Anti-influenza therapy: the emerging challenge of resistance

Influenza is a common cause of respiratory infections, with an annual peak incidence in the late fall, winter and early spring. It is associated with significant morbidity and mortality, particularly in those at the extremes of life and with underlying medical conditions, as well as self-limited illness with reduced productivity in otherwise healthy individuals. Two classes of antiviral medications, M2 inhibitors and neuraminidase inhibitors, are widely available. Use of these agents is associated with reduction in severity and duration of illness, and may be associated with reduced risk of death in certain patient populations. They also are effective in preventing influenza, in addition to or instead of immunization. Unfortunately, widespread resistance to one of the two classes of drugs is now common among most circulating strains of influenza.

KEYWORDS: adamantine = amantadine = influenza = M2 inhibitor = neuraminidase inhibitor = oseltamivir = peramivir = resistance = rimantadine = zanamivir

Influenza viruses cause annual epidemics of illness characterized by the rapid onset of constitutional and respiratory tract symptoms [1]. There are three subtypes of influenza: A, B and C [1]. Influenza A viruses are further classified into subtypes on the basis of their surface proteins (16 hemagglutinins and nine neuraminidases are currently recognized) [1]. Annually, influenza affects approximately 5-10% of adults, with higher rates in children [2]. In the USA, influenza causes an average of 36,000 deaths and 130,000-170,000 hospitalizations during each epidemic [3,4]. Hospitalization and death appear to be more common in the very young and very old patients, those with abnormal immune systems, and those with significant underlying medical conditions, particularly cardiopulmonary disease [2]. In addition, there is a significant financial impact of influenza in the USA annually, with US\$8-12 billion in direct medical costs and economic losses due to lost productivity [5].

The cornerstone of prevention of influenza is vaccination [2]. These vaccines are reformulated each year to attempt to match circulating strains, and availability varies from year to year [2]. Vaccination has been shown to reduce the risk of hospitalization, morbidity and mortality among high-risk patients and be cost-effective, in part, secondary to retained productivity among working adults [2,5]. Recommendations for their use are updated annually, and the most recent advice should be consulted [2]. Unfortunately, response to vaccine is limited in the elderly and those with underlying immune compromise, such as transplant recipients [2,6]. As we have learned in the development of vaccines for H5N1 [7], developing novel vaccines directed against pandemic strains pose formidable challenges, and such vaccines will likely be either completely or partially unavailable during the first wave of infection. As a result of limitations of the current vaccines, antiviral and nonpharmacologic measures, such as social distancing, will play an important role in retarding the spread of the infection [2,8] during a pandemic.

Once infection is established, antiviral medications have been shown to decrease the severity of influenza, shorten the duration of illness, and reduce infectious and noninfectious complications [9,10].

Available anti-influenza agents Approved agents

Currently, there are four drugs in two antiviral classes available for the prevention and treatment of influenza: M2 inhibitors (amantadine and rimantadine) and neuraminidase inhibitors (NAIs; zanamivir and oseltamivir) (FIGURE 1) [9,10]. Recently, the increase in resistance globally to both classes of agents has significantly limited the effectiveness of our current antiviral armamentarium [11–14].

M2 inhibitors

The M2 ion channel allows the influx of protons into the viral particle which, in turn, facilitates uncoating [9]. M2 inhibitors bind to the M2 ion

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Divisions of Infectious Diseases & Organ Transplantation, Northwestern University Feinberg School of Medicine, 645 N. Michigan Avenue Suite 900, Chicago, IL 60611, USA Tel.: +1 312 695 4186 Fax: +1 312 695 5088 maison@northwestern.edu channel and limit the influx of protons, resulting in its antiviral effect. Since the M2 protein is present only on influenza A viruses, M2 inhibitors have no activity against influenza B [9].

There are two US FDA-approved M2 inhibitors: amantadine (Symmetrel®, Endo, PA, USA) and rimantadine (Flumadine®, Forest Laboratories, NY, USA) [15]. Although the mechanism of action and spectrum of activity are similar, there are important pharmacokinetic differences between the two drugs [16]. Amantadine, which has a half-life of 12-18 h. is not extensively metabolized and is excreted unchanged in the urine [9]. Therefore, amantadine accumulates rapidly in patients with reduced renal function, including the elderly [9]. The most common side effects of amantadine are minor, reversible CNS effects, such as insomnia, dizziness and difficulty in concentrating [9]. Side effects appear to be more common among the elderly; confusion is noted in approximately 18% of elderly recipients [17]. In addition, amantadine use has been associated with seizures in individuals with a prior seizure disorder [18]. Dose adjustment of amantadine is therefore indicated in those with renal dysfunction and in the elderly [9,16]. In contrast, rimantadine is extensively metabolized, with less than 15% of the drug excreted unchanged in the urine [9,16]. As a result, rimantadine is associated with considerably fewer CNS side effects and is better tolerated by the elderly. Rimatadine needs to be adjusted in the elderly and those with severe renal dysfunction (<10 ml/min) [9,16].

Neuraminidase inhibitors

The influenza neuraminidase has enzymatic activity that cleaves terminal sialic acid residues and destroys the receptors recognized by viral hemagglutinin [10,19]. This activity is essential for release of virus from infected cells, for prevention of viral aggregates and for viral spread within the respiratory tract [19]. The NAIs are sialic acid analogs that potently and specifically inhibit influenza A and B neuraminidases by competitively and reversibly interacting with the active enzyme site [10].

There are currently two NAIs approved by the FDA: zanamivir (RelenzaTM, GlaxoSmithKline, London, UK) and oseltamivir (Tamiflu[®], Roche, Basel, Switzerland) [10]. Although each drug has unique pharmacologic properties, both have identical mechanisms of action and similar profiles of antiviral activity [10]. Zanamivir is not orally bioavailable and is therefore administered topically by dry-powder inhalation [10].

The proprietary inhaler device for delivering zanamivir is breath-actuated and requires a cooperative patient [20]. Zanamivir may cause bronchosconstriction with use; it should be used with caution in patients with underlying lung disease, and these patients should have ready access to a rapidly acting bronchodilator in the event of bronchospasm [10]. Few other side effects are noticed, since there is limited systemic exposure [10]. Oseltamivir carboxylate is an orally bioavailable ethyl ester prodrug of oseltamivir phosphate [10]. The prodrug is rapidly converted to active drug by intestinal and hepatic esterases. Oseltamivir is eliminated primarily by tubular secretion unchanged. As a result, oseltamivir requires dose adjustment in individuals with a creatinine clearance rate of less than 30 ml/ min [10]. The most common side effect of oseltamivir is gastrointestinal upset, which is ameliorated with co-administration with food [10].

Investigational agents

The threat of an A/H5N1 pandemic and emerging resistance to both M2 inhibitors and NAIs has stimulated research into several investigational anti-influenza agents; these have been reviewed extensively elsewhere [21,22]. Many of the agents under current investigation are new NAIs [23,24]. Peramivir is also undergoing investigation as both an intravenous and an intramuscular formulation [23,24]. Two topical long-acting NAIs are also being developed; their major advantage is the less frequent dosing for prophylaxis. In addition, several compounds with novel mechanisms of action are being developed (TABLE 1) [21-24]. These newer agents typically remain active against viruses resistant to M2 inhibitors and NAIs, and have been recently reviewed elsewhere [21,22].

M2 inhibitor resistance

Resistance to the available M2 inhibitors has been recognized since early in their development. Mutations in the M2 inhibitor gene at one of five commonly recognized sites (position 26, 27, 30, 31 or 34 of the M2 protein) results in reduced binding of the M2 inhibitors or in enlargement of the pore diameter; by either mechanism, the function of the M2 pore is preserved in the presence of the inhibitor [25–27]. Resistance mutations do not affect transmissibility or replication fitness as compared with wild-type viruses; documented transmission from person to person has been well established [28]. Resistance affects both drugs in the class equally, and appears to be persistent over time [26,29].

Table 1. Investigational anti-influenza agents.				
Class	Compound	Route		
Neuraminidase inhibitors	Peramivir	i.v./i.m.		
	Zanamivir*	i.v.		
	Oseltamivir*	i.v.		
	A-32278	Oral		
	CS8959/R-118958	Topical		
	Zanamivir dimers	Topical		
Conjugated sialidase	DAS181	Topical		
Hemagglutinin inhibitors	Cyanovirin-N	Topical		
	Sialylglycopolymer	Topical		
	Entry blocker	Topical		
Polymerase inhibitors	Ribavirin	Topical, i.v., oral		
	Viramidine	Oral		
	T-705	Oral		
siRNA		Topical, i.v.		
Protease inhibitor	Aprotinin	Topical		
Antibodies		i.v., i.m.		
Interferons		i.m., s.c.		
Interferon inducers	Poly (I) Poly (C)	Inhaled		
*Zanamivir is approved for oral inhali i.m.: Intramuscular; i.v.: Intravenous; Data taken from [22–24].	ation and oseltamivir is approved for oral therapy. s.c.: Subcutaneous.			

During routine treatment with M2 inhibitors for documented influenza, resistant variants emerge frequently. Approximately 30% of adults treated with M2 inhibitors will have resistant variants detected during the course of their illness, with high frequency (up to 80%) of resistance emergence in immunocompromised patients, patients hospitalized for influenza and children [30-34]. Until recently, the frequency of M2 inhibitor resistance among seasonal isolates was low (1-3%) [14]. However, in recent years the prevalence of resistance to M2 inhibitors among circulating influenza A/H3N2 increased globally, and now the majority of influenza A/ H3N2 globally is resistant to this class of drugs [14,35]. Resistance has resulted from the S31N substitution of the M2 inhibitor. M2 inhibitor resistance has also been documented in two important novel strains of influenza: A/H5N1 and swine-origin A/H1N1 [8,36]. Most clade 1 A/H5N1 viruses and all swine-origin A/H1N1 are resistant to the M2 inhibitors as a result of the S31N substitution, while most (~80%) of clade 2.1 A/H5N1 are resistant secondary to S31N or V27A substitution [8,36,37]. Of note, most of the clade 2.2 and 2.3 A/H5N1 viruses remain susceptible to M2 inhibitors [37].

There are currently no rapid tests that can screen for and identify the presence of M2 inhibitor resistance. M2 resistance may be diagnosed using plaque assay or gene sequencing. Although plaque assays are well described, they are not widely available [38]. Pyrosequencing methods for rapid analysis of mutations in the M2 gene associated with resistance have been described and are used in several reference laboratories [27,39]. Neither assay is typically available in most clinical laboratories. As a result, most clinicians rely on data generated from groups actively monitoring the resistance among circulating strains – in the USA this is actively carried out by the Centers for Disease Control and Prevention (CDC) [14].

Neuraminidase inhibitor resistance

Resistance to NAIs has been recognized since early in the development of these approved agents. Since the neuraminidase and hemagglutinin have a close functional relationship, viral resistance to NAIs can arise through mutations in either glycopeptides. Neuraminidase mutations affect the binding site and reduce affinity for the inhibitors, while mutations in the hemagglutinin reduce the affinity for its receptor [29,40,41]. Although new mutations conferring resistance are constantly being recognized, several key mutations have been well described (TABLE 2) [42,43]. Resistance to one NAI does not predict resistance to other NAIs. This is mostly related to differences in the chemical structures of the drugs. Oseltamivir, for example, has a bulky side chain, requiring the neuraminidase to undergo a significant conformational change in order to bind the active site. Any mutation

Location of residues Mut	Mutation	Viral subtypes identified with mutation	Neuraminidase inhibitor susceptibility		
			Oseltamivir	Zanamivir	Peramivir
functional D R R E	R292K	H3N2, H5N1, B	R	RS	R
	D151E	H3N2	RS	R	_
	R152K	В	R*	R/RS*	R/RS
	R224K	H3N2	R	R	_
	E276D	H3N2	R	R	_
	R371K	H3N2	R	R	_
framework	H274Y	H1N1, H3N2, H5N1	R*	S	S/R
	N294S	H1N1, H5N1	R	RS	_
	E119V	H3N2, B	R	S	S
	E119D	H3N2	S	R	S
		В	R	R	R
	E119G‡	H3N2, H5N1, B	S/RS	R	S/R
	E119A	В	R	R	R

Table 2. Commonly recognized neuraminidase mutations associated with neuraminidase inhibitor resistance.

that inhibits this conformational change would be expected to reduce the binding affinity of oseltamivir, while not affecting other inhibitors that do not require such conformational changes (i.e., zanamivir) [42,44]. In addition, differences in the neuraminidase protein of type 1 (N1, N4, N5 and N8) and type 2 (N2, N3, N6, N7 and N9) influenza A viruses would also predict differential effects of mutations and may explain differences in NAI susceptibility that are seen between subtypes of influenza [43].

Resistance to NAIs appears to occur less frequently in immunocompetent patients [40]. In clinical studies, resistance has been detected in 0.4% of adults [45]. Higher levels of resistance have been described in children (2.9-27.3%), particularly in Japan [33,46-49]. During the 2007–2008 influenza season, influenza A/H1N1 that had a H274Y mutation conferring oseltamivir resistance was recognized with variable frequency throughout Europe among circulating strains [12]. Over the subsequent months, it became apparent that this resistant virus was detected globally, and during the 2008-2009 influenza season in the USA, nearly all circulating A/H1N1 viruses were resistant to oseltamivir secondary to the H274Y mutation [11,50]. Interestingly, previously recognized oseltamivirresistant mutants containing the H274Y mutation were associated with reduced replication in vitro and reduced virulence in mice and ferrets [40,41,51,52]. Recent studies suggest that the presence of other mutations in the circulating oseltamivir-resistant A/H1N1 viruses may enhance their fitness through enhancing neuraminidase function, which in turn counteracts the attenuation of substrate affinity brought on by the H274Y mutation [53]. The net effect of all of the mutations present in this virus may confer a competitive advantage, explaining the persistence and global spread of this mutant. There is no clear association with prior exposure to or regional use of oseltamivir and the emergence of this resistant strain [11,12]. There are no significant differences between cases of oseltamivirresistant and oseltamivir-susceptible influenza in terms of demographic characteristics, underlying medical illness or clinical symptoms [11].

Resistance to oseltamivir can occur during treatment of influenza and has best been described in immunocompromised patients and those with severe infections caused by A/H5N1 [29,54–56]. Although it is clinically challenging to detect in real-time, there appears to be evidence of progressive influenza disease with an associated high mortality rate, particularly for A/H5N1 infections, when this occurs [29,54].

Neuraminidase inhibitor resistance can be diagnosed by plaque assays, neuraminidase inhibition assays, and neuraminidase and hemagglutinin gene sequencing [40,57-59]. Unfortunately, standard cell lines, such as MDCK, do not provide reliable or consistent assessments of antiviral potency of NAIs [59-62]. This effect is the result of a mismatch between the receptor types in human airway epithelial cells and cell culture systems, and results in reduced requirement for neuraminidase activity [42,60,61]. Cell lines that

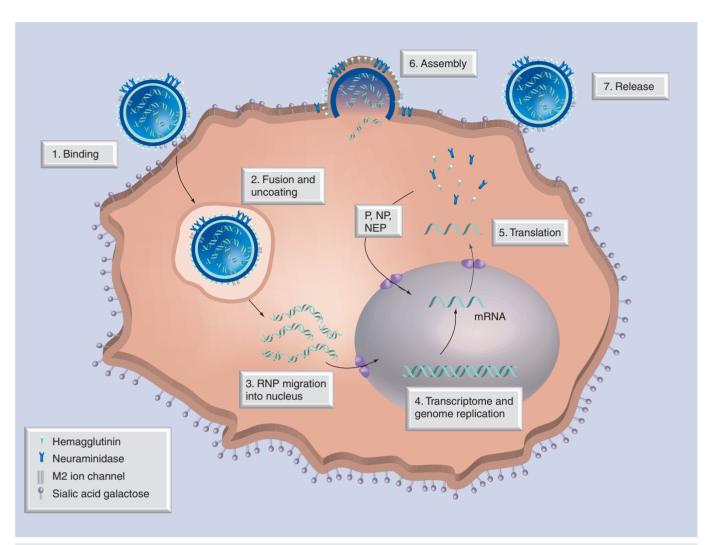


Figure 1. The influenza A virus replication cycle. The available antivirals inhibit either the M2 ion change (replication step 2) or the neuraminidase (replication step 7).

NEP: Nuclear export protein; NP: Nucleoprotein; P: Polymerase; RNP: Ribonucleoprotein. Reproduced with permission from [21].

have been stably transfected with the human 2,6-sialyltransferase gene have been developed and provide more reliable results when using cell cultures [60,61]. These lines are not widely available and are not frequently used to screen clinical isolates. The neuraminidase inhibition assay has been one of the most widely used assays for detecting resistance [63]. Despite being easy to perform, interpreting results may sometimes be challenging, and it may not detect variants with hemagglutinin mutations only [40,42,57]. The assay has been modified recently for clinical studies, since viral neuraminidase levels in samples from the nose and throat may be too low to assay using this method. This modification involves growing the virus in cell culture initially, and therefore sensitivity may be compromised by both reduced replication potential of resistant viruses as compared with wild-type virus and reduced enzymatic activity in resistant variants [42]. Genotypic analysis through sequencing is now utilized by most groups as it can be applied to primary clinical samples and detects the presence of both neuraminidase and hemagglutinin mutations [38,40,42]. Many laboratories have begun screening specifically for the H274Y mutation to allow more rapid identification of oseltamivir resistance in strains predicted to contain this strain [64,65]. Unfortunately, few of these techniques are widely available in clinical laboratories. There are systems for quickly screening for resistance in development, but none are currently commercially available.

Clinical management of influenza in the era of antiviral resistance

The management of influenza is currently complicated by circulating strains of influenza with

Executive summary

Influenza

Influenza causes 36,000 deaths and 130,000–170,000 hospitalizations annually in the USA.

Available anti-influenza agents

- Both M2 inhibitors (amantadine and rimantadine) and neuraminidase inhibitors (oseltamivir and zanamivir) are commercially available for the prevention and treatment of influenza.
- A wide range of investigational anti-influenza compounds are under development; many are neuraminidase inhibitors with novel administration, pharmacokinetics or activity against resistant variants. A sialidase (DAS-181) and a protease inhibitor (T-705) both have novel mechanisms of action and are entering advanced stages of clinical development.

M2 inhibitor resistance

- Mutations in the gene result in resistance to all drugs in the class; the S31N mutation is responsible for resistance in naturally circulating A/H3N2 strains currently.
- M2 inhibitor resistance is diagnosed by plaque assay or gene sequencing; neither is widely available clinically.

Neuraminidase inhibitor resistance

- Mutations in either the neuraminidase or the hemagglutinin gene result in resistance to the neuraminidase inhibitors; frequently resistance is subtype- and drug-specific, with most oseltamivir-resistant variants remaining susceptible to zanamivir.
- The H274Y mutation is responsible for resistance in most circulating A/H1N1 viruses.
- Neuraminidase inhibitor resistance is diagnosed by plaque assay, neuraminidase inhibition assay or sequencing; none of the assays are widely available clinically.

Clinical management of influenza in the era of antiviral resistance

Currently, clinical management of influenza depends on attempting to diagnose the subtype of virus (human A/H1, novel swine-origin A/H1, A/H3) and the recommendations of health authorities, such as the Centers for Disease Control and Prevention, who monitor the changing resistance pattern in circulating viruses.

Conclusion

- Advances in methods of diagnosing resistance in clinical isolates are required; these assays need to be easy to use so that they can be implemented at most hospitals or at the point of care.
- Studies of antivirals with novel mechanisms of action and combinations of antivirals should be carried out to assess the optimal management of influenza in the era of widespread antiviral resistance.

resistance to one of the two classes of available anti-influenza agents. Until reliable resistance testing is widely available in the clinical laboratory, management requires attempting to identify the virus, optimally to the subtype, and reliance on guidance from national reference laboratories, such as the CDC, who monitor for resistance and make treatment recommendations based on up-to-date data [2,101]. There are commercially available antigen detection kits that can differentiate between influenza A and B, in addition to commercially available and home-brew molecular methods that can provide further subtyping of the hemagglutinin of the virus present in clinical samples [2,66,67]. Identifying the virus to at least the subtype level may allow more tailored use of antivirals. Since the resistance in circulating strains is continually changing, consultation with current recommendations of health authorities is recommended [2,101,102]. This is particularly important with regard to the emerging pandemic associated with the swine-origin influenza A/H1N1. This reassorted virus has spread globally and is currently universally resistant to the M2 inhibitors [103]. A few isolates have been identified that have developed resistance to oseltamivir during the course of therapy [68,69]. As a result, management will be guided by emerging data on resistance and optimal treatment, which will be available through the CDC.

Future perspective

Influenza naturally changes over time, resulting in a high risk of emergence of antiviral resistance. Experience has proven that resistance will emerge for all anti-influenza agents and that this resistance may spread globally [11,12,39]. Likewise, resistance may emerge over a treatment course, particularly in patients with suppressed immune systems and those critically ill with novel viruses; when this does occur, morbidity and mortality may be high [29,54]. As a result, it is critical that advances are made to make antiviral resistance testing widely available in most clinical laboratories. Although dual-resistant variants have rarely been isolated, they have not yet circulated globally. If this does occur, there may be limited options for treatment unless new drugs with novel mechanisms of action are developed and approved for clinical use. Likewise, new paradigms in the management of influenza need to be considered

- particularly the use of antiviral combinations or selective rotation of antivirals [70]. The use of these combinations could improve the likelihood that therapy would be active against all circulating strains. In addition, the combination could potentially reduce the emergence of resistant mutants, as has already been demonstrated in one clinical study of combination therapy [71]. Further studies of combination therapy are clearly warranted.

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