



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

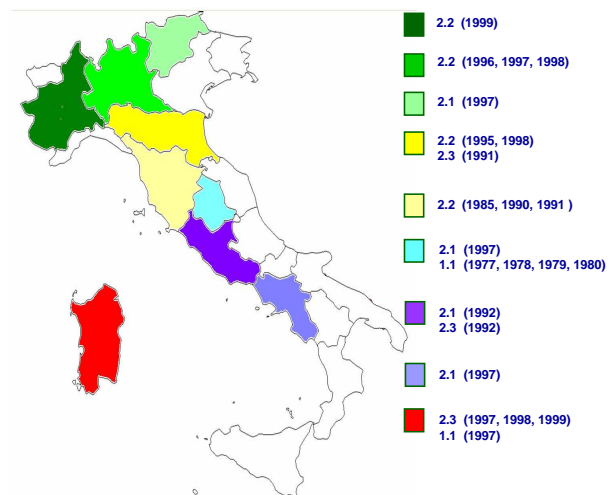
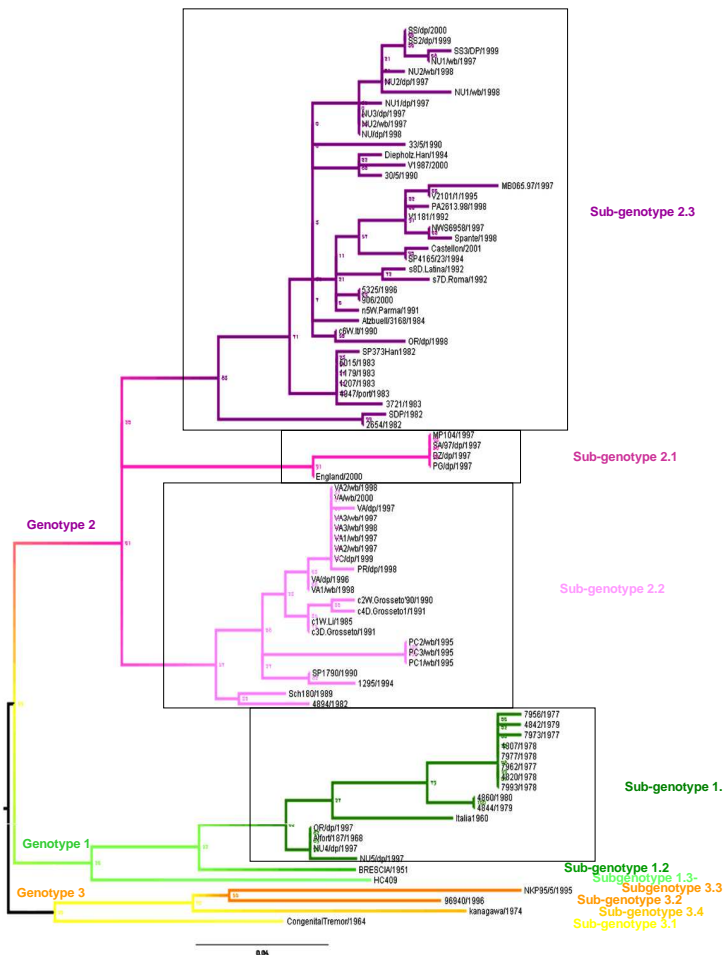
Our results showed that the isolates analysed belonged to subtypes 1.1 (n=15), 1.2 (n=1), 2.1 (n=4), 2.2 (n=21) and 2.3 (n=25). In particular, in the north of the country, viruses of subtype 2.2 have persisted in wild boar, causing sporadic outbreaks in domestic pig. In contrast, viruses of subtypes 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.

Name	Year	Species	Sub-genotype	Intra-group similarity (%)	Acc. Numbers
NU1/97/wb	1997	wb	2.3	86.10-100	AJ312854
SS3/99/dp	1999	dp			AJ312860
SS/00/dp	2000	dp			AJ312873
SS2/99/dp	1999	dp			AJ312883
NU2/97/dp	1997	dp			AJ312886
NU1/98/wb	1998	wb			AJ312853
NU2/98/wb	1998	wb			AJ312858
NU3/97/dp	1997	dp			AJ312856
NU/98/dp	1998	dp			AJ312855
NU2/97/wb	1997	dp			AJ312875
NU1/97/dp	1997	dp			AJ312884
69W/8	1990	wb			L36168
OR/98/dp	1998	dp			AJ312857
n5W Parma91	1991	wb			L36169
s7D.Roma92	1992	dp			L36170
S8D.Latina92	1992	dp	L36172		
3721/83	1983	dp	n.d.		
484/79/dp/83	1983	dp	n.d.		
1178/83	1983	dp	n.d.		
501/5/83	1983	dp	n.d.		
120/7/83	1983	dp	n.d.		
265/4/82	1982	dp	n.d.		
SDP/82	1982	dp	n.d.		
489/4/82	1982	dp	n.d.		
PC1/95/wb	1995	wb	2.2	81.60-100	AJ312865
PC2/95/wb	1995	wb			AJ312872
PC3/95/wb	1995	wb			AJ312874
CZW.Grossato90	1990	wb			L36165
C4D.Grossato191	1991	dp			L36167
C1W.LI/85	1991	dp			L36164
C3D.Grossato90	1990	wb			L36166
VA1/96/dp	1996	dp			AJ312869
VA1/98/wb	1998	wb			AJ312861
PR/98/dp	1998	dp			AJ312876
VA2/97/wb	1997	wb			AJ312863
VA2/98/wb	1998	wb			AJ312866
VA3/97/wb	1997	wb			AJ312867
VA/00/wb	2000	wb			AJ312871
VA1/97/wb	1997	wb			AJ312868
VA3/98/wb	1998	wb	AJ312856		
VA/97/dp	1997	dp	AJ312862		
VC/99/dp	1999	dp	AJ312870		
s7D2.Roma92	1992	dp	L36171		
SA/97/dp	1997	dp	AJ312882		
PG/97/dp	1997	dp	AJ312878		
BZ/97/dp	1997	dp	AJ312860		
BRESCIA	1951	dp	AF091661		
NU5/97/dp	1997	dp	AJ312877		
NU4/97/dp	1997	dp	AJ312859		
CR/97/dp	1997	dp	AJ312864		
Italia/60	1960	dp	AJ312879		
Alfort 187	1968	dp	CSF0902		
486/80	1980	dp	n.d.		
484/79	1979	dp	n.d.		
480/78	1978	dp	n.d.		
797/77	1977	dp	n.d.		
796/77	1977	dp	n.d.		
793/78	1978	dp	n.d.		
797/77	1977	dp	n.d.		
482/78	1978	dp	n.d.		
795/77	1977	dp	n.d.		
484/79	1979	dp	n.d.		

CSFV genotypes circulating in Italy from 1960 to 2000



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