1. INTRODUCTION

1.1 Introduction

Influenza viruses are spherically or longitudinally shaped enveloped particles with an up to eight-fold segmented, single-stranded RNA genome of negative polarity. Influenza viruses belong to in the *Orthomyxoviridae* family and are classified into types A, B or C based on antigenic differences of their nucleo- and matrix proteins. Avian influenza viruses (AIV) belong to type A. Excellent reviews on the structure and replication strategy of influenza viruses have been published recently (Sidoronko and Reichl, 2004).

The main antigenic determinants of influenza A virus are the haemagglutinin (H or HA) and the neuraminidase (N or NA) transmembrane glycoproteins, capable of eliciting subtype-specific and immune responses and protection.

On the basis of the antigenicity of these glycoprotein, influenza A viruses currently cluster into sixteen H (H1 - H16) and nine N (N1 - N9) subtypes. These clusters are substantiated when phylogenetically analysing the nucleotide and deduced amino acid sequences of the HA and NA genes, respectively (Fouchier, 2005).

The conventional nomenclature for influenza virus isolates requires implication of the influenza virus type, the host species (omitted in the case of human origin), the geographical site, serial number, and year of isolation.

1.2 Objectives of the study

1. To compare analytical sensitivity of three diagnostic methods for avian influenza virus isolation and / or detection

2. To compare the effect of re-isolation and detection on the sensitivity

3. To determine the minimum detectable of virus concentration of the assay

1.3 Significance of the study

1. Provide the scientific evidence of the validity of test result in a laboratory

2. Provide the estimate of the laboratory efficiency in detecting AI

3. Provide information necessary for the ISO 17025 application