

Analysis of the shift of the transmission pattern for hepatitis C in a community in Central Italy

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SUMMARY

Anti-HCV and HCV-RNA prevalence among adults from an isolated Central Italian community were 16.3% and 9.0%; 3.0%, 2.3% among 25-to-49-year-olds, 27.6%, 14.7% among older subjects. 1b genotype prevailed (88.5%). 1a, 1a/1b, 4 were also isolated. Seropositivity was associated with age >50 years, public dental health care, glass syringe use, surgical interventions. The transmission pattern seems to be shifting from that typical of Southern Italy (high prevalence, particularly in the elderly, 1b genotype predominant, various routes of transmission involved, cohort effect), to that typical of Europe (lower prevalence, particularly among younger adults, other genotypes involved, association with intravenous drug use and immigrants).

KEY WORDS: hepatitis C virus (HCV), HCV transmission, HCV risk factors, public health care, dentistry

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Hepatitis C virus (HCV) is a serious public health problem due to its high global prevalence, the tendency to develop chronic infection, and the absence of symptoms among most infected individuals. In Europe, two broad patterns of HCV transmission have been identified. The most frequent, with an overall prevalence of 1%-2%, among 30-to-50-year-old adults and sustained by genotypes 1a, 3, 4 has been introduced by intravenous drug (IVD) use and immigrants from endemic areas. The second prevailing in the elderly, genotypes 1b and 2c associated with a wide group of transmission routes more frequent in the distant past, such as the use of glass syringes, unsafe medical health care. Both these patterns co-exist in Italy (Ansaldi *et al.*, 2005).

A high anti-HCV prevalence (14%) was found in a rural community living in the Central Italian village of Fontechiari.

Three hundred subjects, aged >25 years were randomly selected from the patient list of the only local general practitioner (GP) and directly interviewed by the GP. Serum samples were collected and tested for anti-HCV using a second-generation Enzyme Immunoassay (EIA 2.0, Abbott Laboratories, Chicago, Illinois, US). Anti-HCV positive sera were confirmed by recombinant immunoblot assay (RIBA) by the local Hospital. The anti-HCV positive samples were tested for HCV RNA and HCV genotyped by a line-probe assay (INNOLiPA HCV II, Innogenetics, Belgium).

The association between anamnestic variables and HCV seroprevalence was investigated using multiple logistic regression analysis.

Prevalence of anti-HCV infection was as high as 16.3% (Tab. 1). Viremia was ascertained in 55.3% of seropositive subjects. Therefore, HCV RNA prevalence was 9.0%; 91.5% of seropositive sub-

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TABLE 1 - Prevalence and 95% Confidence Interval (95CI) of anti-HCV positives, HCV-RNA positives and of HCV genotypes in the investigated sample and in the two age groups.

Group	Sample % (n)	Anti-HCV		HCV RNA		1a		1a/1b		1b		4	
		% (n)	95CI	% (n)	95CI	% (n)	95CI	% (n)	95CI	% (n)	95CI	% (n)	95CI
25-49 yrs	46.0 (133)	3.0 (4)	0.1-5.9	2.3 (3)	1.6-3.0	0.8 (1)	0.0-1.5	0.8 (1)	0.0-1.5	0.8 (1)	0.0-1.5	0.0 (0)	0.0-0.0
≥50 yrs	54.0 (156)	27.6 (43)	20.6-34.6	14.7 (23)	9.1-20.3	0.0 (0)	0.0-0.0	0.0 (0)	0.0-0.0	14.1 (22)	8.6-19.6	0.6 (1)	0.0-1.9
Total	100.0 (289)	16.3 (47)	12.0-20.6	9.0 (26)	3.3-12.3	0.3 (1)	0.0-1.0	0.3 (1)	0.0-1.0	8.0 (23)	4.9-11.1	0.3 (1)	0.0-1.0

jects and 88.5% of viremic subjects were older than 50 years. HCV genotype 1b was isolated in 88.5% of cases, with an estimated overall point prevalence of 8.0%. Genotypes 1a, 1a/1b and 4 were isolated on one occasion each. The carriers of the genotype 1a/1b and 1a were young adults, IVD users, whereas the carrier of the genotype 4 was the sister of a 1b positive subject. Sixteen of the twenty-six 1b positives were family contacts of seropositive subjects (7 daughters/sons, 4 brothers, 5 spouses) and were older than 50 years.

The statistically significant predictors for anti-HCV positivity from the strongest to the weakest were age older than 50 years (OR 12.0; 95 CI 2.7-52.3; $p < 0.001$), dental therapy in public health care offices (OR 4.7; 95 CI 1.6-13.3; $p < 0.004$), use of glass syringes (OR 4.3; 95 CI 1.6-11.6; $p < 0.004$) and surgical interventions (OR 3.7; 95 CI 1.3-10.5; $p < 0.01$). The whole model's goodness of fit was high ($p < 0.0001$), but with an R^2 of 0.36, almost two thirds of the present anti-HCV positive cases remained unexplained.

The high anti-HCV prevalence in the investigated community is in agreement with other reports from Central-Southern Italy (Guadagnino *et al.*, 1997; Maio *et al.*, 2000) and confirms the observation that these regions are hyperendemic areas, with the highest prevalence in Europe (Ansaldi *et al.*, 2005).

The analysis of risk factors and the high proportion of unexplained cases did not completely confirm the results of a previous case-control study on only the elderly residents in Fontechiari, which found family contacts with HCV and glass syringe sharing associated with the condition (Simonetti - D'Arca *et al.*, 1999). The present com-

munity has been isolated for decades, with irrelevant immigration and most residents working in the countryside, within the area of the municipality. The HCV infection was presumably sustained by the 1b genotype and was associated with the use of glass syringes and many other daily HCV exposures, most of them unidentified (Dal Molin *et al.*, 2002). In such a small and isolated community, all residents had similar risk levels of HCV exposure. Therefore, family contacts of infected individuals, particularly spouses with more than twenty years of marriage, generally considered at highest risk were not at greater infection risk than the remaining residents. For the HCV infection sustained by 1b genotype, a classical cohort effect was observed, with the incidence of the condition progressively decreasing among subsequent generations. However, the shift of the community from isolated to open, observed in recent decades in Fontechiari, led to a parallel shift of the transmission pattern, with lower morbidity, the introduction of other genotypes, different age and gender distribution, with younger male adults at highest risk, and the transmission associated, yet not significantly, with IVD use (Guadagnino V. *et al.* 1997, Maio *et al.*, 2000; Dal Molin *et al.*, 2002).

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