

Susceptibility of Influenza A, B, C, and D Viruses to Baloxavir¹

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Baloxavir showed broad-spectrum in vitro replication inhibition of 4 types of influenza viruses (90% effective concentration range 1.2–98.3 nmol/L); susceptibility pattern was influenza A > B > C > D. This drug also inhibited influenza A viruses of avian and swine origin, including viruses that have pandemic potential and those resistant to neuraminidase inhibitors.

Influenza viruses are classified into 4 types: A, B, C, and D (1). Influenza A viruses infect a wide range of species and pose threats to human and animal health. Influenza A viruses belonging to 16 hemagglutinin and 9 neuraminidase subtypes have been identified in the natural reservoir (wild birds). Zoonotic infections with avian H5N1, H5N6, and H7N9 viruses are concerning because of their high fatality rates in humans and pandemic risk (2).

Swine are recognized as mixing vessels because influenza A viruses from multiple hosts can infect pigs and produce novel reassortants. Numerous subtypes of reassortant swine influenza A viruses are enzootic throughout North America and pose a threat to human health. For instance, H3N2 triple reassortant viruses caused a multi-state outbreak affecting hundreds of persons in the United States during 2012, and a quadruple reassortant H1N1 virus caused the 2009 pandemic and now circulates as a seasonal virus (2,3).

Influenza B viruses are considered strictly human pathogens, although occasional outbreaks in aquatic mammals have been reported (1). Influenza C viruses are known to infect humans, pigs, camels, and dogs (1). Unlike influenza A and B viruses, influenza C viruses typically cause

mild illness. However, in recent years, severe illness in children infected by influenza C virus has raised concerns over the lack of virus-specific therapeutics and vaccines (4). Recently discovered influenza D viruses were isolated from swine and bovines. No virologically confirmed human infections have been reported, but influenza D virus antibodies have been found in persons exposed to cattle (1). Evolutionarily, influenza C and D viruses are more closely related to each other than to influenza A or B viruses (1).

Antiviral drugs have been used to mitigate zoonotic virus outbreaks and are central to pandemic preparedness. However, therapeutic options remain limited and drug-resistant viruses can emerge after treatment, spontaneous mutation, or reassortment. Until recently, only matrix (M) 2 blockers and neuraminidase inhibitors (NAIs) were approved to control influenza. M2 blockers are effective only against influenza A viruses and are not recommended because of widespread resistance. NAIs are used for treatment of influenza A and B virus infections, but NAI-resistant viruses have emerged (5). NAI-resistant seasonal influenza H1N1 viruses circulated worldwide during late 2007 through early 2009 (6) and raised concerns over limited therapeutic options.

In 2014, favipiravir was licensed in Japan for restricted use in the event of a drug-resistant influenza pandemic (7). Favipiravir is a broad-spectrum antiviral drug that inhibits viral RNA polymerase, an enzyme recognized as an attractive target because of its critical role in virus replication and high degree of conservation (8). In 2018, another inhibitor of the viral RNA polymerase, baloxavir marboxil, was approved in Japan and the United States for treatment of influenza A and B virus infections (9). Its active metabolite, baloxavir acid, inhibits cap-dependent endonuclease activity of polymerase acidic (PA) protein (10). Amino acid substitutions at position 38 in the PA active site were recognized as the primary pathway to baloxavir resistance (11). PA substitutions at this and other positions have variable impact on resistance and are rarely found in nature (11,12). The purpose of this study was to determine the effectiveness of baloxavir against the 4 types of influenza viruses.

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The Study

The active site of the PA protein (P3 in C and D viruses) is nearly identical in all 4 influenza virus types (1,8). Therefore, we hypothesized that baloxavir would inhibit replication of not only influenza A and B viruses but also influenza C and D viruses. First, we tested 2 viruses of each type by using a virus yield reduction assay. We used baloxavir acid (baloxavir) in experiments and included favipiravir as a control.

Baloxavir broadly inhibited virus replication of all 4 types (Table 1). On the basis of 90% effective concentration values determined at 48 hours postinfection, influenza A viruses were most susceptible to baloxavir and influenza D viruses least susceptible. Baloxavir susceptibility for influenza B viruses was \approx 3-fold lower and that for influenza C viruses was \approx 6-fold lower than that for influenza A viruses. Analysis of 34 P3 sequences of influenza D virus and 221 of influenza C virus (retrieved from GISAID, <https://www.gisaid.org>, and GenBank) showed that all influenza D viruses have valine at position 38, whereas influenza C viruses have isoleucine, similar to most influenza A and B viruses. Nevertheless, valine at 38 in influenza A and B viruses had little or no effect (\leq 3-fold) on baloxavir susceptibility (10–12). Favipiravir also showed inhibitory effects against all virus types, although much higher concentrations were required to achieve similar levels of reduction (Table 1).

Although the virus yield reduction assay has been used to assess baloxavir susceptibility of seasonal and avian viruses (10,13), other phenotypic assays, such as the focus-reduction assay (FRA) and the high-content imaging neutralization test (HINT), offer an improved throughput (12,14,15). Regardless of the assay used, baloxavir effective concentrations for influenza A viruses were similar (\approx 0.1–3 nmol/L) (10,12–15). Unlike the FRA, HINT

relies on single-cycle virus replication, which is achieved by withdrawing trypsin needed to activate infectivity of progeny virus. HINT eliminates variance caused by different replication kinetics. However, the FRA is optimal for testing highly pathogenic avian viruses because multicycle replication of these viruses is trypsin independent. We used 2 seasonal A(H1N1)pdm09 viruses, one of which contains the naturally occurring substitution PA-I38L, for reference purposes (12) (Table 2).

First, we tested 25 influenza viruses of avian origin, representing H5, H6, H7, H9, and H10 subtypes, by using FRA or HINT as described (12) (Table 2; Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/25/10/19-0607-App1.pdf>). Most viruses were isolated from infected humans. Most viruses had markers of M2 resistance and some had NAI-resistance markers. Data showed that these diverse viruses were susceptible to baloxavir and had 50% effective concentration (EC_{50}) values in a low nanomolar range (Table 2; Appendix Table 1). In the FRA, favipiravir EC_{50} values were much higher than those for baloxavir (Appendix Table 1). However, favipiravir did not produce a measurable antiviral effect by HINT because this drug requires several hours for activation in cells. Baloxavir susceptibility of 30 swine-origin viruses, representing different lineages and subtypes and collected over many years, demonstrated HINT EC_{50} values comparable to avian and seasonal influenza A viruses (Table 2; Appendix Table 2) (10,12,13).

It is prudent to analyze PA sequences of emerging influenza A viruses for markers previously associated with reduced baloxavir susceptibility (11,12). Among swine-origin viruses available for testing in this study, polymorphism PA-38I/M was detected in A/Iowa/33/2017 (H1N1) v. Virus populations with either PA-I38 or PA-I38M were recovered by biologic cloning and tested by using HINT.

Table 1. Drug susceptibility of influenza A, B, C, and D viruses by viral yield reduction assay in MDCK cells*

Type	Virus	Virus titer, log ₁₀ TCID ₅₀ /mL†		EC ₉₀ , nmol/L		
		24 hpi	48 hpi	Baloxavir, mean \pm SD		Favipiravir 48 hpi
				24 hpi	48 hpi	
A	A/Texas/138/2018 (H1N1)pdm09	6.4 \pm 0.5	9.1 \pm 0.1	0.8 \pm 0.2	1.2 \pm 0.1	NT
	A/Illinois/08/2018 (H1N1)pdm09	5.8 \pm 0.5	8.9 \pm 0.3	2.7 \pm 0.5	3.3 \pm 0.2	3,005
B	B/Maryland/29/2018	3.5 \pm 0.5	7.1 \pm 0.6	8.9 \pm 1.6	5.8 \pm 1.1	1,789
	B/Iowa/18/2018	3.5 \pm 0.5	7.6 \pm 0.4	13.8 \pm 2.0	7.8 \pm 1.7	1,635
C	C/Taylor/1233/47	<1.5	5.9 \pm 0.5	NA	13.0 \pm 3.3	27,476
	C/Aomori/74	<1.5	4.9 \pm 0.4	NA	18.4 \pm 6.5	31,603
D	D/swine/Oklahoma/13334/2011	4.4 \pm 0.3	7.7 \pm 0.1	110.2 \pm 27.6	98.3 \pm 23.9	2,764
	D/bovine/Oklahoma/660/2013	4.8 \pm 0.0	8.0 \pm 0.5	105.6 \pm 37.0	64.3 \pm 16.2	3,106

*Cell monolayers were inoculated at a multiplicity of infection of 0.0005 and virus was allowed to adsorb for 1 h. Virus inoculum was removed, serially diluted drug (baloxavir: 0.5–500 nmol/L; favipiravir: 310–318,000 nmol/L) was added, and cells were incubated at 33°C in a 5% CO₂ incubator. At 24 and 48 hpi, cell culture supernatants were harvested to determine infectious virus titers. Replication of influenza A and B viruses was detected by neuraminidase activity (Fluor-NA Kit; Applied Biosystems, <https://www.thermofisher.com>), and replication of influenza C and D viruses by esterase activity (3-acetyl-umbelliferone in 20 mmol/L Tris-HCl, pH 8.0, reaction buffer (Sigma-Aldrich, <https://www.sigmaaldrich.com>)). The EC₉₀ corresponds to a drug concentration causing a 90% reduction in virus titer compared with control wells without drug. The EC₉₀ for each virus and drug were determined by using nonlinear regression analysis (GraphPad, <https://www.graphpad.com>). For baloxavir, results are shown as mean \pm SD of 3 independent experiments; favipiravir results are shown as single or average of 2 independent experiments. EC₉₀, 90% effective concentration; hpi, hours postinfection; NA, not applicable; NT, not tested; TCID₅₀, 50% tissue culture infectious dose.

†Virus titers were determined in control wells without drug.

Table 2. Baloxavir susceptibility of zoonotic and animal influenza A viruses in MDCK-SIAT1 cells*

Virus subtype	FRA		HINT	
	No. viruses tested	EC ₅₀ , nmol/L, mean ± SD†	No. viruses tested	EC ₅₀ , nmol/L, mean ± SD†
Avian origin				
H5N6‡	3	0.31 ± 0.19	–	–
H6N1	1	0.12	1	0.48
H7N9	19	0.48 ± 0.32	9	1.44 ± 1.08
H9N2§	1	0.18	1	0.53
H10N8	1	0.30	1	0.63
Swine origin				
H1N1¶	–	–	3	0.72 ± 0.27
H1N1v	–	–	3	0.51 ± 0.12
H1N2v	–	–	9	1.19 ± 0.36
H3N2v	–	–	15	0.86 ± 0.50
Reference viruses#				
A/Illinois/08/2018 (H1N1)pdm09 PA-I38		2.12	–	1.75 ± 0.59
A/Illinois/37/2018 (H1N1)pdm09 PA-I38L		14.96 (7-fold)**	–	13.09 ± 3.56 (8-fold)**

*Both assays were conducted by using MDCK-SIAT1 cells. Details on viruses tested are in the Appendix (<https://wwwnc.cdc.gov/EID/article/25/10/19-0607-App1.pdf>). According to World Health Organization nomenclature, the swine-origin influenza viruses isolated from humans are named variant viruses (e.g., A[H1N1]v). EC₅₀, 50% effective concentration; FRA, focus reduction assay; HINT, high-content imaging neutralization test; –, not tested.

†Mean ± SD or average of 2 test results.

‡One of 3 viruses was isolated from chicken (Appendix Table 1).

§Virus was isolated from chicken (Appendix Table 1).

¶All 3 viruses were isolated from swine (Appendix Table 2).

#A pair of seasonal influenza A(H1N1)pdm09 viruses were included in each test as reference viruses (12).

**Fold change to EC₅₀ of virus carrying PA-I38L compared with sequence-matched control virus carrying PA-I38.

Substitution PA-I38M conferred 12-fold reduced baloxavir susceptibility, consistent with previous reports for PA-I38M-containing H3N2 viruses (11,12). Analysis of PA sequences from 2,485 H7N9 viruses (from GISAID and GenBank) showed 1 virus with PA-I38M, 2 with PA-E199G, and 1 with PA-A36V (11,12). The effect of these substitutions on baloxavir susceptibility for H7N9 viruses is currently unknown. Moreover, PA sequence of 1 swine influenza A virus showed PA-I38T, a marker associated with clinically relevant baloxavir resistance (11). None of these viruses were available for phenotypic testing.

Conclusions

Baloxavir displayed broad antiviral activity against diverse influenza viruses, including all 4 types and animal-origin influenza A viruses with pandemic potential. Our findings suggest that baloxavir might offer the first therapeutic option against influenza C virus infections. Further studies are needed to provide comprehensive assessment of baloxavir susceptibility by using a large panel of representative influenza C viruses. Ongoing monitoring of baloxavir susceptibility of emerging avian and swine influenza A viruses with pandemic potential is needed to inform clinical management and public health preparedness efforts.

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isolates; and the US Department of Agriculture, Agricultural Research Service and National Veterinary Services Laboratories, for providing viruses collected from birds and animals.

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About the Author

Dr. Mishin is a biologist in the Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA. His primary research interests are influenza viruses, antiviral drugs, development and optimization of in vitro assays for monitoring drug susceptibility, and influenza antigenic characterization.

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Susceptibility of Influenza A, B, C, and D Viruses to Baloxavir

Appendix.

Appendix Table 1. Drug susceptibility of zoonotic and avian influenza A viruses*

Subtype	Virus name	M2 blocker resistance marker in M2 protein	NAI resistance marker in NA protein	PA gene accession no.	FRA		HINT
					Favipiravir, EC ₅₀ , nmol/L†	Baloxavir, EC ₅₀ , nmol/L†	Baloxavir, EC ₅₀ , nmol/L†
H5N6	A/Sichuan/26221/2014‡	None	None	EPI533587	–	0.11, 0.22	–
	A/Yunnan/14563/2015‡	S31N	None	EPI587617	–	0.58, 0.56	–
	A/chicken/Vietnam/NCVD-16A26/2016‡	–	None	EPI1335786	39,530, 48,270	0.17, 0.19	–
H6N1	A/Taiwan/2/2013	S31N	None	EPI459854	33,620, 33,180	0.10, 0.14	0.38, 0.57
H7N9 (wave 1)	A/Anhui/1/2013	S31N	None	EPI439508	–	0.39, 0.41	1.03, 1.28
	A/Shanghai/1/2013	S31N	R292K	EPI439490	28,800	0.40, 0.42	0.99, 1.29
H7N9 (wave 2)	A/Shanghai/2/2013	S31N	None	EPI439498	–	0.29, 0.33	–
	A/Taiwan/1/2013 clone 1	S31N	None	EPI515451	–	1.04, 0.85	0.63, 0.68
	A/Taiwan/1/2013 clone 2	S31N	E119V	EPI515458	26,940	0.92, 1.30	0.66, 0.56
	A/Taiwan/1/2013 clone 3	S31N	I222K	EPI515474	–	0.66, 0.58	1.71, 1.34
	A/Taiwan/1/2013 clone 4	S31N	R292K	EPI516361	18,820	0.62, 0.50	0.62, 0.56
	A/Taiwan/1/2013 clone 5	S31N	I222R	EPI515466	–	0.35, 0.46	0.78, 0.87
	A/Hong Kong/5942/2013	S31N	None	EPI490878	–	0.47, 0.43	–
	A/Hong Kong/2212982/2014	S31N	None	EPI502369	–	0.05, 0.07	–
H7N9 (wave 3)	A/Hong Kong/734/2014	S31N	None	EPI498796	–	0.26, 0.21	–
	A/Hong Kong/56/2015	S31N	None	EPI1489673	–	0.11, 0.15	–
H7N9 (wave 4)	A/British Columbia/1/2015	S31N	None	EPI560397	–	0.15, 0.19	–
	A/Hong Kong/793/2016	S31N	None	Pending	–	0.72, 1.01	–
H7N9 (wave 5)	A/Hong Kong/61/2016	S31N	None	EPI1335764	27,390	0.46, 0.33	2.39, 2.36
	A/Hong Kong/4553/2016	S31N	None	EPI1335756	44,250, 34,200	0.68, 0.92	3.98, 4.18
	A/Hong Kong/125/2017	S31N	None	EPI977391	–	0.18, 0.17	–
H9N2	A/Hong Kong/214/2017	S31N	None	EPI884218	–	0.07, 0.07	–
	A/Taiwan/1/2017‡	S31N	R292K	EPI917064	56,240, 53,170	0.95, 1.08	–
H10N8	A/chicken/Vietnam/NCVD-LS52/2016	S31N	None	EPI1335772	20,120, 20,870	0.17, 0.18	0.63, 0.43
H10N8	A/Jiangxi/09037/2014	S31N	None	EPI530446	34,000, 32,980	0.26, 0.34	0.81, 0.45

*All procedures were conducted in Biosafety Level 3–enhanced containment. Both assays were conducted by using MDCK-SIAT1 cells. Most viruses were tested in duplicate to determine EC₅₀. EC₅₀, 50% effective concentration; FRA, focus reduction assay; HINT, high-content imaging neutralization test; M2, matrix 2; NA, neuraminidase; NAI, neuraminidase inhibitor; PA, polymerase acidic; –, not tested.

†Duplicate EC₅₀ values for each virus are shown.

‡Highly pathogenic avian influenza virus.

Appendix Table 2. Baloxavir susceptibility of swine and variant influenza A viruses determined by HINT*

Subtype	Virus name	M2 blocker resistance marker in M2 protein	PA gene accession no.	Baloxavir EC ₅₀ , nmo/L†
H1N1	A/swine/Iowa/15/30	None	EPI129822	0.45, 1.05
	A/swine/1976/31	–	–	1.03, 1.06
	A/swine/Tennessee/1/75	None	EPI62684	0.42, 0.33
H1N1v	A/South Dakota/03/2008	V27T	EPI291878	0.45, 0.48
	A/Texas/14/2008	V27T	EPI291886	0.62, 0.73
H1N2v	A/Minnesota/33/2014	S31N	EPI558110	0.40, 0.40
	A/Michigan/09/2007	None	EPI291823	1.39 ± 0.15
	A/Ohio/24/2017	S31N	EPI1056721	0.53 ± 0.14
	A/Ohio/35/2017	S31N	EPI1056729	1.30, 1.20
	A/California/62/2018	S31N	EPI1311357	1.80, 1.90
	A/California/63/2018	S31N	EPI1311365	1.40, 1.30
	A/Michigan/382/2018	S31N	EPI1271030	0.80, 1.10
	A/Michigan/383/2018	S31N	EPI1271062	0.80, 0.90
	A/Michigan/384/2018	S31N	EPI1271038	1.60, 1.20
	A/Ohio/25/2018	S31N	EPI1311349	1.30, 1.00
H3N2v	A/Ohio/88/2012‡	S31N	EPI541959	1.15; 0.95
	A/Iowa/04/2013	S31N	EPI482821	1.34, 2.30
	A/Ohio/4319/2014	S31N	EPI397958	0.90 ± 0.17
	A/Wisconsin/24/2014	S31N	EPI557538	1.46 ± 0.46
	A/Ohio/02/2014	S31N	EPI539158	0.46 ± 0.14
	A/Michigan/39/2015	S31N	EPI642509	0.36, 0.78
	A/Michigan/83/2016	S31N	EPI824771	1.60, 1.60
	A/Michigan/84/2016	S31N	EPI838247	1.00 ± 0.12
	A/Ohio/28/2016	S31N	EPI824753	0.10, 0.21
	A/Ohio/27/2016	S31N	EPI824745	0.58, 0.62
	A/North Dakota/19/2017	S31N	EPI1311461	0.32, 1.05
	A/Ohio/14/2017	S31N	EPI1056657	0.06, 0.10
	A/Ohio/15/2017	S31N	EPI1056665	1.19, 1.23
A/Ohio/29/2017	S31N	EPI1311405	0.29 ± 0.12	
A/Ohio/13/2017	S31N	EPI1056649	0.70, 1.19	

*HINT was conducted by using MDCK-SIAT1 cells. All procedures involving swine-origin viruses were conducted in Biosafety Level 2–enhanced containment. EC₅₀, 50% effective concentration; HINT, high-content imaging neutralization test; M2, matrix ; PA, polymerase acidic; –, not tested.

†EC₅₀ values from 2 tests. Mean ± SD values are shown for viruses which were tested more than twice.

‡Contains NA-S247P, a marker associated with decreased susceptibility to neuraminidase inhibitors.