Reassortment of American and Eurasian genes in an influenza A virus isolated from a Great Black-backed Gull (*Larus marinus*), a species demonstrated to move between these regions

Michelle Wille[1], Gregory J. Robertson[2], Hugh Whitney[3], Davor Ojkic[4], Andrew S. Lang[1*]

[1]Department of Biology, Memorial University of Newfoundland, St. John's, NL A1B 3X9, Canada

[2]Wildlife Research Division, Environment Canada, Mount Pearl, NL A1N 4T3, Canada

[3]Animal Health Division, Department of Natural Resources, St. John's, NL A1E 3Y5, Canada

[4]Animal Health Laboratory, University of Guelph, Guelph, ON, N1G 2W1, Canada

*To whom correspondence should be addressed:

phone 1-709-737-7517; fax 1-709-737-3018; email aslang@mun.ca

Note: Nucleotide sequence data reported are available in the GenBank database under the accession numbers: GU724150 – GU724157

Online Resource 1: Primers used for whole genome sequencing of A/Great Black-backed Gull/Newfoundland/296/2008(H13N2).

Gene Region	Primer name	Primer sequence	PCR Conditions[a]	Reference
PB2.1	Bm-PB2-1	TATTGGTCTCAGGGAGCGAAAGCAGGTC	2	[26]
	PB2-1250R	TCYTCYTGTGARAAYACCAT		[27]
PB2.2	PB2-1105F	TAYGARGARTTCACAATGGT	1	[27]
	B010 PB2-1962R	ATTCCKGAGCCTCTCACATTCACAG		[28]
PB2.3	B022 PB2.2-1814F	TGAGGACACTGTTCCAGCAGATG	1	[28]
	AVAKPB222R	CAAGGTCGTTTTTAAACAATTCG		[8]
PB1.1	Bm-PB1-1	TATTCGTCTCAGGGAGCGAAAGCAGGCA	2	[26]
	A006R PB1-621R	CATTTTCTTGGTCATGTTG		[28]
PB1.2	A014F PB1-533F	TAGATTTTCTCAAGGATGTGATGGA	2	[28]
	PB1-1262R	TTRAACATGCCCATCATCAT		[27]
PB1.3	PB1-1124F	ARATACCNGCAGARATGCT	2	[27]
	A012 PB1-1964R	GGCATTACCACAGCATTGTT		[28]
PB1.4	A011 PB1-1944F	AACAATGCTGTGGTGATGCC	2	[28]
	Bm-PB1-2341R	ATATCGTCTCGTATTAGTAGAAACAAGGC		[26]
PA.1	Bm-PA-1	TATTCGTCTCAGGGAGCGAAAGCAGGTA	1	[26]
	C006 PA607R	CGGATTGACGAAAGGAGTCCC		[28]
PA2	C005 PA587F	GGGAYTCCTTTCGTCAGTCCG	1	[28]
	PA-1498R	TNGTYCTRCAYTTGCTTATCAT		[27]
PA.3	PA-747F	CATTGAGGGCAAGCTTTC	1	[27]
	C011 PA1919R	GARCCTTCYTCCACYCCYTTRGG		[28]
PA4	C016 PA1897F	CCYAARGGRGTGGARGAAGGYTC	1	[28]
	Bm-PA-2233R	ATATCGTCTCGTATTAGTAGAAACAAGGT		[26]
NP.1	SZANPF	CTCGAGAGCAAAAGCAGGGT	1	[29]
	E010 NP-734R	AATTTCCCTTTGAGGATGTTGCACATTC		[28]
NP.2	E003 NP-517F	GGAATGGAYCCCAGGATGTGCTC	1	[28]
	SZANPR	AGTAGAAACAAGGGTATTTTTC		[29]
M	SZAMF	CTCGAGCAAAAGCAGGTAGAT	1	[29]
	SZAMR	ATGAGAAACAAGGTAGTTTTT		[29]
NS	SZANSF	AGCAAAAGCAGGGTGACAAA	1	[29]
	SZANSR	ATGAGAAACAAGGGTGTTTTTT		[29]
HA.1	HAF M	TATTACGCGTCGAGGAGCAAAAGCAGGG	2	[29]
	HA13intR	TCAATGGCCTTTTGTGTTGA		This study
HA.2	HA1134F	CCATACCANCCRTCDATCATTCC	1	[31]
	HAR K	ATATGGCGCCGTATTAGTAGAAACAAGG		[30]
NA.1	NAF M	TATTACGCGTCGAGGGAGCAAAAGCAGG	1	[30]
NA.2	NAR K	ATATGGCGCCGTATTAGTAGAAACAAGG	1	[30]
N1	N1.1	GAACAGGCAGTTGTGGTC	3	[32]
	N1.2	TYAGTTCTGGATGCTGGA		[32]
N2	N2.1	TCCGTTTCATTTGGGAAC	3	[32]
	N2.2	CTGACAATGGRCTAATGTG		[32]
N3	N3.1	ATCATGTGAYTCYCCAAG	3	[32]

	N3.2	TCCCGATCCAGGTTCAT		[32]
N4	N4.1	ATGTGCATGCAACAGGGTTC	3	[32]
	N4.2	CTGTTGTCTCYCCTCTAATGC		[32]
N5	N5.1	AYCCTGCAACACCACTGAG	3	[32]
	N5.2	TCTCTTTCATTTGTCACCAT		[32]
N6	N6.1	AACCGGAGGGAGCCCAGATC	3	[32]
	N6.2	TCCCAATCGCTCYTTGGATC		[32]
N7	N7.1	ATGYTGAARATACCYAATGC	3	[32]
	N7.2	ARGAACCRGAACCAACTG		[32]
N8	N8.1	ACAGTCRTTAGGGAATAC	3	[32]
	N8.2	TACACATTGGGTGATG		[32]
N9	N9.1	TGTAATGACCCTTATCCAGG	3	[32]
	N9.2	GTTCCATTGTCCAAGGAATTC		[32]

[a] Reactions contained 0.5 µl cDNA, 0.3 mM $MgCl_2$, 0.2 mM each dNTP (New England Biolabs), 0.2 mM of each primer, and 0.5 U Platinum Taq DNA Polymerase (Invitrogen) in a final volume of 25 µl 1x PCR Buffer (Invitrogen).

1. Thermocycler conditions: 2 min at 94°C, followed by 40 cycles of 94°C for 30s, 55°C for 30s, 72°C for 2min, followed by 72°C for 10min.

2. Thermocycler conditions: 2 min at 94°C, followed by 40 cycles of 94°C for 30s, 52°C for 30s, 72°C for 2min, followed by 72°C for 10min.

3. Thermocycler conditions: 2 min at 94°C, followed by 40 cycles of 94°C for 40s, 60°C for 40s, 72°C for 40s, followed by 72°C for 10min.