## P127 - Molecular analyses on HPV infections in semen

<u>Giuseppina Capral</u>, Rosaria Schillaci2, Liana Bosco3, Maria C. Roccheri3, Antonino Perino2, Maria Pia Caleca1, Maria A. Ragusa3

<sup>1</sup>Department of Sciences for Health Promotion and Mother-Child Care "G. D'Alessandro", UOC of Microbiology, Virology and Parasitology, Polyclinic Hospital, "P. Giaccone"; <sup>2</sup>Department of Sciences for Health Promotion and Mother-Child Care "G. D'Alessandro", UOC of Gynecology and Obstetrics; <sup>3</sup>Department of Biological, Chemical, and Pharmaceutical Sciences and Technologies (STEBICEF)-University of Palermo, Palermo, Italy.

**Introduction:** Human Papillomaviruses (HPVs) are non-enveloped double stranded DNA viruses classified in different genera and several different genotypes. Depending on the genotypes, HPV infections can be asymptomatic or can cause from warts to malignant tumours. Some genotypes, such as HPV18 and HPV16, are considered high risk (HR) HPVs and they are the major cause of cervical cancer. HPV is highly tissue-tropic and infects epithelial cells, but it can also binds other cell types. It is known that HPV can be found in semen but its effects on spermatozoa and male reproductive system are not completely clarified.

**Materials and Methods:** In order to study the HPV infection in semen, we developed a new molecular approach, based on a differential cell lysis step and DNA extraction, which allows to evaluate virus localization in the different semen components. Samples are genotyped by reverse hybridization assay and DNA presence and quantity in sperms, somatic cells and semen plasma are evaluated by nested PCR and type-specific real time PCR. Moreover, RNA is also extracted from the separated semen fractions and the expression of selected genes is assessed by RT-qPCR. Seminal parameters are also carefully analysed.

**Results:** Results show that HPV can be identified in every fraction of semen. Different samples can contain the virus in different fractions and more than one HPV genotype can be found in the same fraction. Additionally, our data suggest that only when HPV DNA is detected in spermatozoa can cause a reduction of sperm cell motility that resulted proportional to the viral load. Moreover, preliminary results suggest that samples infected by HR-HPVs show a low viral load. Interestingly, the viral load of the low risk (LR) mucosal HPVs is often much higher. RT-qPCR results suggest that HPV infection could modify sperm maturation pathway causing the impairment of motility, altering the expression of some maturation genes. Indeed, in LR-HPV infected samples the

**Discussion and Conclusions:** Our results highlight the heterogeneity of semen infections: all semen components can contain viral DNA and viral load can be very different for HR- and LR-HPVs; some samples may carry HPV either in cells or in sperms and other samples in both. Only when viral DNA is localized in the sperm fraction, sperm motility is impaired, otherwise, the infection of ductal cells exfoliating in the semen could influence the expression of genes important for sperm maturation. Therefore, these data confirm that HPV infection in semen, even if asymptomatic in the man, can decrease male fertility and prompt new possible consequences of the viral infection in semen.