# MOLECULAR DIAGNOSIS OF SEXUALLY TRANSMITTED INFECTIONS (STIS) WITH MULTIPLI CATALUNYA (SPAIN).

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## BACKGROUND

STIs are very common worldwide. Africa and Southeast Asia are the epicenters with the highest number of cases. In I has been an increase of STIs for a decade as a result of changes in sexual habits (Russian Roulette parties, corr dogging, etc.), abandonment of condom use, migration and increased sex tourism. *C. trachomatis* is the most common and the leading cause of infectious blindness. Its detection has been improved by molecular techniques. *N. gonorr* sensitivity to antibacterial agents has declined over the past 60 years. Currently some strains have been identified in high resistance to third generation cephalosporins (treatment recommended by the CDC), resulting in the need for clos antibacterials. *M.genitalium* is an emerging organism and cause of PID, salpingitis, infertility, cervicitis and nongonocci by some to be the new *C.trachomatis*. *T. vaginalis*, in spite of decreasing incidence levels of detection, continues *Mycoplasma hominis* in the mucosa increases the chances of contracting HIV and affects immunocompromised patter NGU and is associated with childbirth and postpartum events. Our laboratory has a service area of 850,000 inhabit hospitals of 450 beds and 93 satellite extraction centers. The transport of samples from the centers to the laboratory c microorganisms (*N.gonorrhoeae*). In these, we are unable to perform *C.trachomatis*, and cultivation of *M. genitalium* tal and time led us to decide in favor of the incorporation of a multiplex PCR.

## OBJECTIVES

-Detect *Chlamydia trachomatis* and *Mycoplasma genitalium*. -Analyze the co-infections.

## MATERIALS AND METHODS

We analyzed 2602 endocervical, vaginal and urethral samples between January 2010 and October 2011. The samples were subjected to automated extraction system QUIACUBE QUIAGEN<sup>R</sup>. We then performed a multiplex PCR, Seeplex STD6 ACE (Segeene), and detection was accomplished with capillary electrophoresis. STD6 can detect: *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (NG), *Mycoplasma genitalium* (MG), *Mycoplasma hominis* (MH), *Ureaplasma uralyticum* (UU), *Trichomonas vaginalis* (TV), and combinations thereof.

## RESULTS

Of a total of 2602 samples positive results were found in 1346 (52%). Of the total samples tested one organism was detected in 661 (25%) and co-infection with two, three and four microorganisms in 685 (26.5%). The most frequent co-infections were always the combination of two agents. Of the single infections the most prevalent microorganism was UU, with 253/1346 positive samples (19%); MH 173/1346 (13%); CT 131/1346 (10%); NG 60/1346 (4%); MG 24/1346(2%) and TV 20/1346 (1%). Regarding co-infection the most frequent combinations were UU and MH (96/1346 samples, 7%); UU and CT (44/1346 samples, 3%) and MH and CT (34/1346 samples, 2.5%). Results for simple and co-infection rates are shown in Table No. 1

TAULL N.1		
2602 TOTAL SAMPLES	SIMPLE	
UU	253/1346 (19%)	
МН	173/1346 (13%	
СТ	131/1346 (10%)	
NG	60/1346 (4%)	
MG	24/1346 (2%)	
TV	20 /1346 (1%)	
TOTAL POSITIVE	661/2602 (25%)	

## CONC

- 1. With just one procedure, six different at once, both alone and in combined and in combined
- We stress the importance of MG frequently in co-infections (p <0.0</li>
- 3. The use of molecular techniques grow microorganisms.