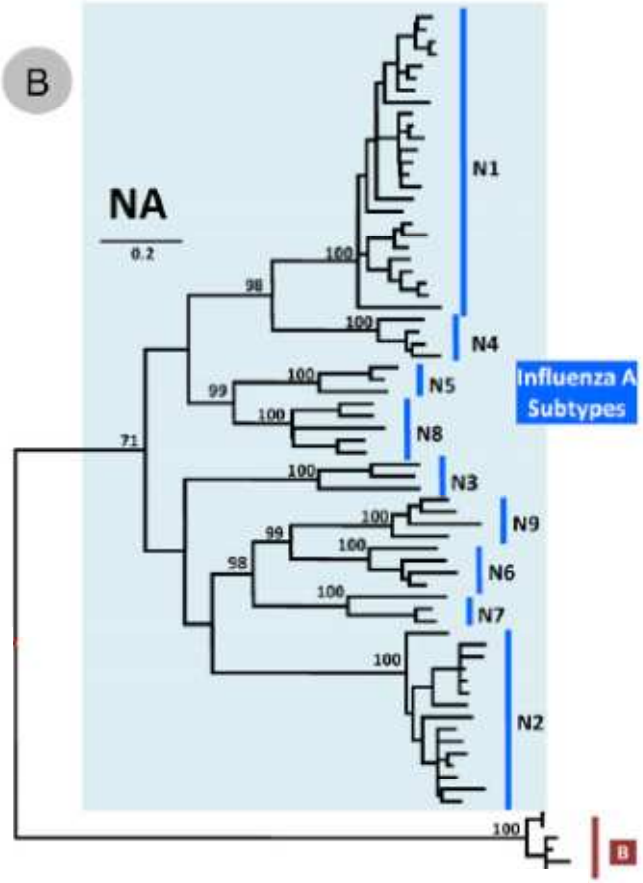
N1				
N2				
N3				
N4				
N5				
N6				
N7				
N8				
N9				

Transmission inter-espece de Influenza A



Phylogénie des glycoprotéines de surface des virus influenza A et B





Les chauve-souris : des réservoirs de virus impressionnants

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Reviews in Medical Virology

REVIEW

Bats as a continuing source of emerging infections in humans

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A distinct lineage of influenza A virus from bats

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Ou?

Guatemala City
Los Tarrales
Montañas Azules
El Naranjo
Agüero
El Jobo
Bat Influenza A virus
El Viña
Los Hilos
El Penate
Mexico
Belize
Guatemala
Honduras
El Salvador

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Gulf of Mexico
NORTH AMERICA
Mexico
Cayman Islands
Jamaica
Ambergris Cay
Belize
Turneffe Islands
Belmopan
Gulf of Honduras
Bahia Islands
Caribbean Sea
Guatemala
Guatemala City
Honduras
Tegucigalpa
San Salvador
El Salvador
Nicaragua
Providencia Is. (Colombia)
San Andres Is. (Colombia)
Gulf of Fonseca
Lake Managua
Managua
Maiz Islands (Nicaraqua)
Lake Nicaragua
Pacific Ocean
Costa Rica
Bocas del Toro (Panama)
Panama Canal
San Jose
Mosquito Gulf
Gulf of Nicaya
Panama City
Panama
Gulf of Panama
Gulf of Chiriqui
Coiba Island
CENTRAL AMERICA
SOUTH AMERICA
Colombia
worldatlas
18° N
15° N
12° N
9°N
6°N
90° W
87° W
84° W
81° W
78° W
150 mi
150 km

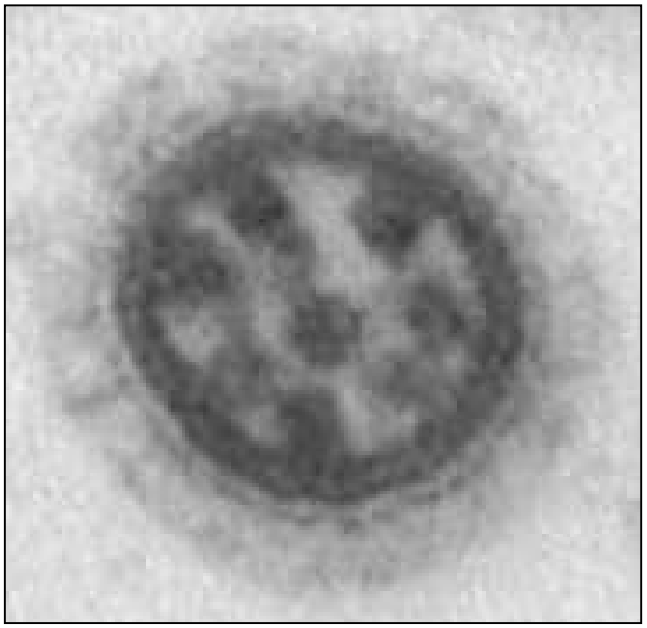
Qui?

Petite chauve souris a épaule jaune (*Sturnira lilium*)

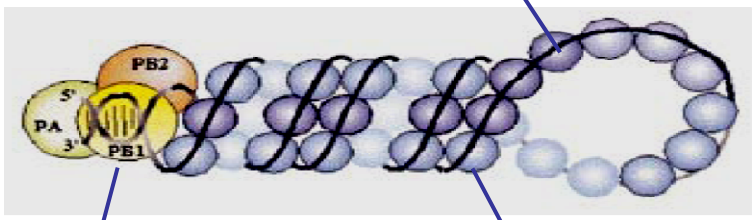
Réalisation de l’étude

- Collecte de 316 animaux de 21 espèces différentes à 8 endroits différents sur 2 périodes différentes
- Prélèvement par écouvillonnage rectal
- Analyse des prélèvements par RT-PCRq pan-génomique
- Détection concomitante de séquences virales dans la gueule des animaux, et dans certains organes (poumons, foie, intestins et reins)
- Séquençage complet de l’ensemble du génome lorsqu’un virus était détecté
- Alignement des séquences obtenues avec les séquences disponibles sur les bases de données
- Tests de mise en culture dans l’œuf, et sur différentes lignées cellulaires

Organisation générale du virus



Ribonucleoprotein particle (RNP)



NP

Polymerase (PB1, PB2, PA)

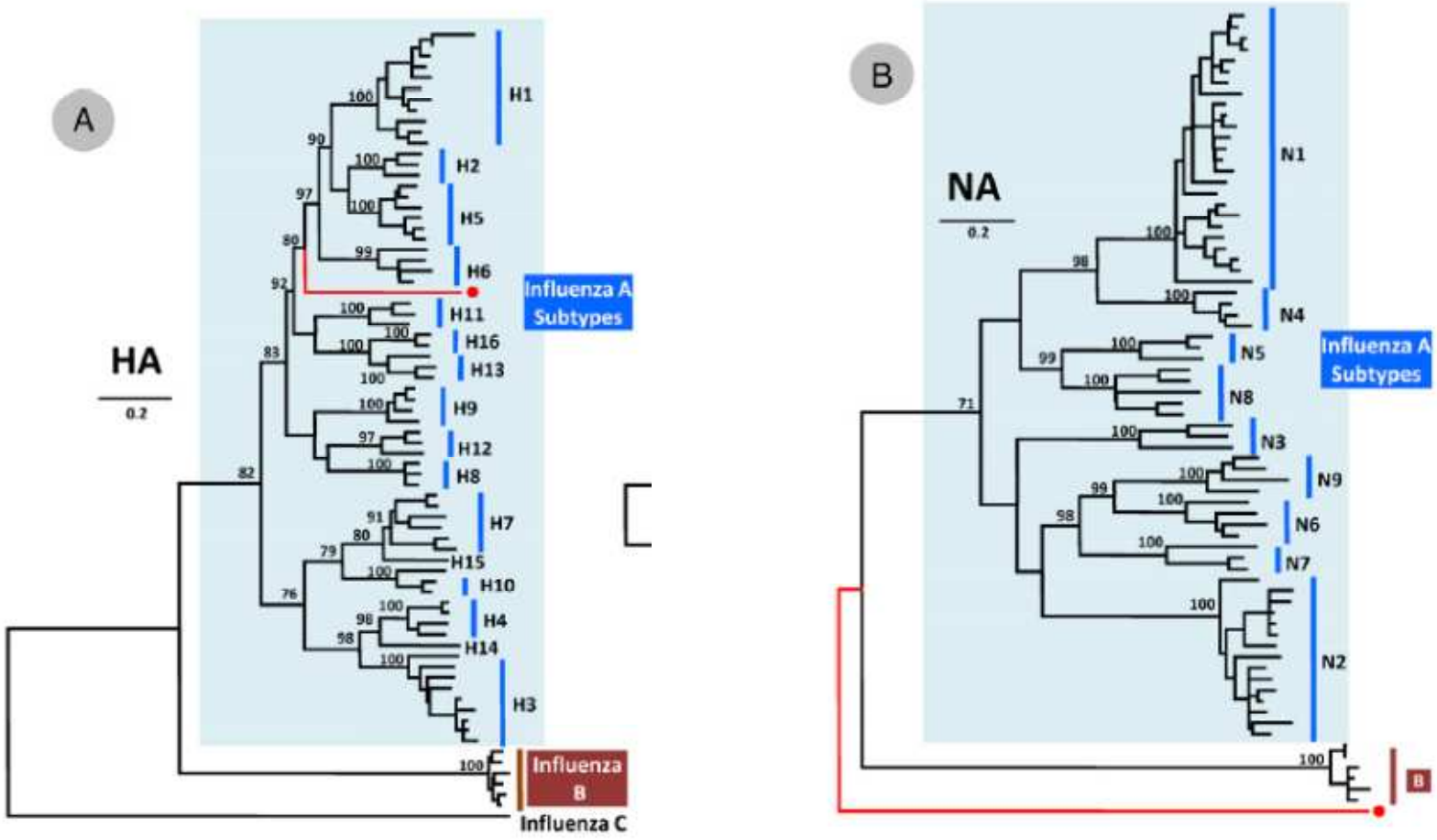
vRNA (-)

Analyse et comparaison avec des virus humains

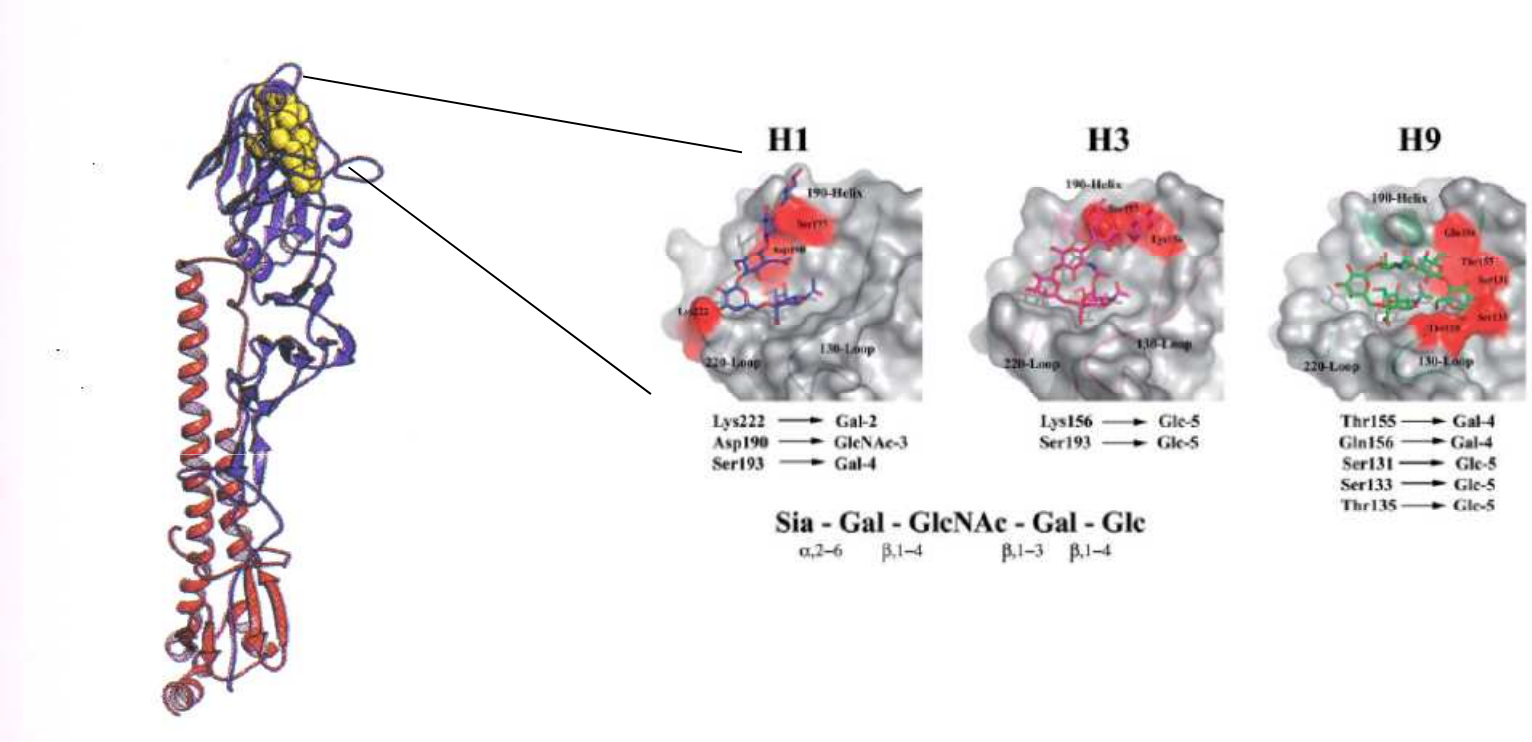
	A/bat/Guat/09		A/Panama/2007/1999 (H3N2)		
Gene	Segment Size in nt (ORF amino acids)	% AU content	Segment Size in nt (ORF amino acids)	% AU content	Number of internal gaps (indels) in best nucleotide alignment
PB2	2338 (760)	57.4	2341 (760)	55.9	0
PB1	2339 (756)	57.3	2341 (758)	55.6	0
PA	2216 (713)	59.0	2233 (717)	56.3	1 (15)
HA	1784 (564)	58.2	1762 (567)	58.6	4 (15)
NP	1558 (497)	54.2	1566 (499)	53.1	1 (3)
NA	1390 (442)	56.5	1466 (470)	57.1	16 (75)
M	1027 (M1: 252; M2: 96)	54.8	1027 (M1: 254; M2: 98)	51.0	0 in M1; 3 (18) in M2
NS	895 (NS1: 221; NS2: 122)	58.0	887 (NS1: 231; NS2: 122)	57.3	2 (6) plus 12 aa del. C term in NS1; 0 in NS2
Total	13547		13623		

Table S3. Comparison of the genome of A/bat/Guat/09to known influenza A viruses

Comparaison avec l'existant

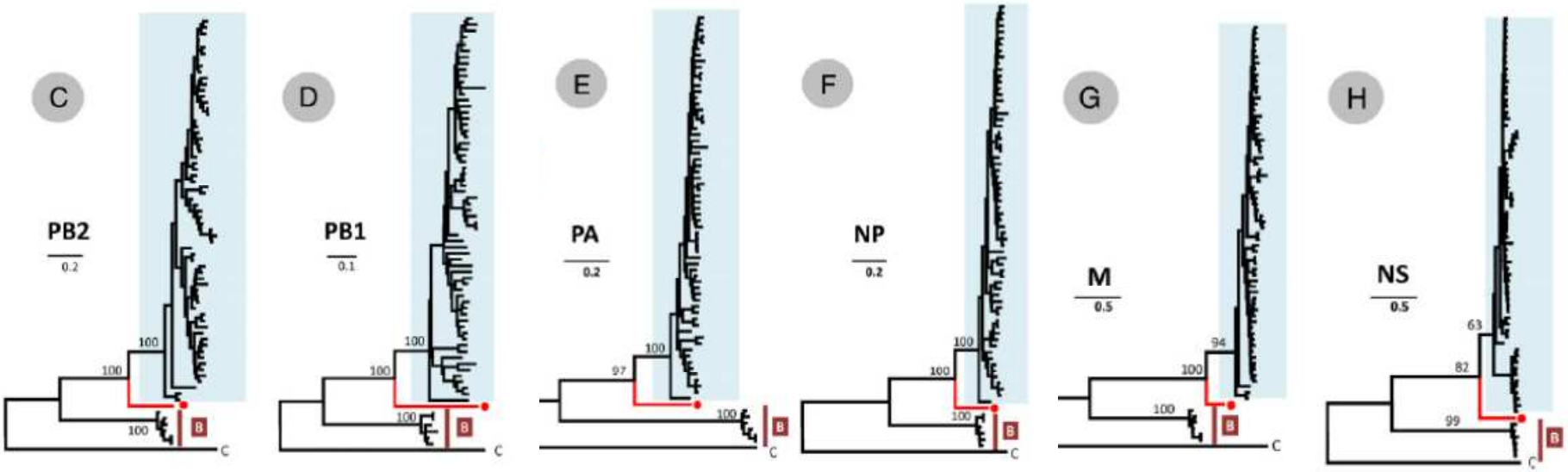


Attachement sur le RBS



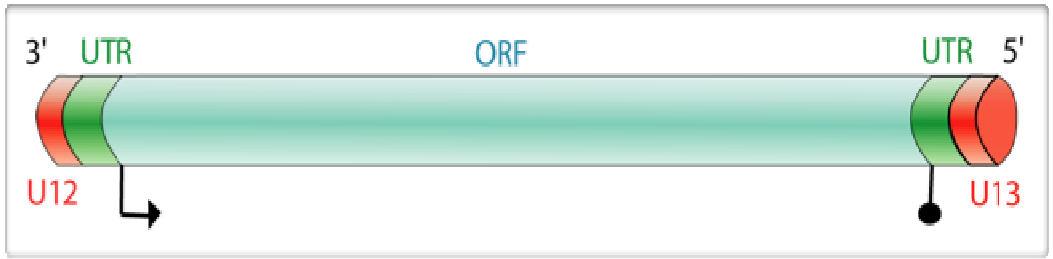
Subtype	Base of RBS				Avian/human-specific		Other relevant positions							
	91	150	180	191	187	222	133	190	213	218	219	223	224	225
H1, H2, H5, H6	Y	W	H	L	D(hu); E(av)	D(hu); G(av)	T	S/K/T	E/K	P/S	K	Q	E/S	G
A/bat/Guat/09	F	W	H	L	Q	A	D	N	E	D	E	H	Q	D
A/bat/Guat/10	F	W	H	L	Q	A	D	N	D	D	E	H	Q	D

Les autres segments de gènes

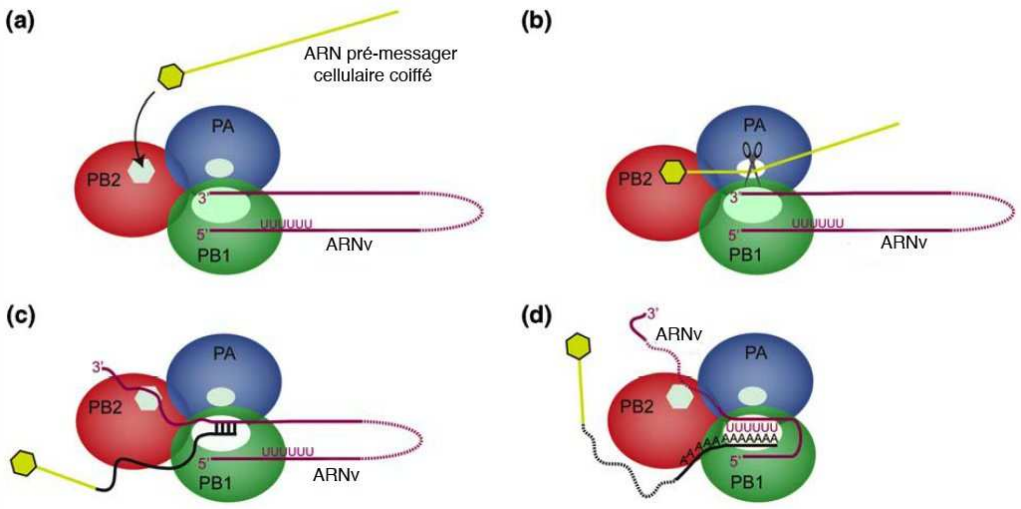


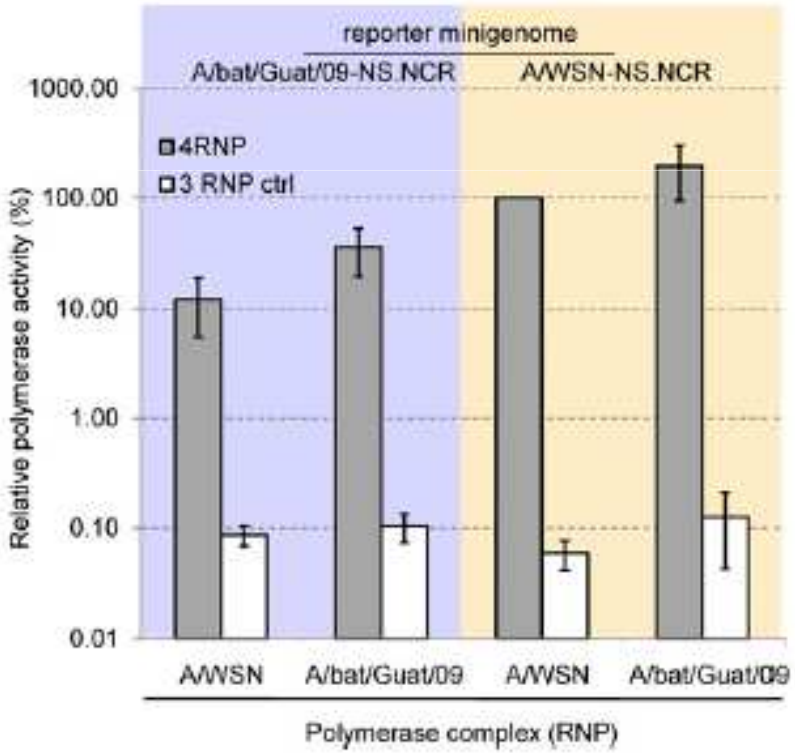
Organisation génomique générale

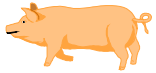
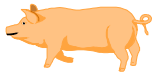
Gene	NCR	A/little yellow-shouldered bat/Guatemala/164/2009		A/Panama/2007/1999(H3N2)		Ratio
		Sequence	UTR nt	Sequence	UTR nt	
PB2	3′	UCGUCUUCGUCCAGUCUCUAACAGUUAUAC	27	UCGCUUUCGUCCAGUUAAUAUAAGUCAUAC	27	1.0
	5′	AGUAGAAACAAGGUCAUUUUUAGUAUUGuua	28	AGUAGAAACAAGGUCGUUUUUAAACUAUUCUAUUCAACAuua	39	0.7
PB1	3′	UCGUCUUCGUCCGUUUGAUAAAAUUUUAC	26	UCGCUUUCGUCCGUUUGGUAAACUUAC	24	1.1
	5′	AGAUGAAACAAGGCAUUUUUUCGUUUCAACAACUAAUGACCCuua	42	AGUAGAAACAAGGCAUUUUUUCAUGAAGGACAAGCUAAAUUCAuua	43	1.0
PA	3′	UCGUCUUCGUCCAUGAAUUUGUUAC	22	UCGCUUUCGUCCAUGACUAAGCUUUAC	24	0.9
	5′	AGUAGAAACAAGGUACUUUUUUCUUACAUUGAAUCAAAGCUGAUAGAGUUCUuca	52	AGUAGAAACAAGGUACUUUUUGGACAGUACGGAUAACAAAUAGUAGCACUGCCAUAAcua	57	0.9
HA	3′	UCGUCUUCGUCCCAUUGAUAAUGAGACACGAUGAUAC	34	UCGUUUUCGUCCCCUAUUAAGAUAAUUGGUAC	29	1.2
	5′	AGUAGAAACAAGGGUCUUUUUUGCUUUUCUGAAUGACAAGGUUAAUUCCACCGUUcua	55	AGUAGAAACAAGGGUGUUUUUAAUUAAUGCACUCAAAUGCAAAUGUUGCACcua	51	1.1
NP	3′	UCGUCUUCGUCCCAAUUAUUAGUGUAACACUGUAAAUUUCUAC	40	UCGUUUUCGUCCCAAUUAUUAGUGAGUGACUCACUGUAGUUUUAGUAC	45	0.9
	5′	AGUAGAAACAAGGGUAUUUUUUGCuca	24	AGUAGAAACAAGGGUAUUUUUUCCuua	24	1.0
NA	3′	UCGUCUUCGUCCUCAAAAAUUAUUAC	23	UCGUUUUCGUCCUCACUUCUAC	19	1.2
	5′	AGUAGAAACAAGGAGUUUUUUCAUUCGCUGUCCAUUGGuca	28	AGUAGAAACAAGGAGUUUUUUCUAAAAUUGCGAAAGCuua	28	1.0
M	3′	UCGUCUUCGUCCGUAAUAGGUUUUAC	23	UCGUUUUCGUCCAUCUAUAACUUUCUAC	25	0.9
	5′	AGUAGAAACAAGGGAUUUUUUCAUUuca	25	AGUAGAAACAAGGUAGUUUUuua	20	1.3
NS	3′	UCGUCUUCGUCCCAAAGAUUUCUGUAUUAC	27	UCGUUUUCGUCCCACUGUUUCUGUAUUAC	26	1.0
	5′	AGUAGAAACAAGGGUAUUUUUUAAuca	24	AGUAGAAACAAGGGUGUUUUUUAuua	23	1.0



Capacité de synthèse protéique avec des virus humains





H1				
H2				
H3				
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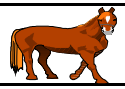
H7				
H8				
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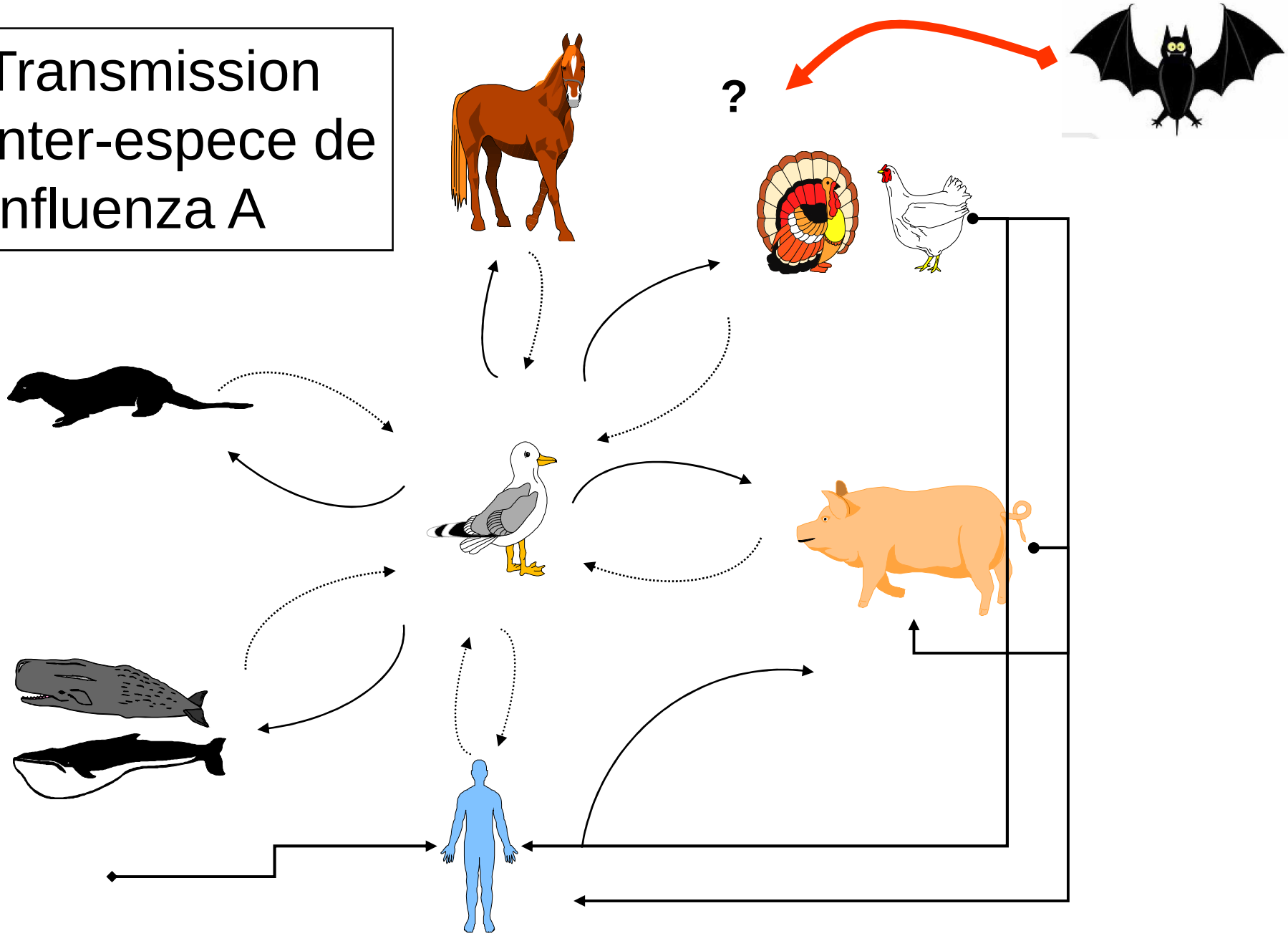
Nouvelle classification et distribution par hôte des hémagglutinines des virus Influenza de type A

Transmission inter-espece de Influenza A



Au total

- Les oiseaux aquatiques ne sont pas le seul réservoir des virus influenza
- Les virus détectés chez les 3 chauves-souris sont identiques, mais différents des virus décrits jusqu'alors. Environ 15% de la population des *Sturnira lilium* est infectée
- Ces virus ne répliquent pas dans le systèmes utilisés classiques, mais sont capables d'interagir avec des virus humains
- La Neuraminidase de ces virus présente des divergences considérables d'avec les virus connus
- Le niveau de circulation de ces virus reste a évaluer, notamment par des enquêtes sero-épidémiologiques
- Les animaux ne sont pas de simples porteurs, ils sont véritablement infectés par ces virus (atteinte de différents organes, titre infectieux élevé)

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