MOLECULAR EPIDEMIOLOGY OF CLASSICAL SWINE FEVER IN ITALY: A RETROSPECTIVE ANALYSIS

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INTRODUCTION

Historically in Italy, Classical swine fever (CSF) was observed in the first half of the 19th century, however little is known about its origin as well as the epidemiological situation. In the 1960s and 1970s a big epidemic of CSF occurred in Italy causing hundred of outbreaks and severe economic losses. Although the incidence of the disease was afterwards much reduced, CSF was successfully eradicated only in 2003. To extent the relatedness between Italian isolates, CSFV isolates collected from wild and domestic pigs over a 40-year period (1960-2000) were analysed.

RESULTS AND DISCUSSION

Our results showed that the isolates analysed belonged to subtypes 1.1 (n=15), 1.2 (n=1), 2.1 (n=4), 2.2 (n=21) and 2.3 (n=25 ). In particular, in the north of the country, viruses of subtype 2.2 have persisted in wild boar, causing sporadic outbreaks in domestic pig. In contrast, viruses of subtypes 2.1 and 2.3 appeared only intermittently in different regions of the mainland. CSFV isolates belonging to the subtype 2.1 are genetically and epidemiologically related to the Dutch isolate in Venhorst originating from the large epizootic in 1997. Since 1970, isolations of genotype 1 viruses have been extremely infrequent in Europe. Interestingly, all the viruses isolated from 1977 to 1980 in mainland Italy and in Sardinia in 1997, belonged to the subtype 1.1, indicating that type 1 viruses were still circulating at that period. In conclusions our results showed that in Italy occurred several independent epidemiological events.

MATERIALS AND METHODS

A total of 23 historical isolates were included in this study, 43 additional sequences of other representative isolates were acquired from the GenBank. A 190 base fragment of the E2 envelope glycoprotein was sequenced and used for genetic analysis. Bands of correct sizes were purified and used as templates in sequencing reactions. Precipitated products were run on an ABI PRISM 3130 Genetic Analyzer (Applied Biosystems). Both the sense and antisense strands were sequenced performing three independent reactions for each isolate. Sequences data were analyzed using the program SeqMan II from the DNASTAR package and subsequently with Clustal X version 2.00, in respect of the amino acidic coding frame. The phylogenetic tree was inferred using the PhyML v.2.4.4., used the Maximum Likelihood (ML) method.

Phylogenetic tree constructed using E2 region of 66 CSFV Italian isolates and reference strains retrieved from the GenBank database. Bar: number of substitutions per site.

Spatial and temporal distribution of CSFV subgroups in Italy.