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Réseau des Hygiènistes du Centre

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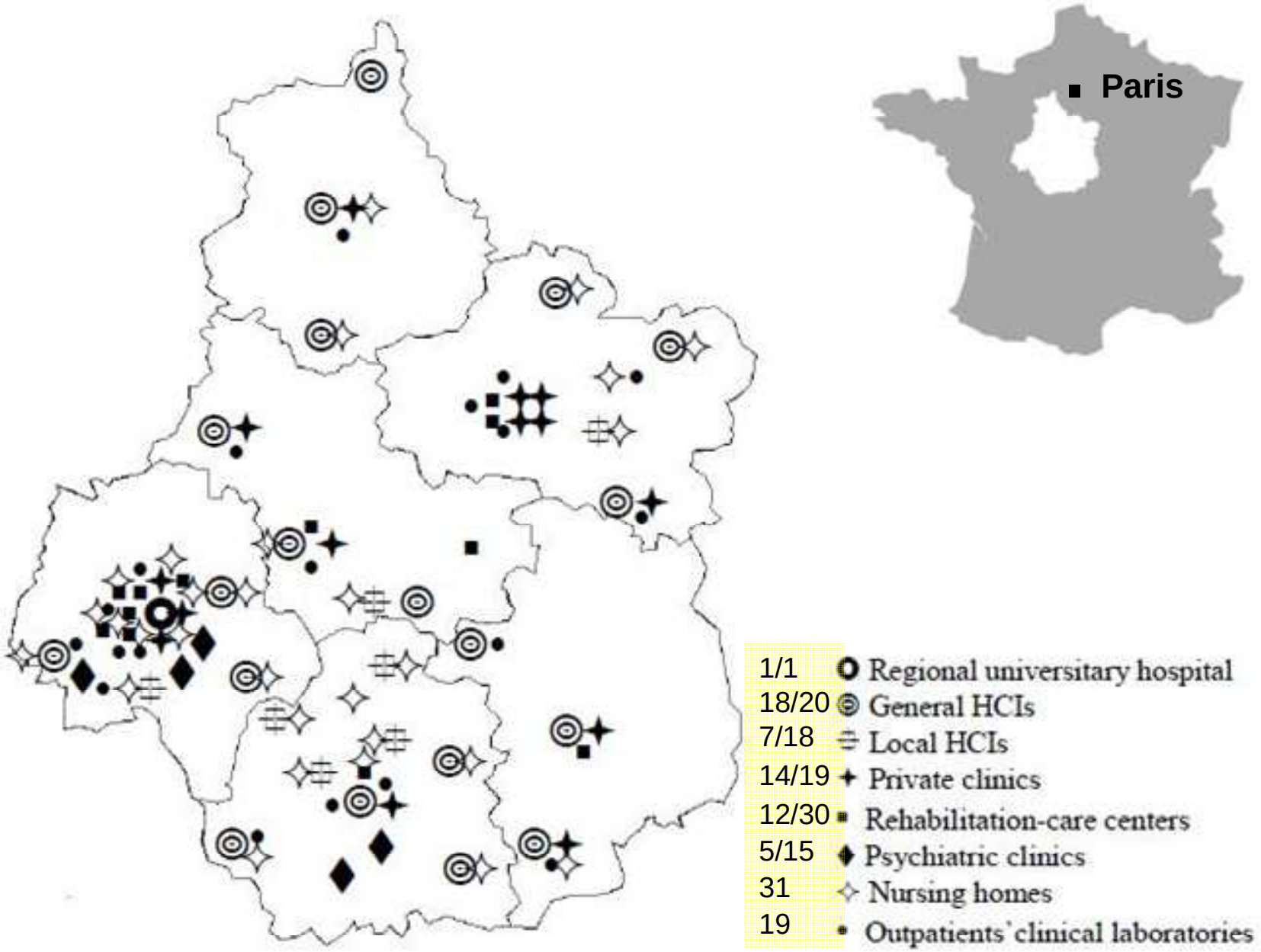
MDR organisms
Epidemiological study involving healthcare institutions, nursing homes and the community setting

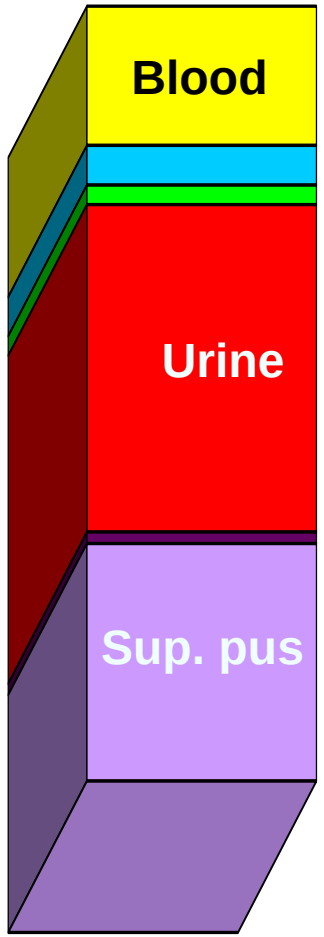

Paris
1/1 Regional universitary hospital
18/20 General HCIs
7/18 Local HCIs
14/19 Private clinics
12/30 Rehabilitation-care centers
5/15 Psychiatric clinics
31 Nursing homes
19 Outpatients' clinical laboratories

Objectives

- Evaluate precisely the epidemiological state of the spread of MDR organisms into the region Centre of France
- Epidemiological study involving HCIs and the community setting
- All infections caused by MDR organisms identified during the study period documented (15 days at least)
- Strains centralized and studied (antibiotic susceptibility and genetic diversity)

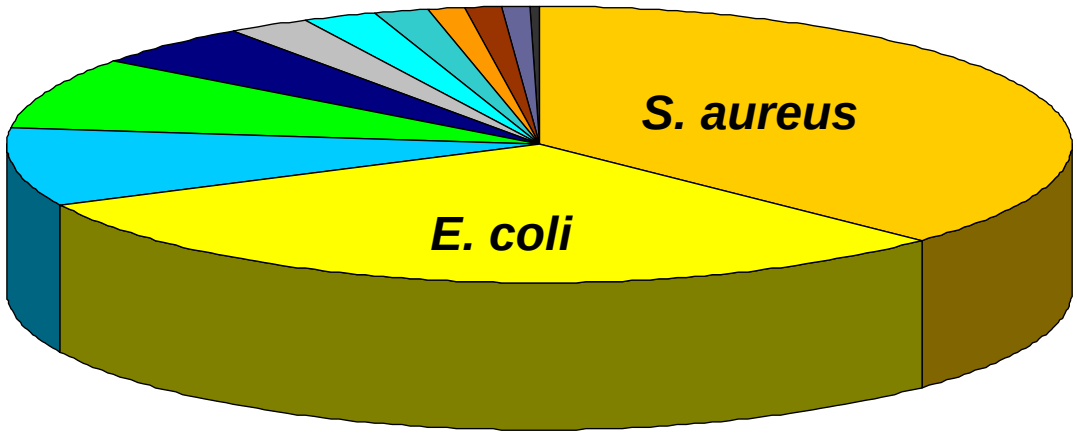
The study

- 346,251 patient-days
  - 164,008 in short-stay unit
  - 64,107 in rehabilitation care unit
  - 79,107 in long-stay unit
  - 38,869 in psychiatric unit
- 233,835 resident-days
- 43,379 diagnostic clinical samples
  - 7,564 blood cultures (17 %)
  - 2,130 deep pus (5 %)
  - 1,054 respiratory tract samples (2 %)
  - 17,768 urines (41 %)
  - 606 intravenous devices (1 %)
  - 12,889 superficial pus (30 %)

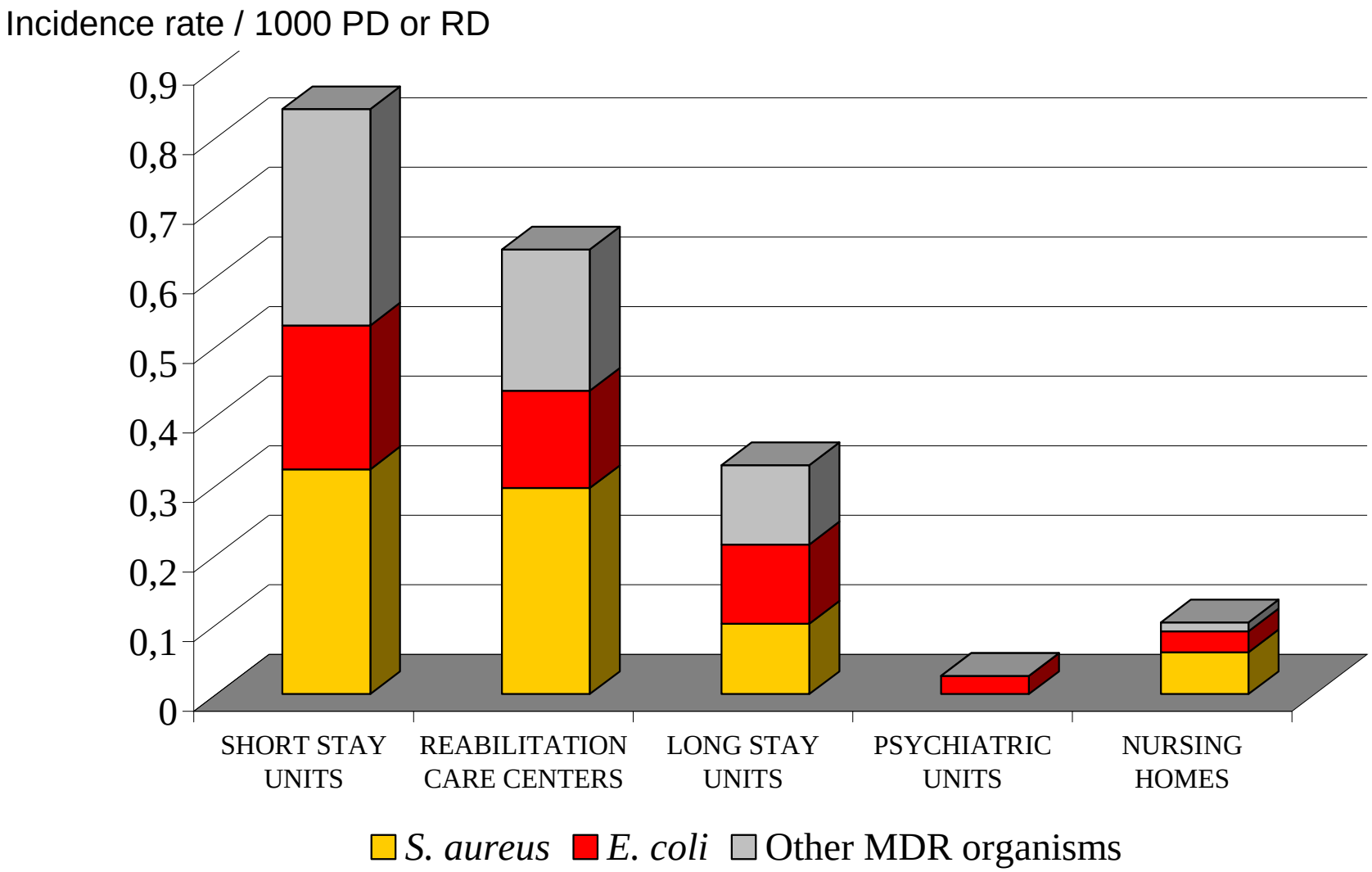


275 MDR organisms

- 12 different species
  - ***S. aureus* (103, 37%)**
  - ***E. coli* (84, 31%)**
  - **No VRE**
  - 25 *E. cloacae* (9 %)
  - 23 *P. aeruginosa* (8 %)
  - 13 *K. pneumoniae* (5%)
  - 7 *A. baumanii* (3%)
  - 6 *P. mirabilis* (2%)
  - 5 *C. freundii* (2%)
  - 3 *E. aerogenes* (1%)
  - 3 *C. koseri*
  - 2 *K. oxytoca*
  - 1 *K. ornithinolytica*

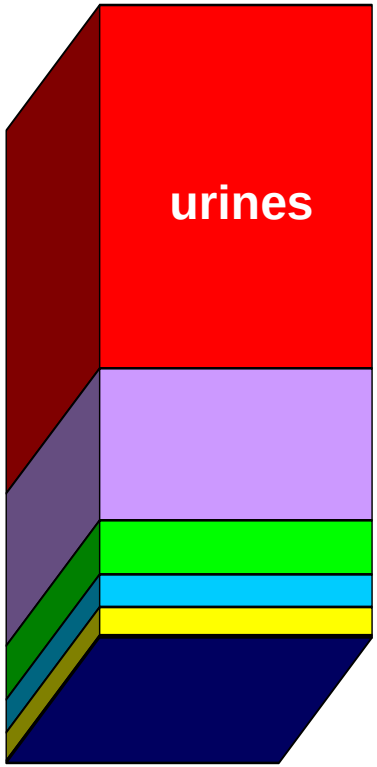


MDR organisms incidence rate



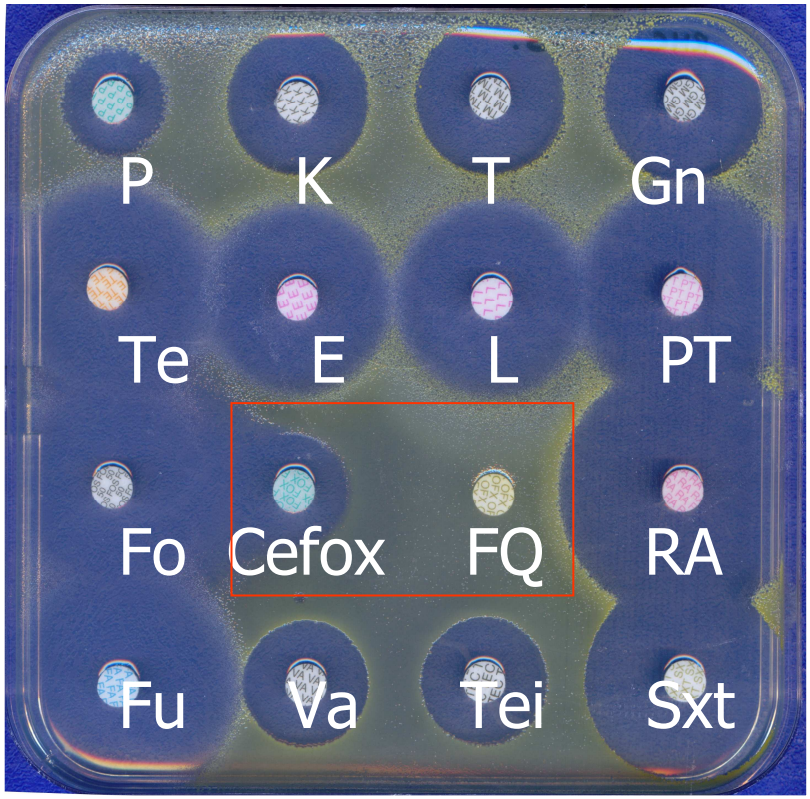
275 MDR organisms

- **155 (56%) from urine (p < 0.001)**
- 65 from superficial pus (24%)
- 23 from respiratory tract (8%)
- 14 from deep pus (5%)
- 12 from blood cultures (4%)
- one from IVD (< 1 %)
- 5 not known



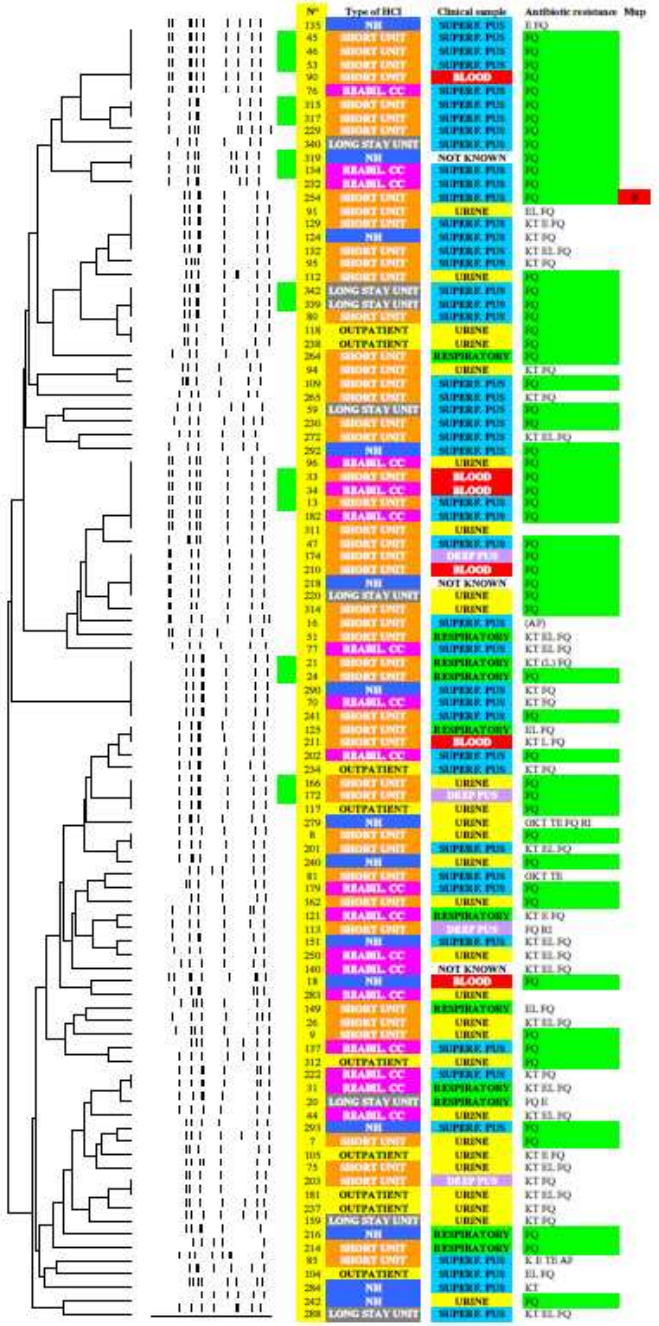
MRSA

- 71/103 “new clones” (69%)
- 57/103 FQ R-MRSA (55%)
- FQ R : 95/103 (92%)
- No GISA
- R to Mupirocin : 1/103 (1%)
- 4/103 *tst* gene +
- 1/103 *luk* genes +



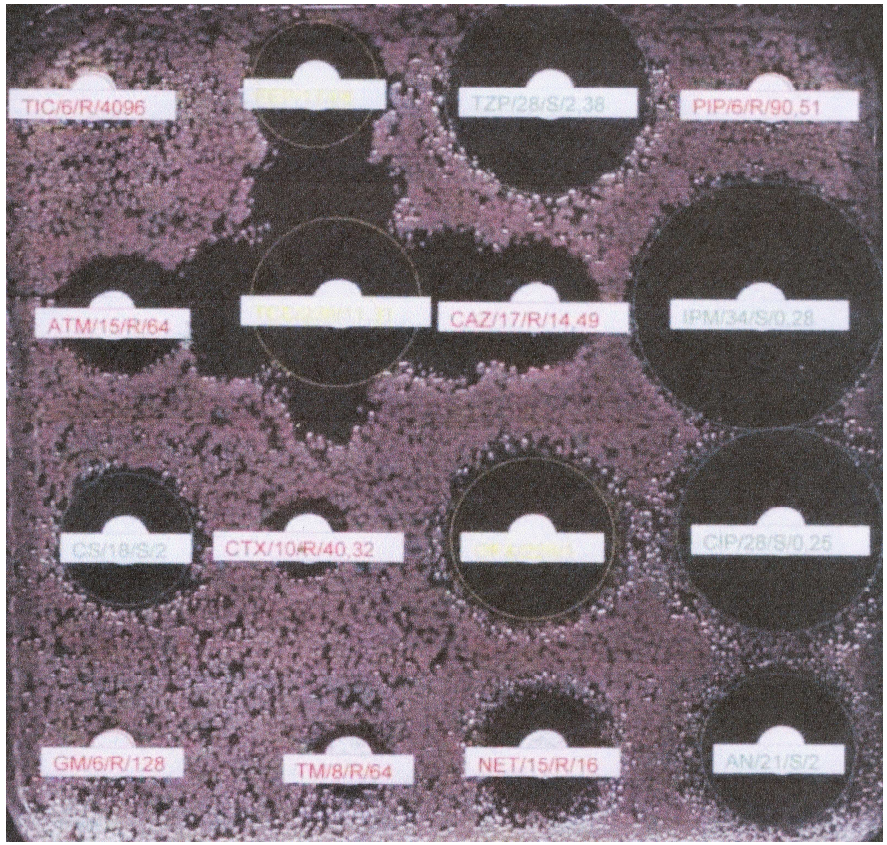
MRSA Genetic diversity

- 64 patterns /103 strains
- 1 NT
- 7 clusters
  - 6 with FQ R-MRSA
- ID $_{H\&G}$ 0.99
  - 0.97 for FQ R-MRSA
  - 0.99 for classical MRSA



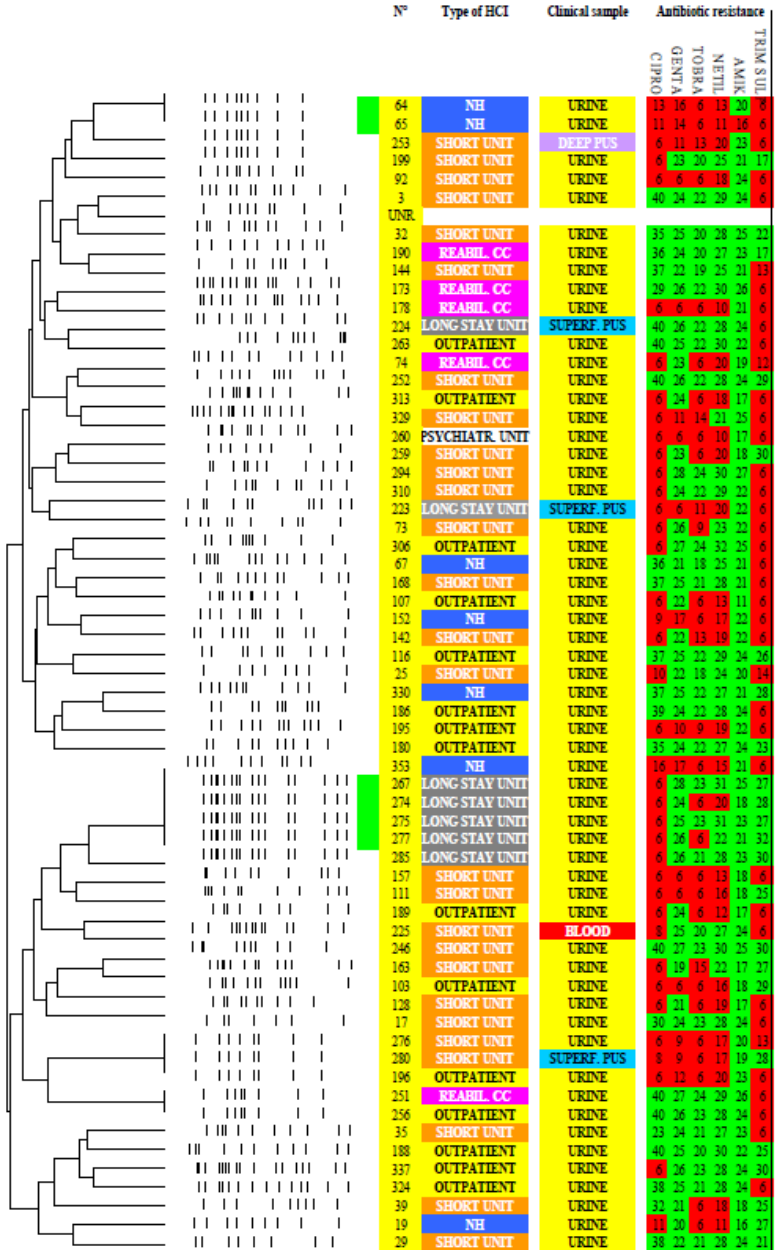
E. coli

- ESBL-producing : 66/84 (79%)
- 56/66 (85%) : CTX-M
- FQ R : 51/ 84 (61%)
  - 43/66 ESBL + (65 %)

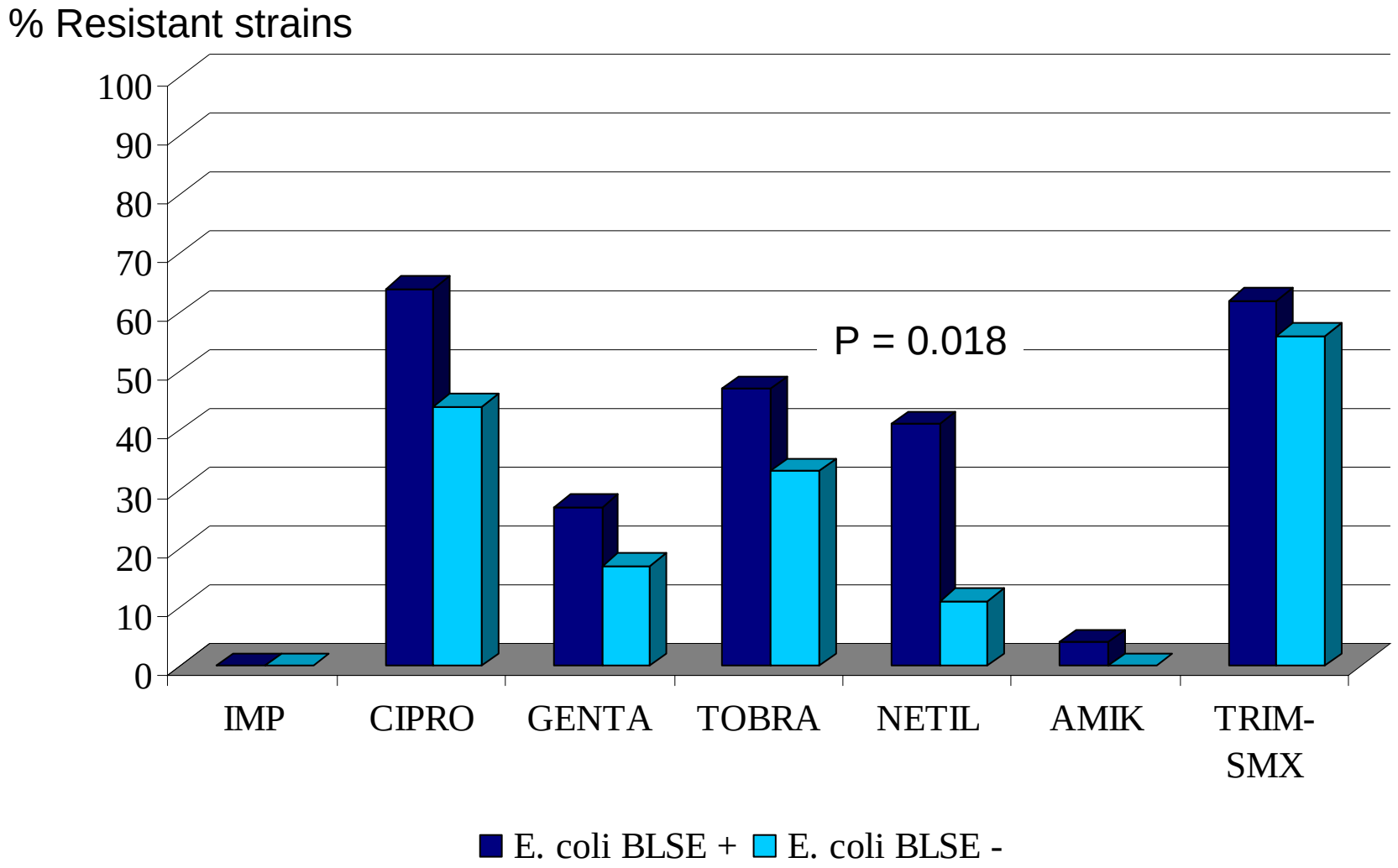


ESBL producing E. coli
Genetic diversity

- ✦53 patterns /63 strains
- ✦3 NT
- ✦2 clusters
  - ✦1 with CTX-M-15 ST131
- ✦ID $_{H\&G}$ 0.99



E. coli & Antibiotic resistance



Likely epidemic phenomenons

MRSA	*E. coli*	*E. cloacae*	*K. pneumoniae*	*A. baumannii*	*P. mirabilis*
7	4	2	1	1	1
4 Hospitals 1 Reab. C. Center	2 BLSE + 1 Hospital 1 NH 2 BLSE - 1 Hospital 1 Clinic	1 BLSE + 1 Hospital 1 BLSE - 1 Hospital	BLSE + 2 Hospitals 1 Reab. C. Center	BLSE - 1 Hospital	BLSE + 1 Hospital 1 NH Outpatients

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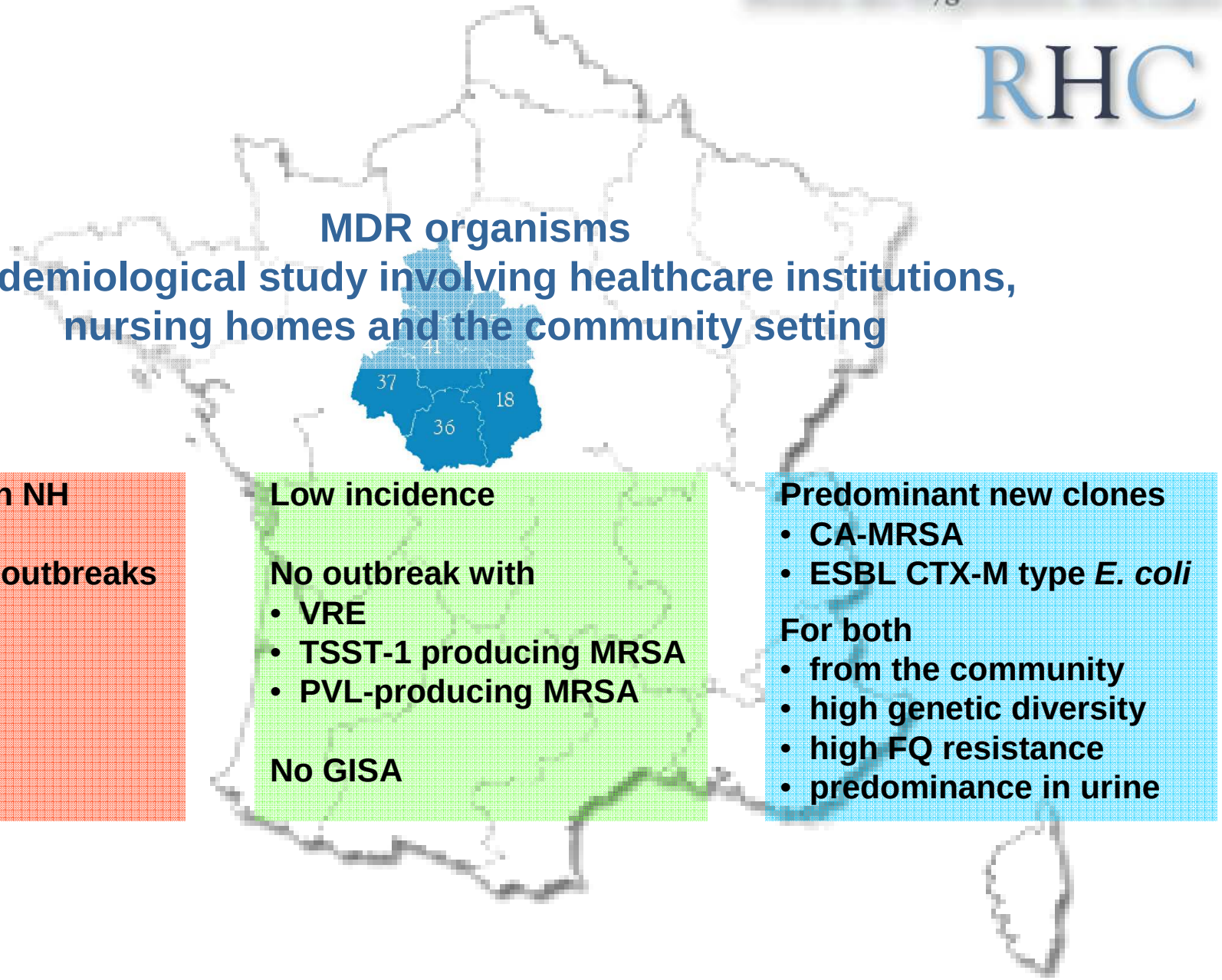

Spread in NH

16 likely outbreaks

Low incidence

No outbreak with
- **VRE**
- **TSST-1 producing MRSA**
- **PVL-producing MRSA**

No GISA

Predominant new clones
- **CA-MRSA**
- **ESBL CTX-M type *E. coli***

For both
- **from the community**
- **high genetic diversity**
- **high FQ resistance**
- **predominance in urine**

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