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Abstract Book

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CONCORDANCE AND DISTRIBUTION OF HPV GENOTYPES IN HPV INFECTED SEXUAL COUPLES

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Introduction: The characteristics of HPV infection in women have been extensively investigated, however, only a few studies have analyzed the characteristics of HPV infection in men and in sexual couples.

Materials and Methods: 195 sexual couples positive for HPV-DNA were examined, at the Virology laboratory of the Department of Sciences for Health Promotion and Mother and Child Care (Policlinico, University of Palermo, Italy). HPV-DNA detection was performed by the INNOLiPA HPV Genotyping Extra II Test (Fujirebio) and nested PCR/sequencing method. All women (range: 20-60, mean age: 31.5 ys) had performed a pap smear and knew the cytological diagnosis: 73 (37.4%) negative at Pap smear, 21 (10.8%) with atypical squamous cell of undetermined significance (ASCUS), 82 (42.1%) with low grade squamous intraepithelial lesion (LSIL), 18 with high grade squamous intraepithelial lesion (HSIL) and 1 carcinoma. For ease of computation, these two latter categories were grouped together, and thus represented a total of 19 cases of $\geq$ HSIL (9.7%). As for the partners (range 20-70; mean age: 36.7 ys) only two had genital warts.

Results: 36 types of HPV were identified: 27 were present in both men and women, two (HPV-67, -90) only in women and seven types (HPV-43, -81, -82, -83, -87, -91, -107) only in men. Infection with or containing high risk HPV types (HR-HPV) was in 112/195 (57.4%) women and in 57/195 (29.2%) men; low risk HPV types (LR-HPV) was in 17/195 (8.7%) women and in 32/195 (16.4%) men. Multiple infections was in 66/195 (33.8%) women and in 106/195 (54.4%) men. Mostly frequent types, the same in men and women, were: HPV-16 (27.7% and 21% respectively), HPV-51 (13.8% and 19%), and -66 (13.8% and 18.5%). HPV-group specific (HR or LR) concordance between sexual partners was

found in 163/195 (83.6%; 95%CI = [78.4-88.8]) couples. HPV-type specific concordance was found in 99/195 (50.8%; 95%CI = [43.8-57.8]) couples, of which 82 (82.8%) shared one types, 12 (12.1%) two types and 4 (4.1%) three types, 1 (1%) four types. Cytological diagnosis was not statistically significantly associated neither with HPV-group specific concordance ($p = 0.206$) nor with HPV-type specific concordance ($p = 0.312$).

Conclusions: partners of positive women represent a population at high risk of infection and in turn can be a source of (re)infection to the partner. Studied are needed to improve knowledge of the natural history of HPV infection in sexual couples, to control viral transmission and provide adequate counseling to HPV infected sexual partners.

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DISTRIBUTION OF GENITAL HUMAN PAPILLOMAVIRUS IN SICILIAN MEN WITH AND WITHOUT CLINICAL MANIFESTATIONS

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Introduction: Infection Human Papillomavirus (HPV) is the cause of several disease in men and in women: genital warts, penile and cervical intraepithelial neoplasia, invasive penile carcinoma and cervical cancer. However, less is known about HPV infection, prevalence and distribution of HPV types in men.

Materials and Methods: 820 genital samples of men (age 19-77; mean age: 36.7 ys) who had come to the Virology laboratory of the Department of Sciences for Health Promotion and Mother and Child Care (Policlinico, University of Palermo, Italy) were examined for HPV infection. The study included men with genital warts, men with atypical genital lesion, partners of HPV-positive women and asymptomatic men for Sexually Transmitted Diseases (STD) diagnostic evaluation. HPV-DNA genotyping was performed by the INNOLiPA HPV

Genotyping Extra II Test (Fujirebio) and nested PCR/sequencing method.

Results: 461/820 (56.2%) genital samples were HPV positive. The highest HPV detection rate was found in the 25-34 year age group (41.4%), followed by the 35-44 group (31.7%). Oncogenic types were found in 360/461 (78.1%) positive samples. Multiple HPV type infections were shown in 225/461 (48.8%) samples of whom 109 (23.6%) had two genotypes, 58 (12.6%) three genotypes, 38 (8.2%) four genotypes, 15 (3.2%) five genotypes, 3 (0.6%) six genotypes and then only 2 (0.4%) eight genotypes. Thirty-eight different HPV types were identified: the mostly frequent were HPV-16 (19.9% of HPV positive patients), -51 and -6 (18.2%), -31 (13.9%), -66 (13.7%), -53 (11%), -18 (7.6%), -44 (7.1%), -56 (7%), other viral types occurred at a frequency of less than 7%. Men who have made the HPV test: 138 (16.8%) were diagnosed with genital warts, 3 (0.4%) carcinomas, 413 (50.3%) were HPV-positive women partners, 30 (3.6%) presence of an atypical genital lesion, 236 (28.7%) men who wanted a full assessment of sexual transmitted diseases. HPV infection was evident in 100% of men with carcinomas, in 103/138 (74.6%) men with genital warts, in 254/413 men (61.5%) partners of HPV-positive women, in 11/30 (36.7%) men with presence of an atypical genital lesion and in 90/236 (38.1%) in asymptomatic men. HPV-16 was prevalent in 2 (66.7%) men with carcinoma, in 55 (21.6%) men HPV-positive women partners and in 3 (27.3%) men with atypical genital lesion; HPV-6 in 36 (35%) men with genital warts and in 19 (21.1%) asymptomatic men.

Discussion and Conclusions: Different prevalence and distribution of HPV types in different categories including men in study will contribute to elucidating the epidemiology of HPV infection in men, and it will also be helpful in the implementation of future prevention strategies.

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RESISTANT GENETIC PROFILE OF HEPATITIS C VIRUS GENOTYPE 4 IN DIRECT-ACTING ANTIVIRAL AGENTS NAÏVE PATIENTS

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Introduction: Direct-acting antiviral agents (DAAs) become the new standard of anti-HCV therapy and show a very high sustained virological response (SVR) rate. Due to HCV genetic variability, drug resistance associated substitutions (RAS) are detected in patients prior the start of DAAs therapy according to genotype/subtype. More studies have focused on genotype 1 and little has known about the impact of other HCV intra-genotype variability on DAAs resistance. HCV-4 is highly heterogeneous, with 19 recognized subtypes which relative prevalence changes geographically. In Italy, the prevalence of the HCV-4 increase in recent years, with 2-6% of chronic hepatitis reported in southern regions, and due to migration flows, new subtypes can be introduced. We study the presence of RAS and the genetic barrier of HCV-4d in isolates from Sicilian chronically infected patients naive for DAAs therapy.

Materials and Methods: Serum samples from 50 Sicilian HCV-4 chronically infected patients naive for DAAs were collected. Two fragments of NS3/4A and NS5A genes were amplified with specific primers and sequenced by Sanger method. Thirty-six HCV-4 sequences of all subtypes, obtained from data base, were included. A phylogenetic analysis, using MEGA 6 software, was conducted to identify the subtypes and the presence of RAVs and polymorphisms was evaluated by visual inspection. The genetic barrier was studied using the minimal score (*m.s.*) calculation which assigned a score of 1 to each transition and of 2.5 to transversion.

Results: Phylogenetic analysis of NS3 and NS5A sequences show that forty-nine HCV strains from Sicilian patients were classified as subtype 4d and only one as subtype 4a. The nucleotide distance of HCV-4d strains was 5.8% for NS3/4A and 6.4% for NS5A genes. Most of HCV-4d strains showed RAS