

# Prevalence of multi-resistant micro-organisms in the ambulatory setting in a Swiss region

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## Background

- Antibiotic resistance is increasing worldwide
- Prevalence of multiresistance is increasing in the ambulatory setting
- Surveillance of antibiotic resistance is a corner stone in resistance control
- Resistance data retrieved from routine microbiology may not reflect true resistance rates in outpatient care due to limited diagnostics

## Aims

- To describe the prevalence of resistance and multiresistance in urinary tract and skin isolates in outpatients
- To compare results with data from the passive resistance surveillance system ANRESIS ([www.anresis.ch](http://www.anresis.ch))

## Methods

- All general practitioners and dermatologists in the canton of Berne, Switzerland, were asked to send
  - wound swabs of patients with a purulent wound infection
  - urine samples of patients >15 years with urinary tract infection (UTI)
- Samples were designated "routine" for "would have been sent anyway" and "solicited" samples for "taken for study purpose only"
- Samples were analyzed at the ifik according to CLSI standards
- All wound swabs were screened for Methicillin-resistant *S. aureus* (MRSA)
- Extended spectrum beta-lactamase (ESBL) production was confirmed by the double-disk test
- Patients were included only once for skin infection. They could be included more than once for UTI, if the intervall between two episodes was >30 days

## Conclusion

- Susceptibility rates in *E. coli* were highest for fosfomycin and nitrofurantoin
- For UTI isolates solicited samples had higher susceptibility rates than routine samples. Therefore passive surveillance systems may not reflect resistance rates for all patient groups.
- Prior antibiotic therapy was a predictor for antibiotic resistance UTI.
- The prevalence of MRSA (2.1%) and ESBL (1.0%) is still rare in outpatients, and carriage is associated with classical risk factors for multiresistance.

## Abbreviation of antibiotics

|     |                             |     |                               |
|-----|-----------------------------|-----|-------------------------------|
| amc | amoxicillin-clavulanic acid | nfu | nitrofurantoin                |
| amp | ampicillin                  | nor | norfloxacin                   |
| cip | ciprofloxacin               | rif | rifampicin                    |
| cx  | cefuroxime axetil           | sxt | trimethoprim-sulfamethoxazole |
| ery | erythromycin                | tet | tetracycline                  |
| fos | fosfomycin                  |     |                               |

## Acknowledgment

We would like to thank all physicians for their participation in this study

## Results

### Wound swabs

- 213 skin samples were analyzed, 138 (65%) were culture positive
- Routine samples included a higher percentage of swabs from ulcers and from older patients and patients with prior antibiotic therapy
- Microorganisms did not differ significantly between groups

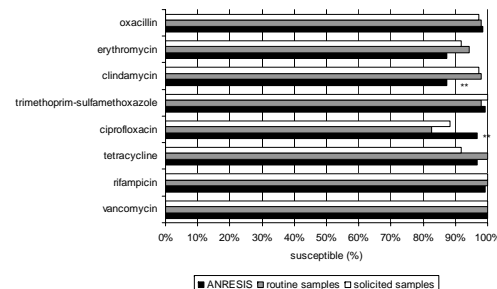
| n <sup>3)</sup> (samples)                            | solicited <sup>1)</sup> | routine <sup>1)</sup> | p-values <sup>2)</sup> | ANRESIS   |
|--|-------------------------|-----------------------|------------------------|-----------|
| age mean (SD) years                                  | 38(21)                  | 50 (23)               | <0.001                 | 49 (50)   |
| females n (%)  | 40 (48)                 | 60 (53)               | ns                     | 84 (50)   |
| rural n (%)  | 20 (24)                 | 28 (25)               | ns                     | 61 (36)   |
| clinical information n (%)                           |                         |                       |                        |           |
| abscess or folliculitis                              | 47 (56)                 | 51 (45)               | ns                     | -         |
| ulceration   | 3 (3.6)                 | 17 (15)               | 0.016                  | -         |
| wound infection                                      | 22 (26)                 | 27 (24)               | ns                     | -         |
| impetigo   | 7 (8.3)                 | 10 (8.8)              | ns                     | -         |
| antibiotics in last 3 months                         | 6 (7.1)                 | 29 (26)               | 0.002                  | -         |
| known MRSA   | 1 (1.2)                 | 3 (2.7)               | ns                     | -         |
| long term facility                                   | 3 (3.6)                 | 6 (5.3)               | ns                     | -         |
| culture positive n (%)                               | 54 (65)                 | 73 (64)               | ns                     | 169 (100) |
| microbiology n (% of positive samples) <sup>4)</sup> |                         |                       |                        |           |
| monobacterial infections                             | 42 (78)                 | 59 (81)               | ns                     | 148 (88)  |
| <i>Staphylococcus aureus</i>                         | 35 (55)                 | 52 (61)               | ns                     | 127 (67)  |
| <i>Streptococcus pyogenes</i>                        | 5 (7.8)                 | 3 (3.5)               | ns                     | 0 (0)     |
| coagulase-negative <i>Staphylococci</i>              | 1 (1.6)                 | 2 (2.4)               | ns                     | 14 (7.4)  |
| other gram-positive cocci                            | 7 (11)                  | 11 (13)               | ns                     | 7 (3.7)   |
| enterobacteriaceae                                   | 8 (13)                  | 9 (11)                | ns                     | 29 (15)   |
| other gram-negative rods                             | 7 (11)                  | 7 (8.2)               | ns                     | 12 (6.3)  |
| anaerobes  | 1 (1.6)                 | 1 (1.2)               | ns                     | 0 (0)     |

<sup>1)</sup> 16 samples excluded, because assignment to solicited or routine samples was not possible  
<sup>2)</sup> ns=not significant  
<sup>3)</sup> demographic data was missing in 16 (age), 6 (sex) and 8 (geography) samples. Missing samples were distributed equally between solicited and routine samples.  
<sup>4)</sup> For clinical data missing values were interpreted as "no". Excluding missing clinical data from analysis had no influence on p-values.  
<sup>5)</sup> all microorganisms detected including dual and triple infections

### Staphylococcus aureus susceptibility

- 2/94 (2.1%) *S. aureus* isolates were MRSA. Both were susceptible to ery, cip, sxt, tet and rif; both patients showed risk factors for MRSA colonisation (long hospitalisation, MRSA known in family members)
- Susceptibility rates for *S. aureus* did not differ significantly between routine and solicited samples

Susceptibility of *S. aureus* (%) in solicited, routine and ANRESIS samples



\*\* significant difference (p<0.05) between routine samples and ANRESIS data

### Urinary samples

- 1018 urinary samples were collected, 68% were culture positive
- Solicited samples included a high proportion of young females without prior antibiotic exposure, living in urban regions
- The proportion of *E. coli* was highest among solicited samples

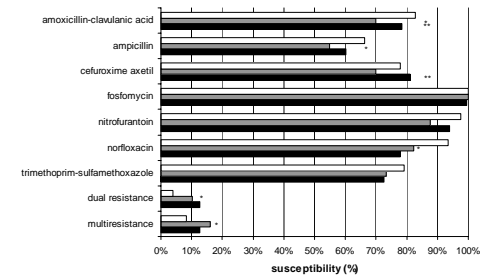
| n <sup>3)</sup> (samples)                            | solicited <sup>1)</sup> | routine <sup>1)</sup> | p-values <sup>2)</sup> | ANRESIS    |
|--|-------------------------|-----------------------|------------------------|------------|
| age mean (SD) years                                  | 48.3 (22)               | 55.7 (23)             | <0.001                 | 56.6 (25)  |
| females n (%)  | 358 (84)                | 409 (78)              | 0.006                  | 742 (71)   |
| rural n (%)  | 128 (29)                | 212 (40)              | 0.001                  | 329 (31)   |
| clinical information n (%)                           |                         |                       |                        |            |
| antibiotic exposure during last 3 months             | 48 (11)                 | 228 (43)              | <0.001                 | -          |
| bladder catheter                                     | 21 (4.9)                | 36 (6.9)              | ns                     | -          |
| known ESBL carrier                                   | 2 (0.5)                 | 8 (1.5)               | ns                     | -          |
| long term facility                                   | 11 (2.6)                | 38 (7.2)              | 0.002                  | -          |
| culture positive                                     | 305 (71)                | 348 (66)              | ns                     | 1046 (100) |
| microbiology n (% of positive samples) <sup>4)</sup> |                         |                       |                        |            |
| <i>Escherichia coli</i>                              | 231 (76)                | 232 (67)              | 0.01                   | 685 (66)   |
| <i>Klebsiella</i> spp.                               | 13 (4.3)                | 22 (6.3)              | ns                     | 93 (8.9)   |
| <i>Proteus mirabilis</i>                             | 10 (3.3)                | 14 (4.0)              | ns                     | 41 (3.9)   |
| other <i>Enterobacteriaceae</i>                      | 16 (5.2)                | 17 (4.9)              | ns                     | 83 (7.9)   |
| <i>Enterococcus</i> spp.                             | 61 (20)                 | 52 (15)               | ns                     | 33 (3.2)   |
| <i>Staphylococcus saprophyticus</i>                  | 10 (3.3)                | 17 (4.9)              | ns                     | 14 (1.3)   |
| other  | 16 (5.2)                | 34 (9.8)              | ns                     | 163 (16)   |

<sup>1)</sup> 65 samples excluded, because assignment to solicited or routine samples was not possible  
<sup>2)</sup> ns=not significant  
<sup>3)</sup> demographic data was missing in 77 (age), 64 (sex) and 10 (geography) samples. Missing samples were distributed equally between solicited and routine samples.  
<sup>4)</sup> For clinical data missing values were interpreted as "no". Excluding missing clinical data from analysis had no influence on p-values.  
<sup>5)</sup> all microorganisms detected including dual and triple infections

### Escherichia coli susceptibility

- Susceptibility rates were higher in solicited than in routine samples for all antibiotics tested except for fosfomycin
- Multiresistance (resistance to at least 3 out of amc, cxa, nor or sxt) was significantly lower in solicited samples
- Resistance data from passive surveillance were comparable to routine samples for most antibiotics
- 5 ESBL producing *E. coli* (1.0% of *E. coli* isolates) were identified. 4/5 had known risk factors for ESBL carriage
- Antibiotic exposure was the only predictor for antibiotic resistance

Susceptibility of *E. coli* (%) in solicited, routine and ANRESIS samples



\* significant difference (p<0.05) between routine samples and solicited samples,  
 \*\* significant difference (p<0.05) between routine samples and ANRESIS data