

DETECTION OF SEXUALLY TRANSMITTED INFECTION ASSOCIATED PATHOGENS THROUGH MULTIPLEX REAL-TIME PCR.

Alice Nava, Valentina Lepera, Alessandra Bielli, Diana Fanti, Luisa Grassi, Giovanni Gesu

S.C. Analisi Chimico Cliniche e Microbiologia – A.O. Ospedale Niguarda Ca' Granda – Milano

RESULTS:

Male samples were 445; 65 (14.61%) were infected with at least one microorganism and globally 72 pathogens were identified. Among the male positive samples, the percentage of single, double and triple infection was 89.23%, 9.23% and 1.54%, respectively. The most common isolated pathogens was UU (46.15%), followed by UP (21.54%). The percentage of CT, NG and TV detection was 12.31%, 10.77% and 3.08%, respectively. The prevalence of MH was 7.69% and of MG was 9.23%. Female samples were 701; 272 (38.81%) were infected with at least one microorganism and a total of 325 pathogens were identified. Among the female positive samples, the percentage of single, double and triple infection was 81.99%, 16.54% and 1.47%, respectively. The most common isolated pathogens was UP (76.86%), followed by UU (16.17%). The percentage of CT, NG and TV detection was 6.62%, 0.36% and 2.94%, respectively. The prevalence of MH was 15.8% and of MG was 0.73%. The prevalence of STI in the female population was higher in the fertile age group (36.95%) relative to the not-fertile one (1.86%).

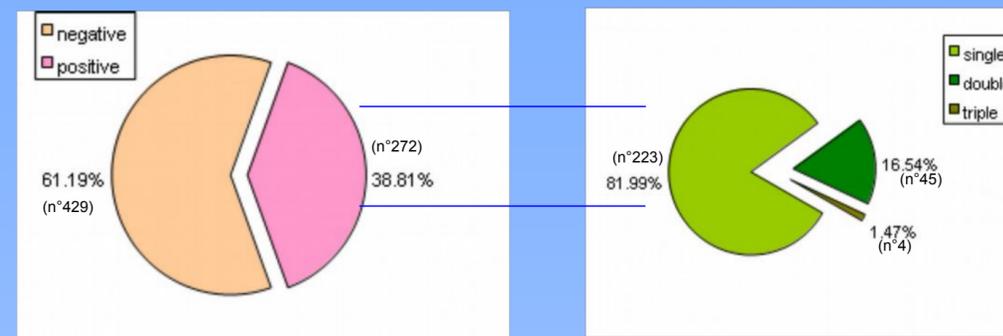
BACKGROUND:

Sexually transmitted infections (STI) are clinical syndromes caused by different pathogens such as bacteria, protozoa, virus and fungi. Their identification is fundamental in order to cure symptomatic patients and to avoid problems of sterility. Clinical manifestations are often atypical with common symptoms. A simultaneous identifications is essential for the establishment of a correct therapeutic regimen. Therefore, multiplex real-time PCR assays are considered a very useful approach for their detection. The aim of this work is an epidemiological analysis on a sexual active population in order to evaluate the prevalence of STI.

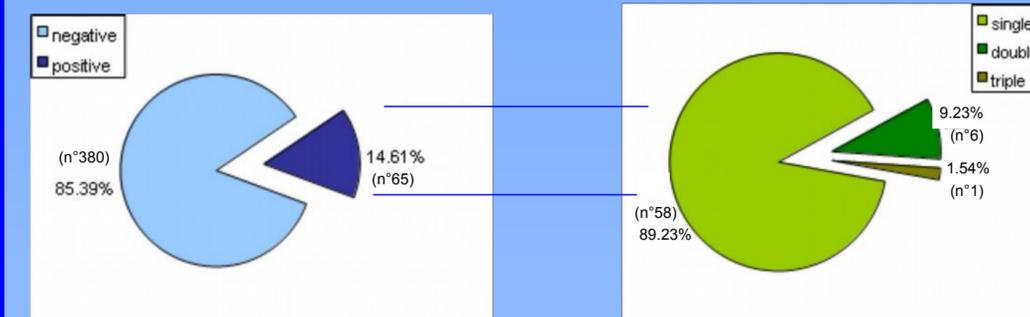
MATERIAL/METHODS:

From 13th March 2015 to 16th November 2015 we tested 1146 samples (569 urines, 85 urethral secretions, 481 cervical secretions and 11 other matrix). We used Anyplex II STI-7TM detection kit (Seegene®) for the qualitative and simultaneous identifications of 7 pathogens: Chlamydia trachomatis (CT), Neisseria gonorrhoeae (NG), Trichomonas vaginalis (TV), Ureaplasma urealyticum (UU), U. parvum (UP), Mycoplasma hominis (MH) and M. genitalium (MG). Nucleic acid extraction was performed on the specific platform Nimbus Microlab (Seegene®). Retrospectively we have analyzed data stratifying for sex and for fertile age in the female population.

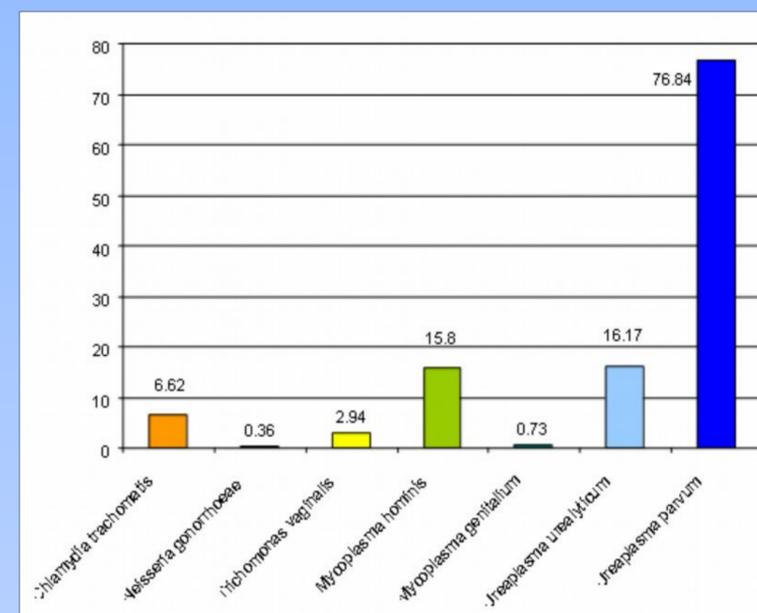
GRAPH 1: Female samples (tot. 701)



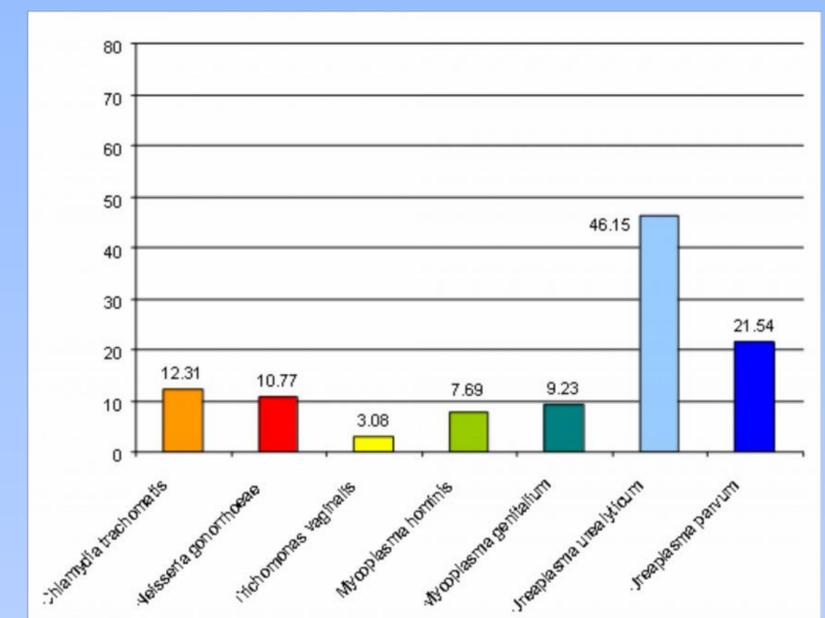
GRAPH 2: Male samples (tot. 445)



GRAPH 3: Percentage of isolated pathogens on positive female samples



GRAPH 4: Percentage of isolated pathogens on positive male samples



CONCLUSION:

The prevalence of NG and CT is major in the male population than in the female one. Their percentages are higher relative to last Italian report on STI (2013). UP is the most common isolated microorganism, it is sometimes associated with other STI (17.37%) but its pathogenic role is still debating.