Sapovirus and Aichi virus associated to imported shellfish from developing countries

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Introduction

The risk of infection by foodborne diseases has increased due to the international trade of food products, including shellfish. Bivalve molluscs naturally concentrate pathogens while filtering, becoming a vector for viral gastroenteritis. In recent years, novel enteric viruses have emerged associated with the human consumption of these foods. The aim of the present study was the detection, quantification and genetic characterization of sapovirus and Aichi virus from shellfish samples imported into Spain.

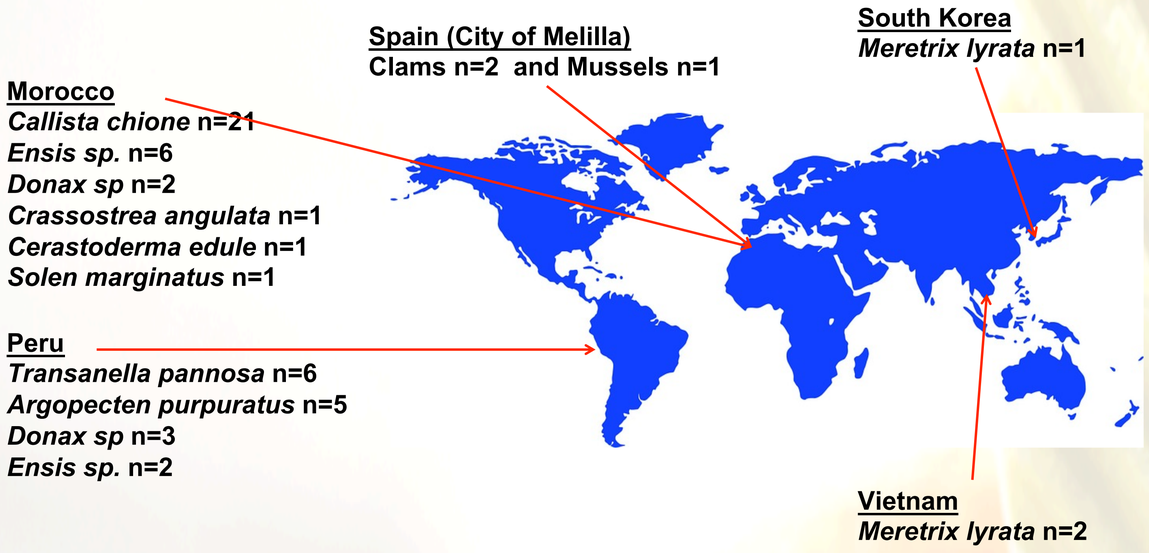

Figure 1. Geaographic origin of the imported samples.

Results

Sapovirus was detected in 29 samples (53.7%): 12 from Morocco (22%), 11 from Peru (20%) , 2 from Vietnam (4%), 1 from South Korea (2%) anod 3 (6%) from Melilla (Table 1); whereas Aichi virus was detected in 18 samples (33.3%): 12 from Morocco (22%), 3 from Peru (6%), 1 from Vietnam (2%), 1 from South Korea (2%) and 1 (2%) from Melilla (Table 2). Of these samples, 10 were positive for the two studied viruses. Genotyping for sapovirus shown 10 strains clustering as genotype GI.2 and 2 as GI.1, while 5 Aichi virus characterized strains clustered as genotype A and 1 as genotype B (Figure 2).

Table 1. Detection and quantification levels of SaV.

SaV	DETECTION							QUANTIFICATION cRNA/g DT	
	TOTAL	Clams	Oysters	Mussels	Scallops	Cockles	Razor clams	Average	Range
TOTAL	53.7 %	43.2 %	100 %	100 %	100 %	100 %	55.6 %	1.2×10^5	$1.4\times10^3 – 9.9\times10^6$
Morocco	22 %	21.7 %	100 %			100 %	71.4 %	6.0×10^4	1.4×10^3 - 9.9×10^6
Peru	20%	66.7 %			100 %		0 %	2.3×10^5	$1.3\times10^4 – 3.2\times10^6$
Vietnam	4 %	100 %						4.8×10^4	$1.8\times10^4 – 1.3\times10^5$
S. Korea	2 %	100 %						-	-
Melilla	6 %	100 %		100 %				2.5×10^5	$2.5\times10^4 – 1.7\times10^6$

Methods

The study included 54 shellfish samples imported with commercial purposes into Spain between September 2006 and January 2011 from Morocco, Peru, Vietnam, South Korea and from a street commerce in Melilla (Africa) (Figure 1). Species studied were clams (*Callista chione, Transanella pannosa*, and *Donax sp.*), oysters (*Crassostrea angulata*), scallop (*Pecten maximus*), cockles (*Cerastoderma edule*), and razor clams (*Solen marginatus* and *Ensis sp.*). Techniques employed were RT-qPCR for detection and quantification, and RT-nested PCR for posterior Sanger sequencing.

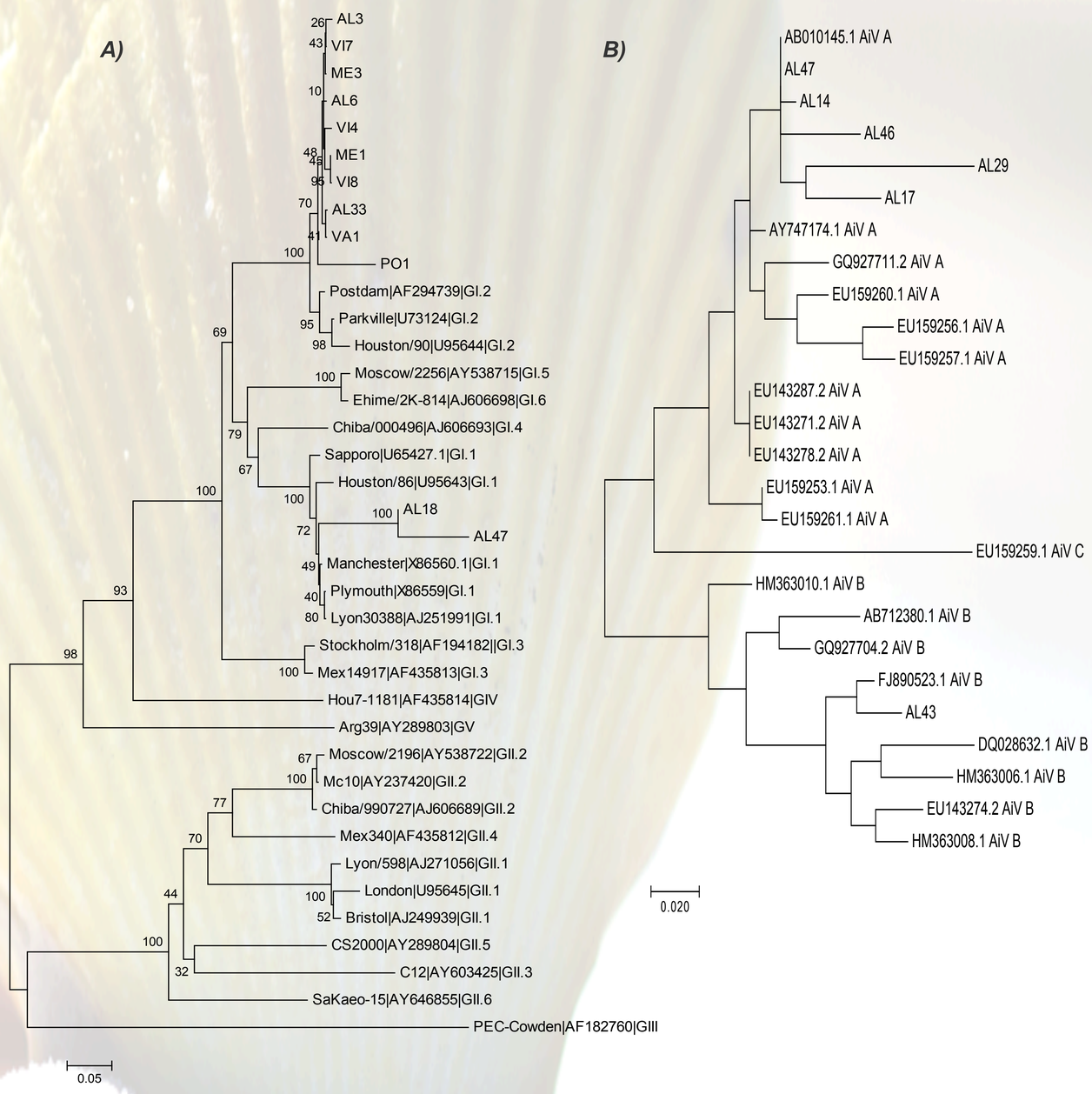

Figure 2. Phylogenetic trees of *A)* the partial capsid gene of SaV ;*B)* VP1 region of AiV samples, by neighbor-joining analysis using MEGA 6.

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Table 2. Detection and quantification levels of AiV.

AiV	DETECTION							QUANTIFICATION cRNA/g DT	
	TOTAL	Clams	Oysters	Mussels	Scallops	Cockles	Razor clams	Average	Range
TOTAL	33.3 %	35.1 %	0 %	0 %	0 %	100 %	44.4 %	2.4×10^4	$4.9\times10^2 – 3.6\times10^6$
Morocco	22 %	34.8 %	0 %			100 %	42.9 %	3.9×10^4	1.6×10^3 - 3.6×10^6
Peru	6 %	22.2 %			0 %		50.0 %	2.8×10^4	1.5×10^4 - 5.9×10^4
Vietnam	2 %	50.0 %						-	-
S. Korea	2 %	100 %						-	-
Melilla	2 %	50.0 %		0 %				-	-

Conclusions

The lack of routine viral analysis in bivalve molluscs and the global trade of these food products open new bias for enteric pathogens and could be a route of viral foodborne outbreaks with important implications in human health.