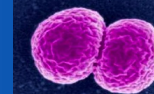


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Molecular typing by NG-MAST of *Neisseria gonorrhoeae* isolated from recurrent genital infections



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Introduction

Sexually Transmitted Infections with *Neisseria gonorrhoeae* (NG) is still a major problem of public health by:

- the increase in gonorrhoea cases in the world (1),
- the emergence of strains resistant to the recommended antibiotic treatment, i.e. 3rd-generation cephalosporins (2),
- the large diffusion in Europe of the ST1407 clone harbouring a decreased sensitivity to 3rd generation cephalosporins (3).

Objectives

Since relapse and therapeutic failure are often related to resistance, the aim of this study was :

- to identify high risk populations suffering from NG recurrent infections,
- to distinguish between recurrence and re-infection,
- to identify the circulating bacterial clones in these populations,

Materials and methods

Patients:

- 84 patients (80 men) consulting at least twice for a genital NG
- mean age: 30 years old
- 60% Men having Sex with Men (MSM) vs 40% heterosexuals
- all patients received by one dose of 500 mg ceftriaxone IM plus azithromycin 1g.

Clinical NG isolates:

- 200 NG from urethral specimens (n=179), cervical (n=7) and 14 rectal swabs (n=14)

Period of study:

from 2004 to 2012 at St Louis Hospital, Paris

Molecular epidemiology typing was performed using the reference multi-antigen sequence typing (NG-MAST) method (4). The genes *tpbB* and *porB* were amplified and sequenced. Each strain ST was determined using the NG-MAST database (5)

Recurrences were defined by repeated genital infections with NG isolates showing the same Sequence –Type (ST) and occurring in a time interval of less than 6 months.

Reinfections were characterized by repeated infections with NG isolates showing a different Sequence –Type (ST).

Results and discussion

- Among the 200 NG clinical isolates, 102 different ST Types were characterized in which 37/102 (36.2%) were novel STs.
- The ST2992, ST225 and ST1407 were overrepresented in the MSM.
- The ST2992 (12%) and ST2 (8.5%) were the most frequently observed and they were associated to the MSM and to the heterosexual population, respectively.
- The predominant NG-MAST genogroups were similar as those previously described from a sampling of French isolates (2009-11) (3).

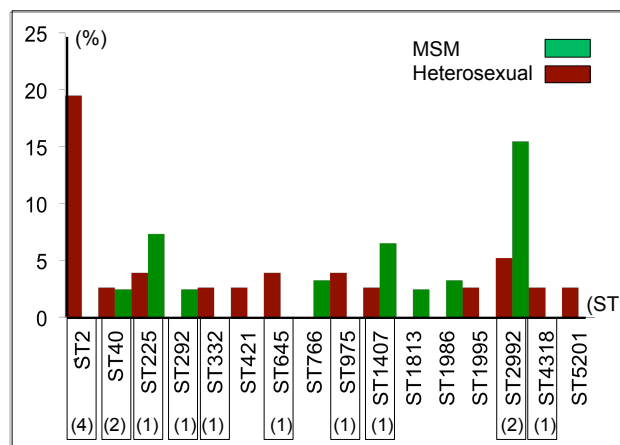


Figure: Prevalent ST-Types of the 200 NG isolates. ST-Type of NG isolates found in cases of recurrence were boxed and the number of patients were indicated below.

Table: Patients characteristics and co-infection

Characteristics	Recurrence	Re-infection	Total
Patients	18 (21.4%)	66 (78.6%)	84
Male	17	63	80
Female	1	3	4
Heterosexual population	11 (65%)	18 (29%)	29 (35%)
MSM population	6 (35%)	45 (71%)	51 (65%)
HIV co-infection	3 (16%)	16 (24%)	19 (23%)
<i>C. trachomatis</i> co-infection	11 (61%)	18 (27%)	29 (35%)
Mean of time interval between episodes (in weeks)	11	70	60

- Recurrences with the same NG isolate and reinfections were respectively observed in 21.4% and 78.6% of the cases (Table).
- Two STs were mainly observed in case of recurrence: ST2992 (MSM) and ST2 (heterosexual) (Figure). The ST1407 was found in only one case.
- Interestingly, recurrences occurred more commonly in the heterosexual population than in the MSM population. This suggests a lack of treatment and prevention of sexual partners.

Conclusions

Our study highlights the usefulness of NG genotyping by the MAST method in order to distinguish recurrence and reinfection.

Although this cannot distinguish between recurrence and true relapse, it could indicate which preventing measures are adequate with regard to the population consulting for a second episode of NG infection.

References

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