

# **Epidemiologic and virologic characteristics of chronic hepatitis C across Europe: Results from EuroSIDA**

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for the EuroSIDA study group.

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# Objectives

- It is unknown which factors determine the rate of spontaneous clearance of hepatitis C virus (HCV) infection in HIV individuals.
- Moreover, the variables influencing serum HCV-RNA levels and HCV genotype distribution are not well defined in this population.

# Patients & Methods

- HCV antibody positive (HCVA<sup>b+</sup>)
- Stored serum samples in the EuroSIDA sample repository
- Serum HCV-RNA testing by a reliable quantitative assay for distinct genotypes (Versant)
- HCV genotyping (LiPA) carried out in viremic subjects

# Statistical Methods

- Logistic regression was used to identify
  - variables associated with spontaneous HCV clearance
  - Variables associated with HCV genotype 1 (HCV-1) infection

Adjusting for demographic, clinical and therapeutic factors.

# Recruitment in EuroSIDA

- Pre-defined number from each clinic for each cohort
- Pre-booked, routine outpatient appointment
- Aged over 16
- Cohorts I-III, CD4 < 500/mm<sup>3</sup> in 4 months before enrollment

# EuroSIDA (n = 14,282)

**Cohort I**  
May 1994, N=3116

**Cohort II**  
January 1996, N=1365

**Cohort III**  
April 1997, N=2841

**Cohort IV**  
April 1999, N=1225

**Cohort V**  
November 2001, N=1223

**Cohort VI**  
November 2003, N=2121

**Cohort VII**  
January 2006, N=2391

# Data collected in EuroSIDA

- Demographic data
- CD4 and viral loads
- Other markers
- HCV/HBV status
- Disease specific prophylaxis
- Antiretrovirals (start/stop dates)
- All AIDS defining illnesses
- Other severe opportunistic illnesses
- Non-AIDS malignancies
- Serious adverse events

# Main characteristics of 2,263 HIV patients with positive HCV antibody in EuroSIDA.

	Total n = 2263	Positive serum HCV-RNA n = 1677 (74.1%)	Negative serum HCV-RNA n = 586 (25.9%)	p
<b>Gender:</b> Male	1577 (69.7%)	1173 (74.4%)	404 (25.6%)	0.88
<b>Median age (years)</b>	37.1	37.1	37.4	0.0025
<b>Risk group:</b> IDU	1586 (70.1%)	1233 (77.7%)	353 (22.3%)	<0.0001
<b>Ethnicity:</b> White	2027 (89.6%)	1504 (74.2%)	523 (25.8%)	0.10
<b>Region:</b> South/Argentina	773 (34.2%)	603 (78.0%)	170 (22.0%)	<0.0001
Central	511 (22.6%)	368 (72.0%)	143 (28.0%)	
North	442 (19.5%)	301 (68.1%)	141 (31.9%)	
East	537 (23.7%)	405 (75.4%)	132 (24.6%)	
<b>Serum HBsAg:</b> positive	197 (8.7%)	107 (54.4%)	90 (45.6%)	<0.0001
negative	1687 (74.5%)	1263 (74.9%)	424 (25.1%)	
unknown	379 (16.7%)	307 (81.0%)	72 (19.0%)	
<b>Antiretroviral therapy:</b> yes	1915 (84.6%)	1399 (73.1%)	516 (26.9%)	0.007
no	348 (15.4%)	278 (79.9%)	70 (20.1%)	
<b>Prior interferon therapy</b>	115 (5.1%)	69 (60.0%)	46 (40.0%)	0.0048

# Results

- Of 2263 HCVAb+ patients, 1677 (74%) were serum HCV-RNA+ (95% CI: 71-78%).

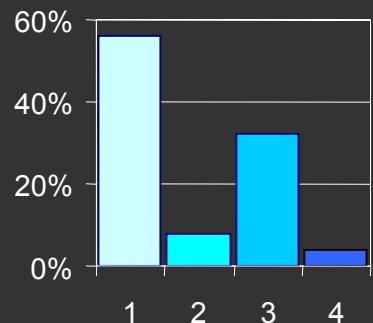
# Variables associated with spontaneous HCV clearance

Variables	Univariate		Multivariate	
	aOD (95% CI)	p	aOD (95% CI)	p
<b>Female gender (vs male)</b>	1.05 (0.86-1.29)	0.65	1.22 (0.99-1.51)	0.069
<b>Older age (per 10 years)</b>	1.24 (1.12-1.39)	<0.0001	1.10 (0.97-1.25)	0.14
<b>Exposure group</b>				
MSM	1.00	-	1.00	-
IDU	0.36 (0.27-0.47)	<0.0001	<b>0.43</b> (0.32-0.58)	<b>&lt;0.0001</b>
Heterosexual	0.55 (0.39-0.79)	0.0012	0.59 (0.40-0.87)	0.0082
Other	0.43 (0.28-0.66)	0.0002	0.47 (0.30-0.73)	0.0007
<b>Serum HBsAg+ status</b>				
Negative	1.00	-	1.00	-
Positive	2.51 (1.85-3.39)	<0.0001	<b>2.48</b> (1.82-3.38)	<b>&lt;0.0001</b>
Unknown	0.70 (1.53-0.92)	0.012	0.62 (0.47-0.83)	0.0014
<b>Region of Europe</b>				
South/Argentina	1.00	-	1.00	-
Central	1.38 (1.07-1.78)	0.015	1.49 (1.13-1.98)	0.0052
North	1.66 (1.28-2.16)	0.0002	1.38 (1.05-1.82)	0.019
East	1.16 (0.89-1.50)	0.27	2.10 (1.50-2.92)	<0.0001

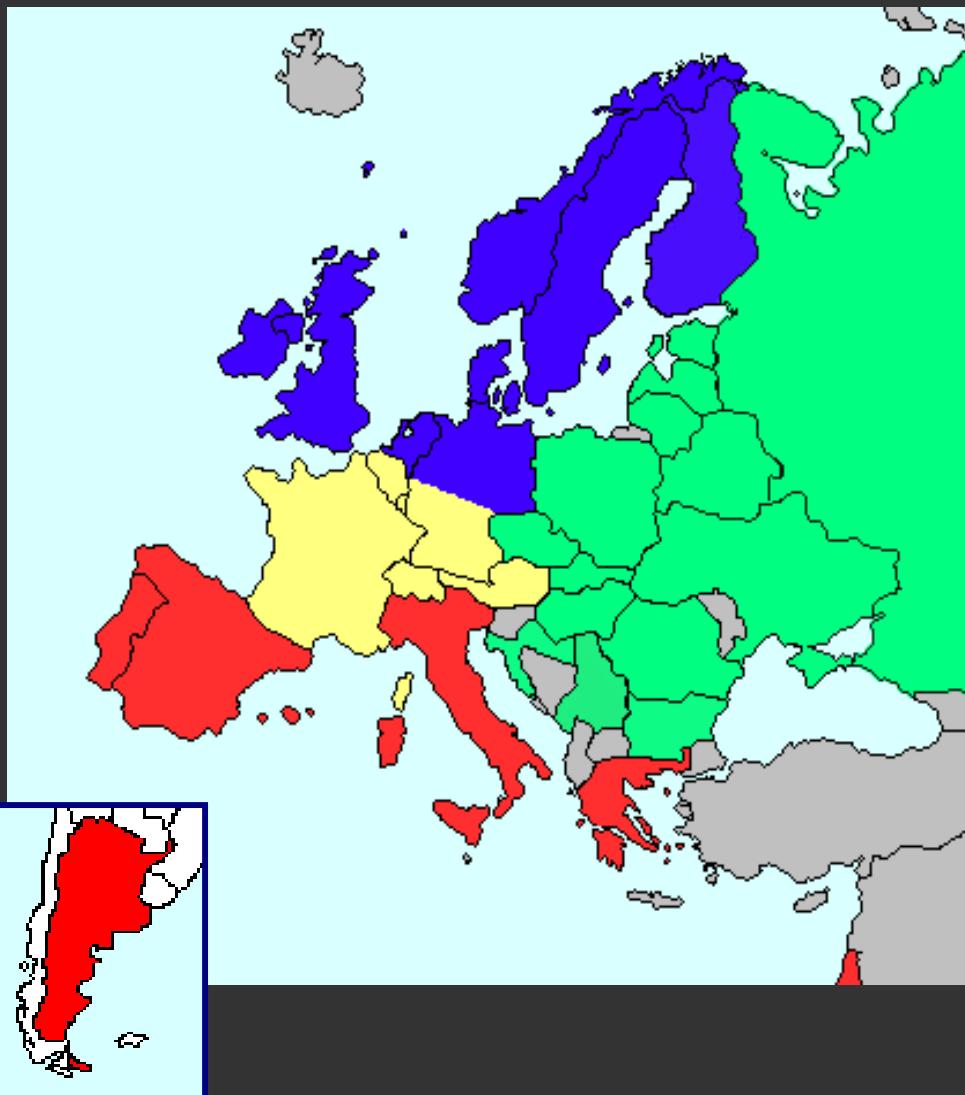
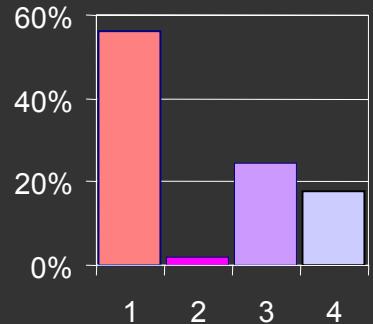
Model additionally adjusted for data source, ethnic origin, exposure group, serum HBsAg serostatus, date of HCV genotyping, date recruited to EuroSIDA, and CD4 count at date of HCV testing.

# Distribution of HCV genotypes by regions

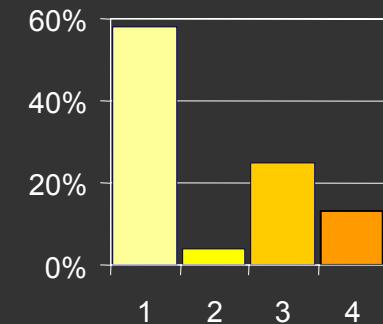
north



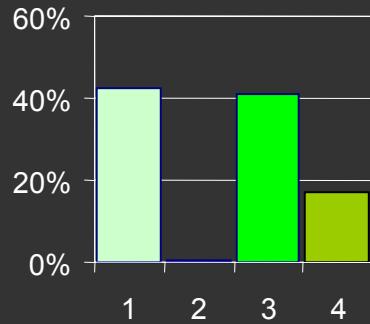
south



central



east



# Variables associated with HCV genotype 1 infection

Variables	Univariate		Multivariate	
	aOD (95% CI)	p	aOD (95% CI)	P
Female gender (vs male)	0.81 (0.66-1.00)	0.049	0.72 (0.56-0.92)	0.0082
Older age (per 10 years)	1.00 (0.89-1.12)	0.99	0.78 (0.67-0.92)	0.0035
Region of Europe				
South/Argentina	1.00		1.00	
Central	1.07 (0.82-1.39)	0.61	0.89 (0.65-1.23)	0.49
North	0.97 (0.74-1.28)	0.83	0.88 (0.63-1.22)	0.45
East	0.57 (0.44-0.73)	<0.0001	<b>0.38</b> (0.26-0.56)	<b>&lt;0.0001</b>
Higher HCV-RNA (per 1 log higher)	1.27 (1.13-1.44)	<0.0001	<b>1.29</b> (1.14-1.47)	<b>&lt;0.0001</b>
Prior AIDS (yes vs no)	1.23 (0.99-1.54)	0.067	1.35 (1.03-1.76)	0.015

Model additionally adjusted for data source, ethnic origin, exposure group, serum HBsAg serostatus, date of HCV genotyping, date recruited to EuroSIDA, and CD4 count at date of HCV testing.

# HCV load by genotypes

- Median serum HCV-RNA (IU/mL):

• G1	n=890 (53.1%)	758,578	p <0.0001
• G2	n=51 (3%)	691,831	
• G3	n=500 (29.8%)	398,107	
• G4	n=236 (14.1%)	436,516	

# Conclusion

- Nearly three quarters of HIV+/HCVAb+ patients in EuroSIDA show active HCV replication.
- HCV viremia is more frequent in IDUs and conversely less common in the presence of chronic hepatitis B.
- Up to 53% of HCV viremic patients are infected by HCV-1; and this genotype is associated with higher serum HCV-RNA levels and male gender, whereas it is less prevalent in Eastern Europe.

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