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Naturally Occurring Antiviral Drug Resistance in Avian H5N1 Virus

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Resistance to the neuraminidase inhibitor, oseltamivir, was found in H5N1 virus isolated from infected patients in Vietnam but no recent avian H5N1 isolates have been reported to possess known neuraminidase inhibitor resistance mutations. It is still not clear whether the NA1 gene neuraminidase mutation, His274Tyr, detected in H5N1 infected human cases originated during disease treatment or came from the avian virus source. A 2002 HK chicken H5N1 isolate was found to contain the His274Tyr mutation on NA1 and resistance to oseltamivir was confirmed using a cell-based assay. To investigate if His274Tyr might naturally occur at low levels mixed with wild type in H5N1 poultry infections we examined isolates from different hosts and geographical locations using a differential RT-PCR assay. The His274Tyr quasi species was more frequently recognized in isolates from infected chickens than in isolates from ducks and geese, but no geographical difference was observed. Close surveillance of mutants in the virus population, combined with pursuit of alternative therapies, is essential to H5N1 pandemic containment strategies.

Introduction

Outbreaks caused by avian influenza H5N1 virus have been reported in poultry in nine southeast Asian countries since 2003 [1,2,3]. Increasing evidence shows H5N1 virus is endemic in poultry in this region; it may not be eradicable from avian hosts by regular control measures. The outbreak in migratory birds at Qinghai Lake in 2005 led to further expansion of the geographical distribution of H5N1 virus from Asia to Europe, the Middle-east and Africa [4,5]. Meanwhile, over 300 human infections by H5N1 virus have occurred in affected countries since 2003 [6]. There is concern that the H5N1 virus, or a derivative of it, may stand to be the next pandemic influenza virus [7]. It may still be some time before an effective vaccine, in adequate quantities, is available. This leaves protection in the face of a pandemic largely to stockpiling antiviral drugs, particularly those for influenza pandemic preparedness, particularly with regard to choice of suitable pharmaceutical agents for stockpiling, and emphasizes the need for alternative therapies, including novel drugs and an effective vaccine.

Materials and Methods

Sequence analysis. Sequences of H5N1 viruses sampled from 1997 onwards were selected from our collection and public databases. Sequence data were aligned with and residue analysis performed using BioEdit (Version 7) [15]. Residues Glu 119, Arg 292, His 274 and Arg 152 of the NA were selected to screen for predicted oseltamivir resistant mutants.

Detection of H274Y mutant with specific PCR. The His274Tyr mutation on subtype 1 neuraminidase (N1) is caused by a C to T substitution at nucleotide position 763. Differential PCR was performed with two forward primers, primer C (5’ GAATGGATGCTCCATATTAC 3’) and primer T (5’ GAATGGATGCTCCATATTAT 3’) that differ by one nucleotide at the 3’ end, and a single reverse primer (5’ AGAGGCACCGGACCAACTAC 3’). The primer pairs were tested with His 274 and Tyr 274 reference templates to optimize conditions for primer specificity in mixtures of the two templates (95°C 10 min, 1 cycle; 95°C 1 min, 62°C 1 min, 72°C 1 min, 35 cycles; 72°C 10 min, 1 cycle; Fig. 1). RNA extraction and cDNA synthesis from virus samples were performed as described previously [2].

Inhibition of H51 virus infection in MDCK cell culture. Virus stocks were propagated in embryonated chicken eggs and TCID₅₀ in MDCK cells was determined. Oseltamivir carboxylate (Roche) was tested at concentrations of 0.1 nM to 100 uM in a cell-based virus reduction assay, modified from that of Yen and co-workers [11]. Briefly, triplicate MDCK monolayer cultures in 96-well format were infected with 100 TCID₅₀ virus doses (1 hour, 37°C, 5% CO₂), then the inoculum removed and cell layers washed with culture media (MEM, Gibco BRL). Two hundred microlitres of culture media containing the appropriate dilution of oseltamivir was added to wells, and cultures incubated for 3 days (37°C, 5% CO₂). The HA titers of individual well supernatants were tested in duplicate.

Quantification of wild type (C type) and mutant (T type) NA gene by quantitative PCR. Quantitative PCR (qPCR) reactions were performed with a Roche Lightcycler system (Roche) using a Lightcycler Faststart DNA Master SYBR Green I kit (Roche) according to the manufacturer’s instructions. For better discrimination between the wild type and mutant NA genes, Locked Nucleic Acid (LNA) primers (Proligo) were used. Wild type and mutant NA genes were cloned into the TOPO PCR 2.1 vector (Invitrogen), sequenced and used as standards for quantification. Mutant and wild type NA gene copy number were calculated with Lightcycler software using the wild type and mutant plasmids as a standard. PCR specificity was checked by melting curve analysis and gel electrophoresis.
Results

Detection of an oseltamivir resistant H5N1 isolate. To date, four neuraminidase residue changes associated with resistance to oseltamivir have been characterized; Glu119Val, Arg292Lys, His274Tyr and Arg152Lys. These appear to be NA subtype specific; Arg292Lys and Glu119Val to N2 and His274Tyr to N1 [16-18]. Published sequences of avian H5N1 virus isolates do not indicate the presence of resistance-associated mutations and the isolates tested are sensitive to oseltamivir inhibition both in vitro and in vivo [10,11]. However, the isolation of oseltamivir-resistant H5N1 viruses from humans in Vietnam indicates that oseltamivir resistance could be an emerging problem [13,14]. As oseltamivir is so important to pandemic preparedness, we wished to investigate if resistant mutant H5N1 viruses might be present in other species and areas in Asia, with a view to determining the potential of a naturally-resistant pandemic strain arising in the future. Available sequences of H5N1 viruses isolated since 1997 were examined. One isolate, A/chicken/Hong Kong/3123.1/02, was found to bear the His274Tyr mutation which conveys resistance to neuraminidase inhibitor drugs in N1 subtype viruses [16-18]. Drug sensitivity tests revealed that this isolate possessed a high degree of resistance to oseltamivir inhibition, with an EC50 of 124.9uM. In comparison, the A/chicken/Vietnam/37/04 isolate, containing the wild type residue at position 274, has an EC50 of 0.4uM oseltamivir.

Quantitative PCR was applied to quantify the relative abundance of His274Tyr mutant and the wild type in virus stocks. In essentially all isolates containing mixed species of wild type and mutant, the mutant represented less than 1% of the virus population, and in many cases less than 0.1% (data not shown).

Discussion

Preparedness for a potential H5N1 influenza pandemic caused by currently-circulating H5N1 viruses has been recommended by the WHO. One well-publicized focus is the stockpiling of antiviral drugs, particularly inhibitors of viral neuraminidase. One
such neuraminidase-inhibitor, oseltamivir, has been considered as one of the few options available for the containment of human-to-human transmission. This study demonstrates that oseltamivir resistant strains bearing the His274Tyr mutation are present in some H5N1 virus populations, albeit at low levels, in the absence of evidence of exposure to the drug. Oseltamivir is not known to have been introduced into the Hong Kong market prior to 2002, but we have detected His274Tyr mutants in virus populations isolated as early as 2000, which suggests that this mutant occurs naturally. Previous studies have shown that oseltamivir-resistant mutants have a growth and virulence disadvantage [19-22]. Given the continuous circulation of H5N1 viruses in poultry and wild birds in the southeast Asia region, there is a chance that His274Tyr mutants could gain the ability to increase in abundance if they obtain other adaptive changes. Even if variant viruses do not become dominant in mixed populations, they may still hamper clinical treatment with oseltamivir by increasing the overall resistance of the population. Isolation of one resistant mutant strain, A/chicken/Hong Kong/3123.1/02, from an infected chicken suggests the possibility that such mutants may possess the potential to become the main population, at least in chickens. Major H5N1 outbreaks in poultry in 1997 and 2001-2002 in Hong Kong were controlled in a timely manner and this might have stopped further expansion of such mutants [23,24]. Antiviral drugs, if appropriately applied and tightly controlled, remain important components of pandemic preparedness. However, the presence of drug-resistant mutants in the pool of potential pandemic H5N1 strains provides additional “options” for the predicted pandemic strain, especially with regard to oseltamivir-resistance. In anticipation of this possible scenario, further control options must be implemented, including stockpiling a wider range of drugs (zanamivir in particular), development of alternative pharmaceuticals, emphasis on vaccine development and, most importantly, increased surveillance for the presence of His274Tyr mutants mixed with wild type strains among new H5N1 isolates.

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References