Mycoplasma genitalium antibiotic resistance in genital and extragenital samples from MSM attending a HIV/STI Clinic in Italy

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Background

- *Mycoplasma genitalium* (MG) is one of the most **warning sexually transmitted pathogens** also due to its ability in **developing resistance** to macrolide and quinolone antibiotics.
- Resistance-guided therapy has demonstrated the best cure rates but can only be based on molecular methods, and the gap between **genotypic resistance** and **microbiological clearance** has not been fully evaluated yet.

→ **This study aims at finding mutations associated with MG antibiotic resistance and investigating the relationship with microbiological clearance amongst men-who-have-sex-with-men (MSM).**

Methods

Samples collection from 1040 MSM: genital (urine), extragenital (pharyngeal and anorectal swabs)

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DNA extraction and MG detection by Anyplex™ II STI-7 assay (Seegene): 107 MG-positive samples from 96/1040 MSM (9.2%)

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47 samples from 42 MSM were available for **detection of mutations** associated with macrolide resistance (**23S rRNA gene**) and quinolone resistance (***gyrA* and *parC* genes**) by Sanger sequencing and Allplex™ MG & AziR assay (Seegene)

Results

- 63.8% (n=30/47) of samples showed mutations in **23S rRNA** gene: A2059G (n=21), A2058T (n=7), A2058G (n=4). In 2 samples, both A2059G and A2058G mutations were detected.
- 17% (n=8/47) of samples had mutations in ***parC*** gene: 6 presented SNPs/AA changes of known clinical relevance (G248T/S83I, G248A/S83N, G259A/D87N, G259T/D87Y).
- 4.3% (n=2/47) of samples had mutations in ***gyrA*** gene: only one carried a SNP/AA change of known clinical relevance (G285C/M95I).
- 17% (n=8/47) of samples had **dual class** (macrolide and quinolone) resistance-associated mutations in 23S rRNA and *parC* genes (n=6) or in 23S rRNA and *gyrA* genes (n=2).
- After first-line **treatment with macrolide azithromycin**, 64.3% (n=27/42) of MSM returned for Test of Cure (ToC): in all those resulting MG-positive (n=15) a mutation in the 23S rRNA gene had been detected; among those resulting MG-negative (n=11), most (n=10) had no mutations in the 23S rRNA gene.
- All patients undergoing second-line **treatment with quinolone moxifloxacin** (n=13) resulted negative at ToC, even those carrying MG strains with mutations in *parC* gene (n=6).

Conclusions

Our observations confirm that mutations in 23S rRNA gene are associated with azithromycin treatment failure while mutations in *parC* gene alone are not always associated with phenotypic resistance to moxifloxacin.

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It is **fundamental to test for mutations** associated with azithromycin resistance to improve antibiotic prescription and reduce antibiotic pressure on MG strains.

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