

OC 9

EVOLUTION AND DETERMINANTS OF THE PREVALENCE OF HCV INFECTION AND HCV GENOTYPE DISTRIBUTION AMONG HIV-INFECTED PATIENTS ENTERING IN CARE BETWEEN 1997 AND 2015 IN ITALY: DATA FROM A PROSPECTIVE NATIONWIDE COHORT (ICONA)

B. ROSSETTI^{1,2}, F. BAI³, A. TAVELLI⁴, M. GALLI⁵, A. ANTINORI⁶, F. CASTELLI⁷, G. PELLIZZER⁸, A. COZZI LEPRI⁹, S. BONORA¹⁰, A. D'ARMINIO MONFORTE³, M. PUOTI¹¹, A. DE LUCA^{1,12} FOR ICONA FOUNDATION STUDY GROUP

¹UNIVERSITY INFECTIOUS DISEASES UNIT, AOU SENESE, SIENA, ITALY, ²CATHOLIC UNIVERSITY OF SACRED HEART, ROME, ITALY, ³SAN PAOLO HOSPITAL, UNIVERSITY OF MILAN, ITALY, ⁴ICONA FOUNDATION, ⁵UNIVERSITY OF MILAN, MILAN, ITALY, ⁶INMI SPALLANZANI, ROME, ITALY, ⁷UNIVERSITY OF BRESCIA, BRESCIA, ITALY, ⁸INFECTIOUS DISEASES, HOSPITAL OF VICENZA, VICENZA, ITALY, ⁹UNIVERSITY COLLEGE OF LONDON, LONDON, UNITED KINGDOM, ¹⁰CLINIC OF INFECTIOUS DISEASES, UNIVERSITY OF TURIN, TURIN, ITALY, ¹¹INFECTIOUS DISEASES, MAGGIORE HOSPITAL, MILAN, ITALY, ¹²DEPARTMENT OF BIOTECHNOLOGIES, UNIVERSITY OF SIENA, SIENA, ITALY

Disclosure

I declare that I received personal fees from Abbvie, Janssen, MSD, ViiV Healthcare, Gilead

Prevalence and burden of HCV co-infection in people living with HIV

- ✓ HCV infection is a major cause of morbidity and mortality in PLWHA

Grint, D. AIDS. 2015 Jun 19;29(10):1205-15

WHO. Hepatitis C. 2016 Mar

- ✓ Worldwide 2 278 400 HIV/HCV co-infections (IQR 1 271 300-4 417 000)
- ✓ Odds of HCV infection are six times higher in PLWHA (5.8, 95% CI 4.5–7.4)
- ✓ Prevalence of HIV/HCV co-infection is 2.4% (IQR 0.8–5.8)
 - 4.0% (1.2–8.4) within pregnant or heterosexually exposed
 - 6.4% (3.2–10.0) in MSM
 - 82.4% (55.2–88.5) in PWID

L. Platt. Lancet Infect Dis. 2016 Feb 24. pii: S1473-3099(15)00485-5

- ✓ HCV prevalence and genotype distribution among PLWHA in Italy are not known

HCV treatment in DAAs era



- ✓ Direct antiviral agents (DAAs) have increased the effectiveness and tolerability of anti-HCV treatments

J McGinnis, EASL 2016. Abs LBP514

K Neukam, EASL 2016. Abs LBP513

- ✓ The efficacy of IFN-free regimens is strongly influenced by viral genotype

WHO, 2016

- ✓ Research is needed to individualize the best care for coinfecting patients

Objectives

- ✓ To analyze variation of HCV prevalence and HCV genotype distribution among persons living with HIV over the time
- ✓ To investigate their determinants
- ✓ To evaluate HCV-Ab positivity and HBsAg-/HBcAb+ status in HCV-Ab+ according to risk factor

Methods

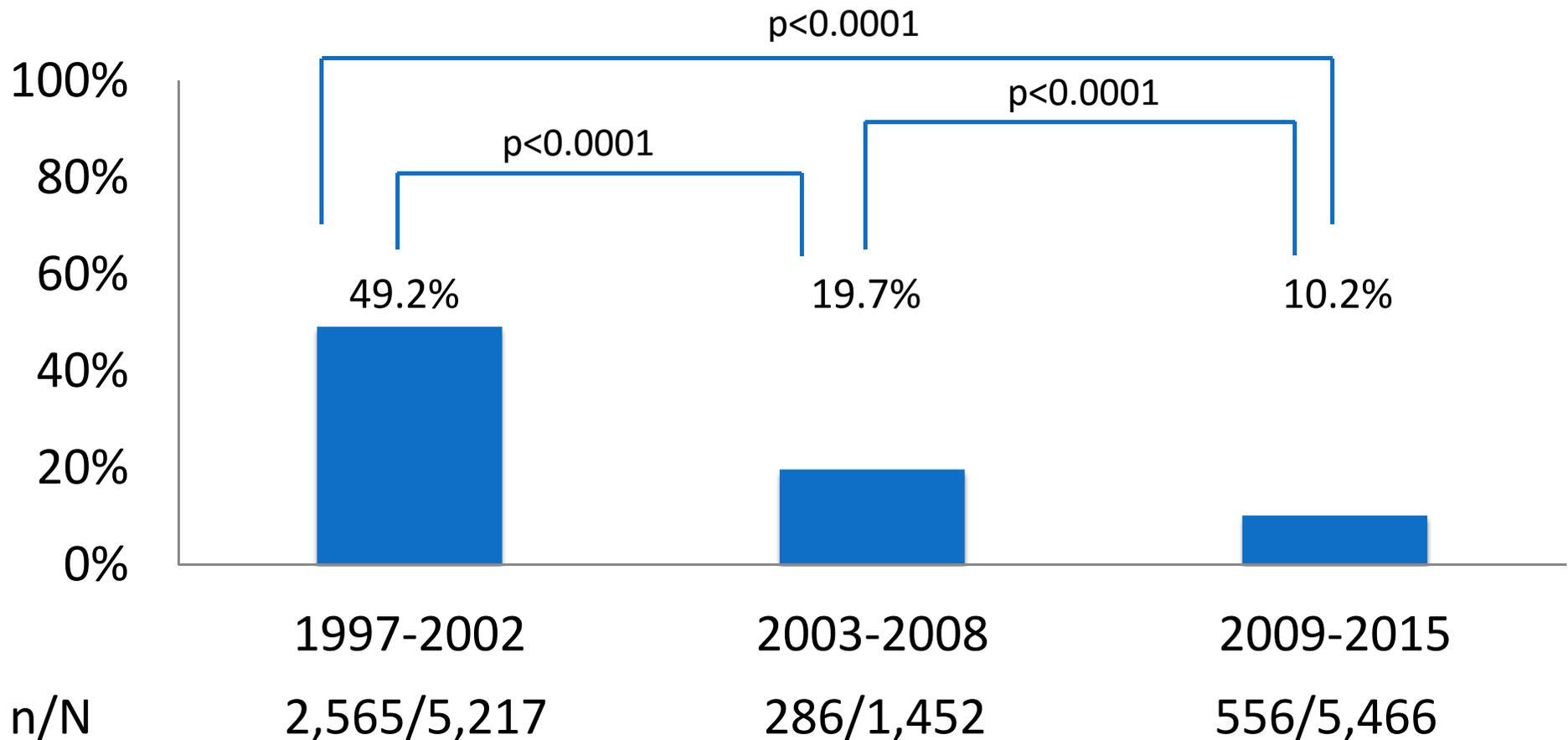
- ✓ HIV-1-infected ART-naïve patients tested for HCV-antibody enrolled from Icona cohort from 1997 to 2015
- ✓ HCV-Ab and HCV genotype prevalence were evaluated over calendar period of enrollment
- ✓ Different distribution of HCV-Ab positivity and HCV genotype and HBsAg-/HBcAb+ status in HCV-Ab+ according to risk factor were evaluated by χ -square test
- ✓ Correlates of HCV-Ab prevalence and HCV genotype distribution were tested by univariable and multivariable logistic regression

Baseline characteristics (N=12,135)

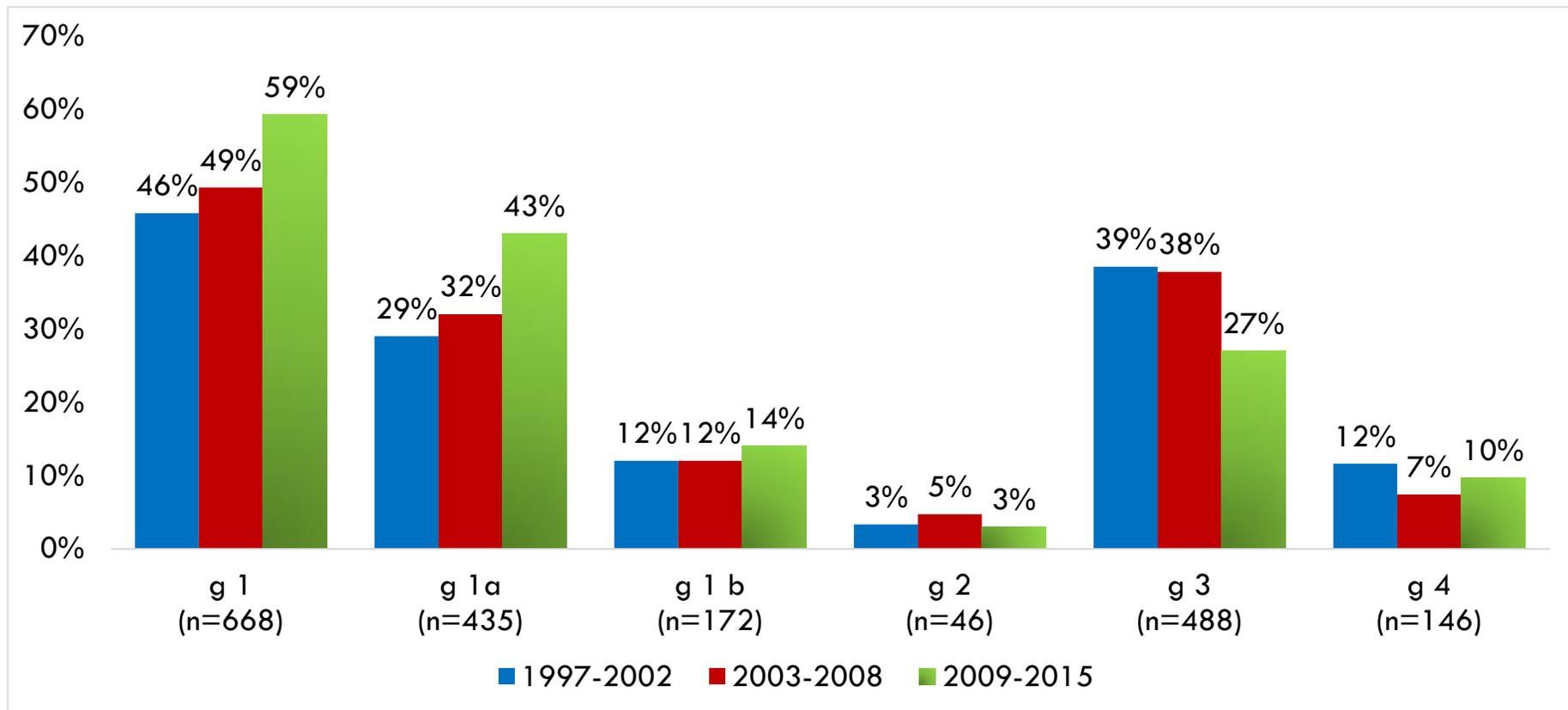
	Overall (n=12,135)	HCV Ab + (n=3,407)	HCV Ab - (n=8,728)	p
Female gender, n (%)	3,001 (24.7%)	871 (24.6%)	2,130 (24.4%)	0.184
Age, years (median, IQR)	36 (31-43)	36 (32-40)	36 (30-45)	0.012
Years from HIV diagnosis to enrollment* (median, IQR)	1 (0-4)	5 (1-11)	0 (0-1)	0.0001
Risk factor, n (%)				
IDU	2,748 (22.6%)	2,502 (73.4%)	246 (2.8%)	
MSM	4,075 (33.6%)	309 (9.1%)	3,766 (43.1%)	0.0001
Heterosexual	4,564 (37.6%)	494 (14.5%)	4,070 (46.6%)	
Other/unknown	748 (6.2%)	102 (3%)	646 (7.4%)	
AIDS, n (%)	1,841 (15%)	586 (17%)	1,255 (14%)	0.0001
Country region, n (%)				
North	6,516 (53.7%)	1,860 (54.6%)	4,656 (53.3%)	
Centre	3,876 (31.9%)	901 (26.4%)	2,975 (34.1%)	0.0001
South and Islands	1,743 (14.4%)	646 (19%)	1,097 (12.6%)	
Italian, n (%)	10,375 (84.1%)	3,238 (95%)	7,137 (81.8%)	0.001
Calendar period of enrollment, n (%)				
1997-2002	5,217 (42.9%)	2,565 (75.3%)	2,652 (30.4%)	0.0001
2003-2008	1,452 (11.9%)	286 (8.4%)	1,166 (13.4%)	
2009-2015	5,466 (45%)	556 (16.3%)	4,910 (56.3%)	
HCV genotypes, n (%)				
1	668 (49%)	668 (49%)		
2	46 (3.4%)	46 (3.4%)		
3	488 (36%)	488 (36%)	-	-
4	146 (10.8%)	146 (10.8%)		
Mixed Infection	11 (0.8%)	11 (0.8%)		
HBsAg positive patients, n (%)	735 (6%)	261 (8.1%)	474 (5.7%)	0.0001

Values are expressed as n (%) except for the * median (IQR)

Prevalence of HCV-Ab positive status according to calendar year of enrollment

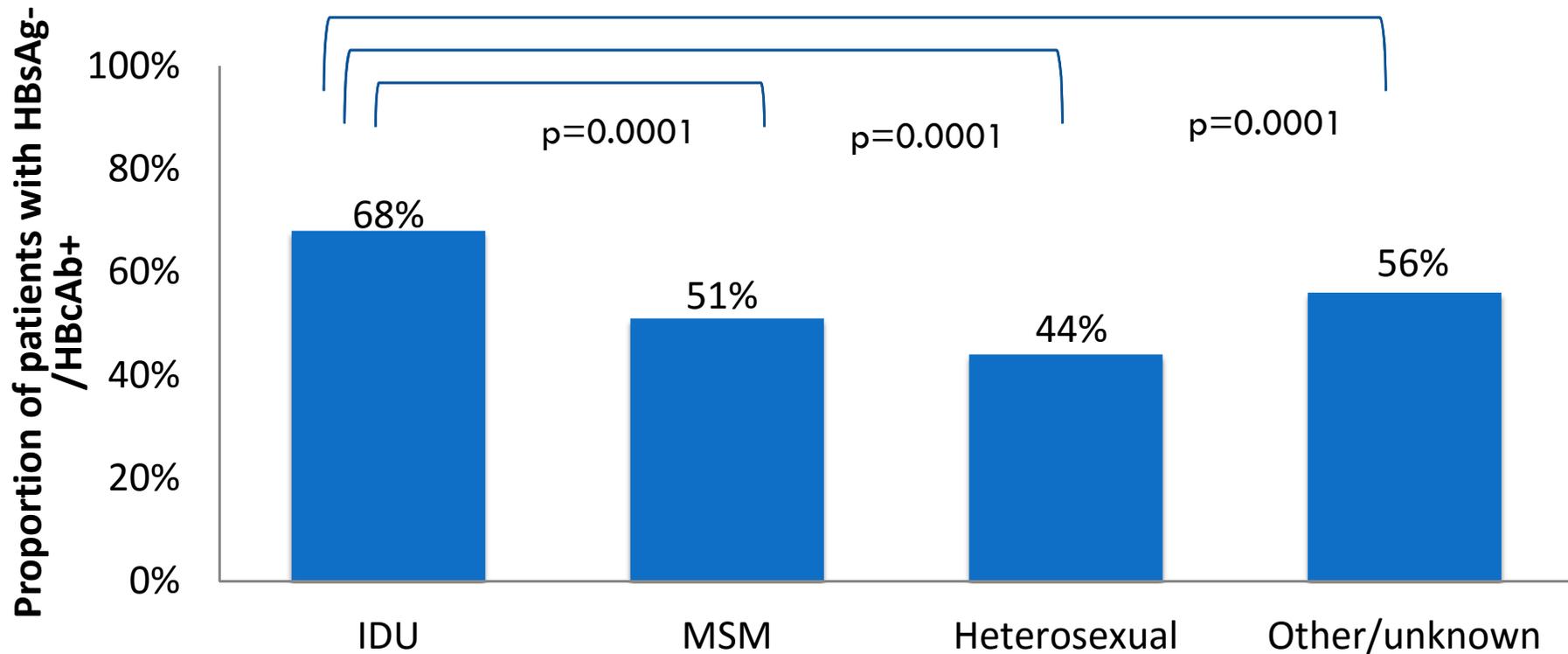


HCV genotype distribution according to calendar year of enrollment (N=1,359*)



*1 not specified: 61 (4.5%); mixed 11 (0.8%)

Prevalence of HBsAg-/HBcAb+ in HCVAb+ (n/N:764/1,249; 61%)



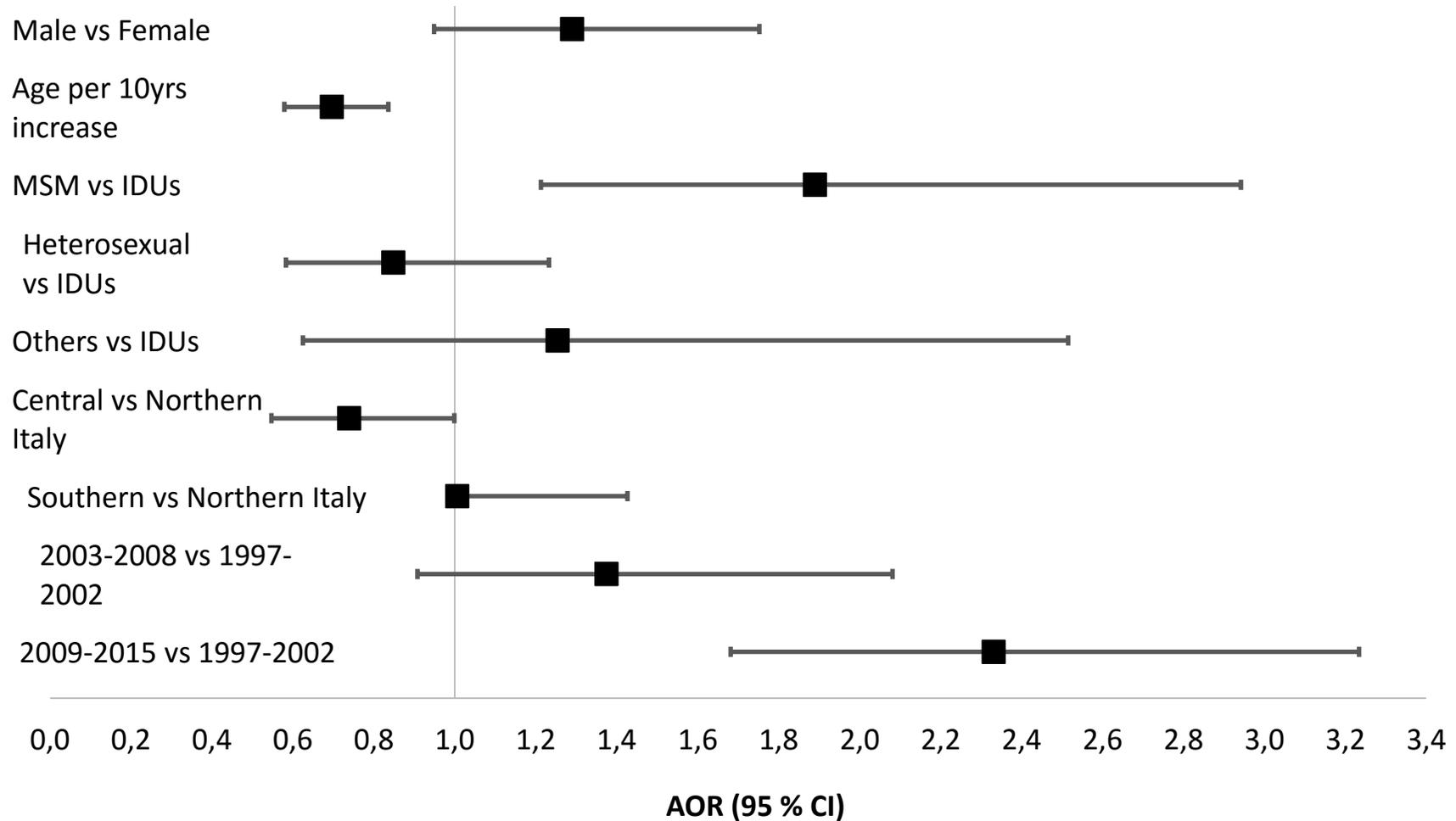
*Other comparisons between groups are non statistically different

Factors associated with HCV-Ab positive status

Variable	Univariate analysis			Multivariate analysis		
	OR	95% CI	P	AOR	95% CI	P
Female gender	1			1		
Male gender	0.940	0.858-1.030	0.183	0.811	0.685-0.957	0.013
Age, for 10 years older	1.523	1.466-1.581	<0.0001	1.039	0.971-1.112	0.276
Risk factor						
IDU	1		<0.0001	1		<0.0001
MSM	0.008	0.007-0.010	<0.0001	0.012	0.010-0.015	<0.0001
Heterosexual	0.012	0.01-0.014	<0.0001	0.013	0.011-0.016	<0.0001
Other/Unknown	0.016	0.012-0.02	<0.0001	0.021	0.015-0.026	<0.0001
Country region						
North	1		<0.0001	1		0.098
Center	0.758	0.692-0.831	<0.0001	0.851	0.734-0.986	0.031
South and Islands	1.474	1.319-1.647	<0.0001	0.951	0.788-1.148	0.601
Foreign born	1			1		
Italian	4.271	3.625-5.032	<0.0001	1.449	1.163-1.807	0.001
Calendar period of enrollment						
1997-2002	1		<0.0001	1		<0.0001
2003-2008	0.254	0.220-0.292	<0.0001	0.497	0.407-0.608	<0.0001
2009-2015	0.117	0.106-0.130	<0.0001	0.229	0.196-0.268	<0.0001
HBsAg-	1			1		
HBsAg+	1.464	1.252-1.713	<0.0001	1.181	0.916-1.521	0.201

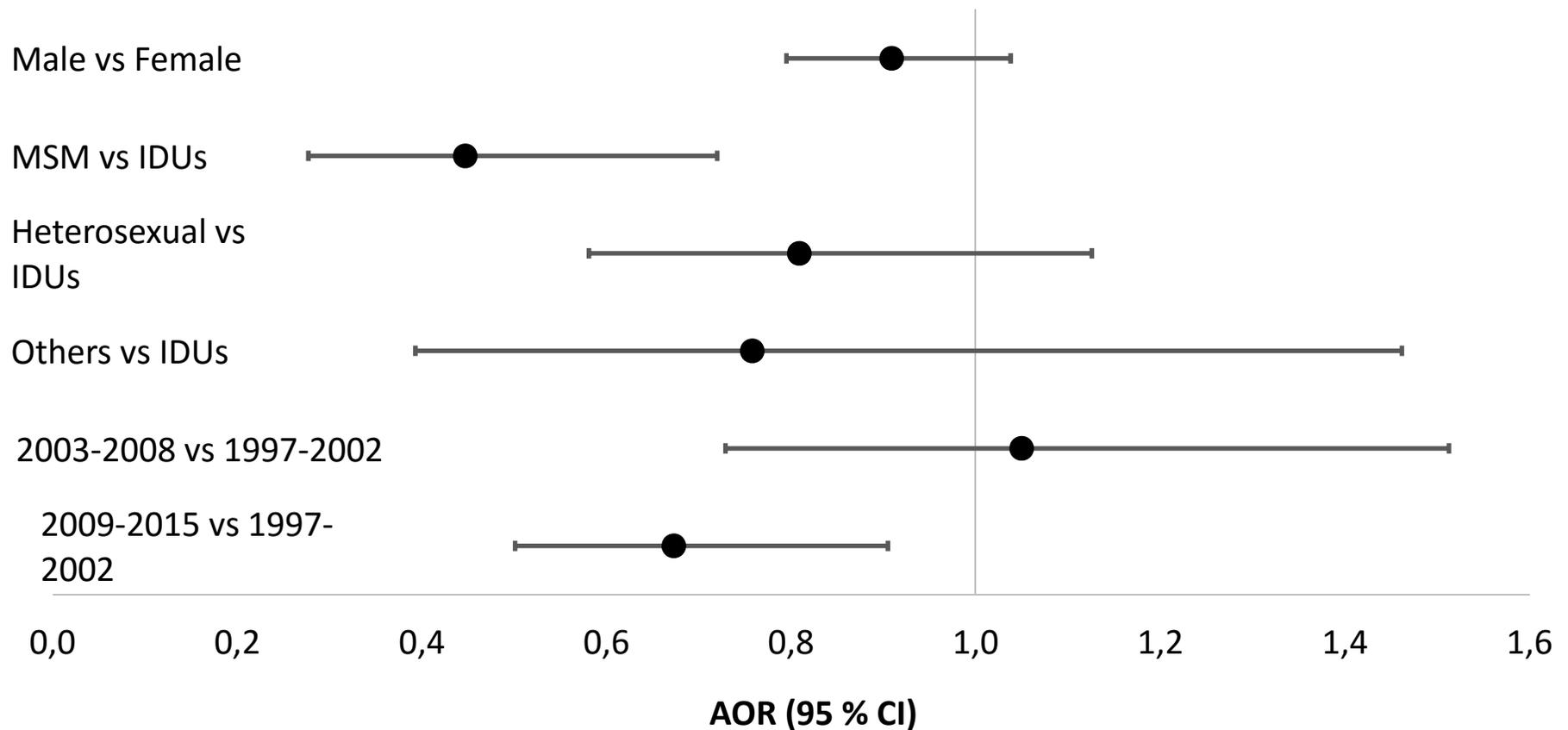
✓ Female sex versus male AOR +1.191, CI 95% 1.014-1.398 p= 0.033, excluding MSM

Factors associated with genotype 1a (N=435)



*Variables are mutually adjusted

Factors associated with genotype 3 (N=488)



*Variables are mutually adjusted

Conclusions

- ✓ Prevalence of HCV infection is significantly declining in PLWHA, independently of risk factors
- ✓ After adjusting for risk factors and calendar year of enrollment, HCV co-infection is more frequent in female patients and in natives
- ✓ In recent years the relative frequency of genotype 3 in co-infected patients is declining, while genotype 1a is increasing, mainly driven by younger patients and MSM

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