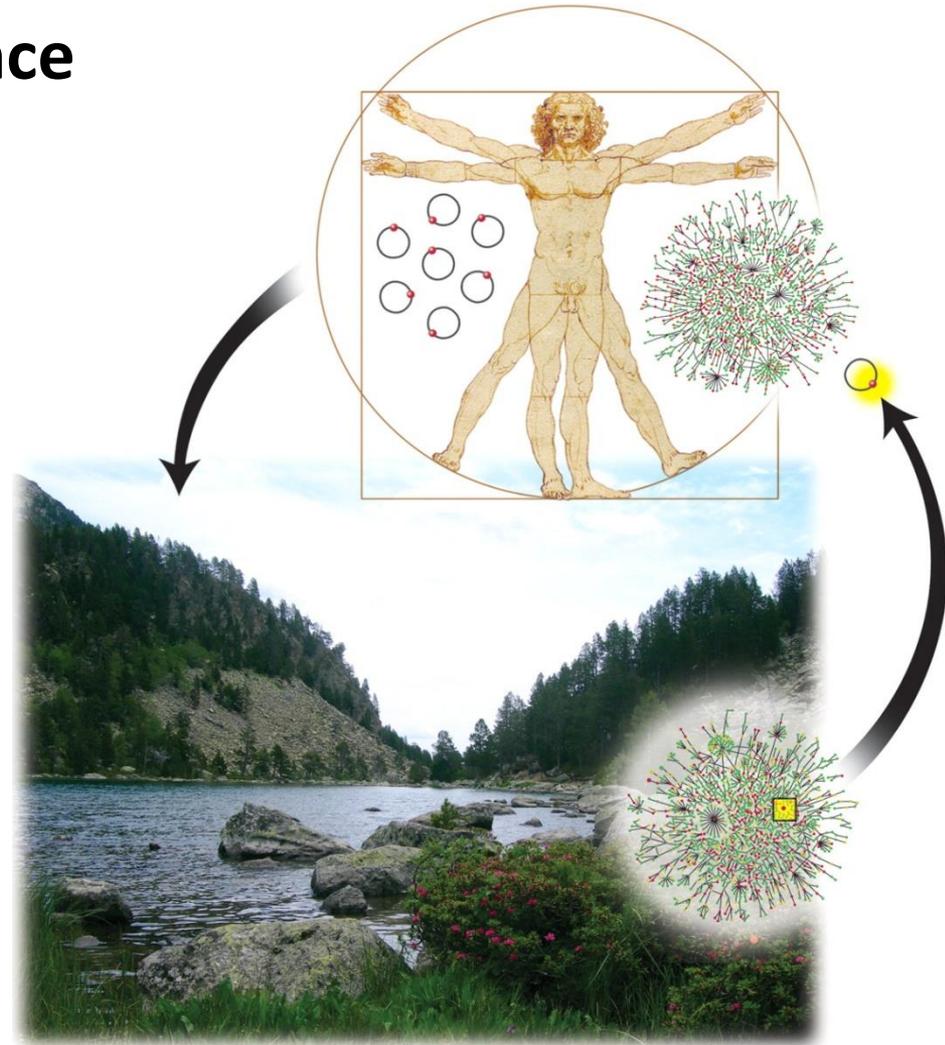


Ecology of Antibiotic Resistance

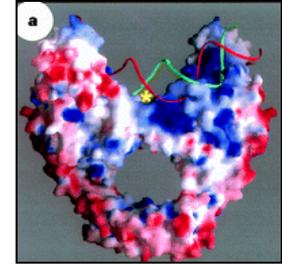
Wolfgang Witte, RKI-Fellow



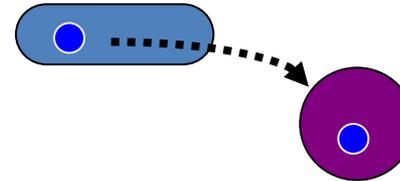
(J. Martinez, Science 2008; 231: 366-367).

Genetic events

- Mutations; e.g. alteration of targets
- Horizontal transfer of resistance genes



homologous T
transfer



heterologous
transfer

Selective pressure :

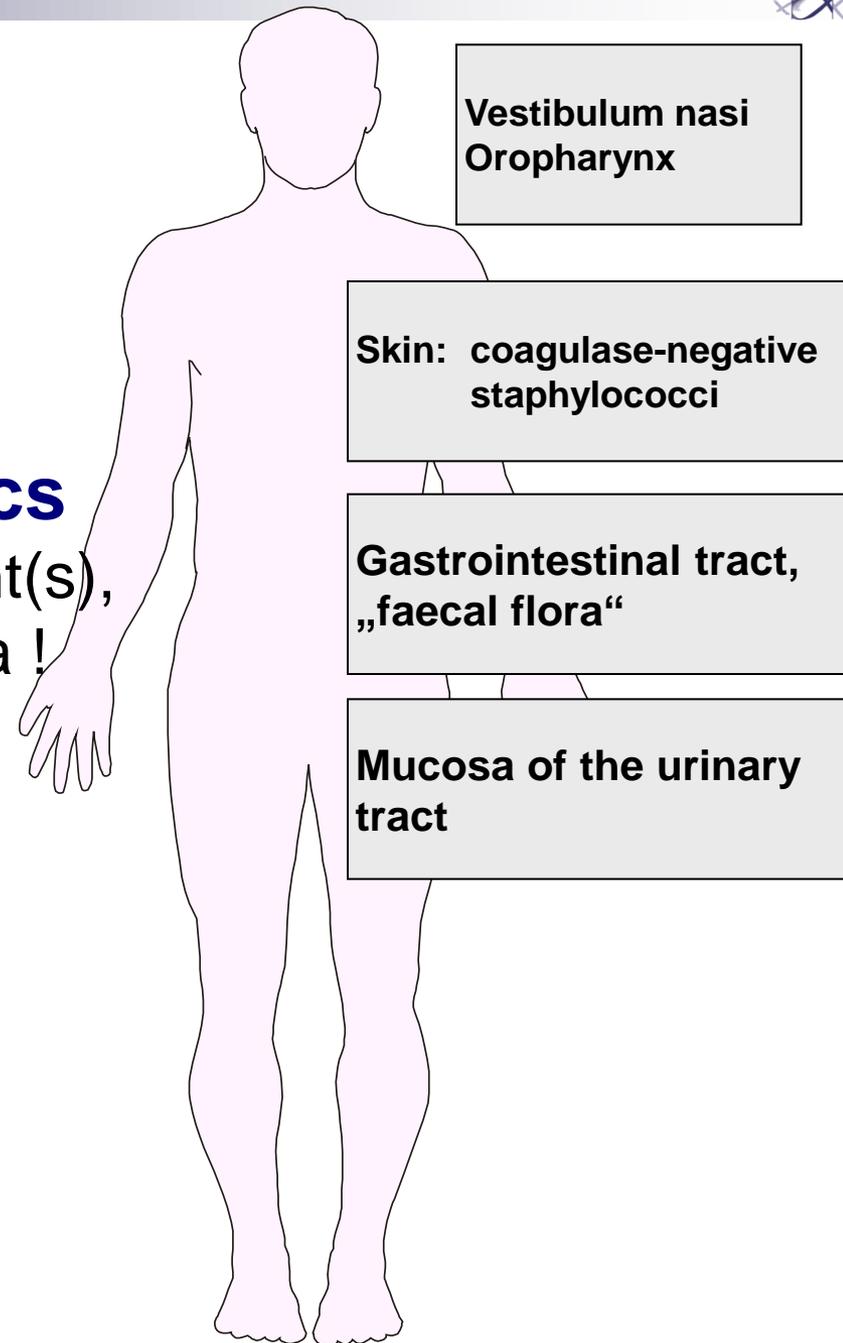
Antibiotics in soil (antibiotii a producers); usage in
human- und veterinary medicin

„Newcomers“ as colonizer

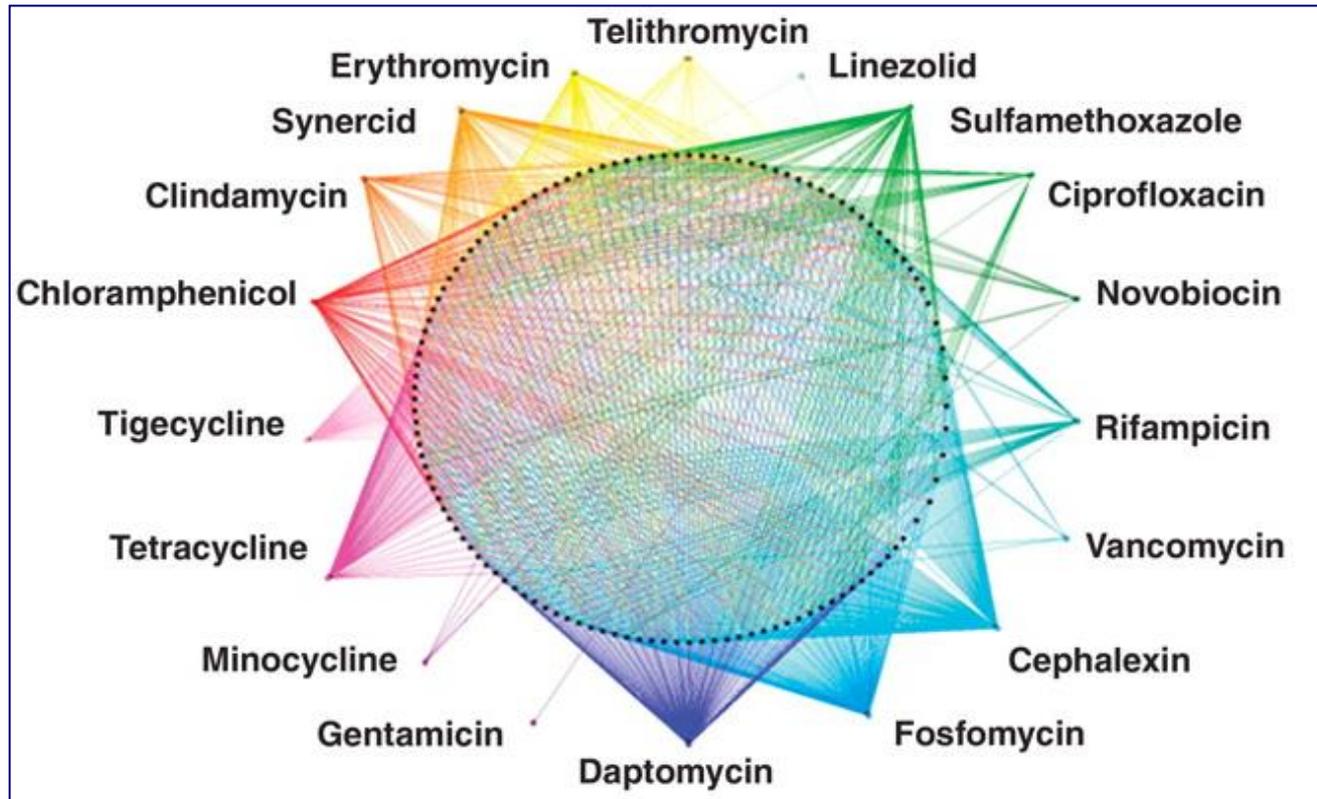
Natural epitopes und microbiota,
Competing microflora

Selective pressure, antibiotics

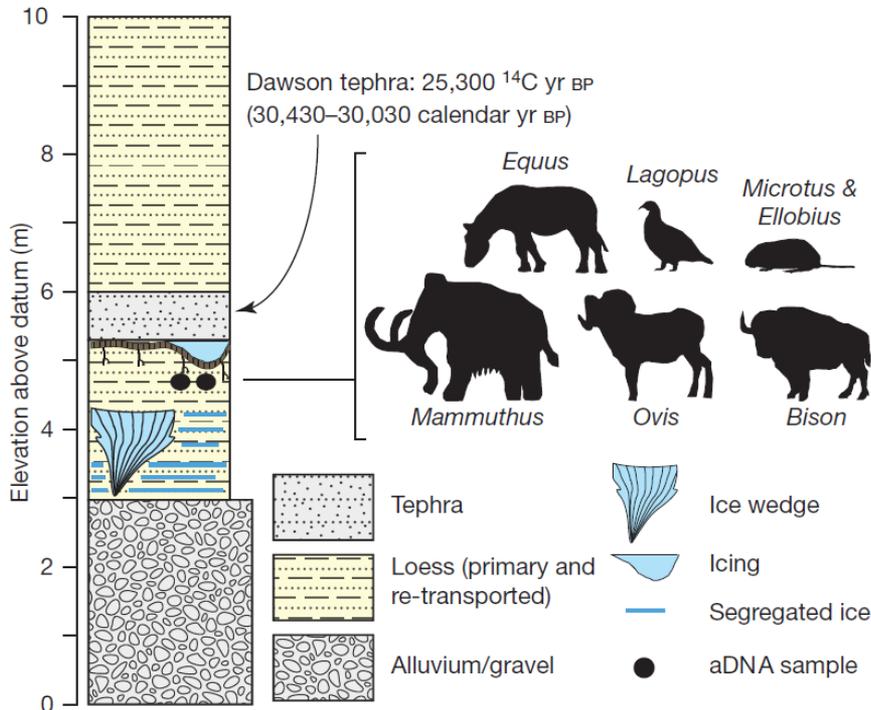
Not only against the infectious agent(s),
always against colonizing microflora !



The unexhaustable reservoir of antibiotic resistance genes



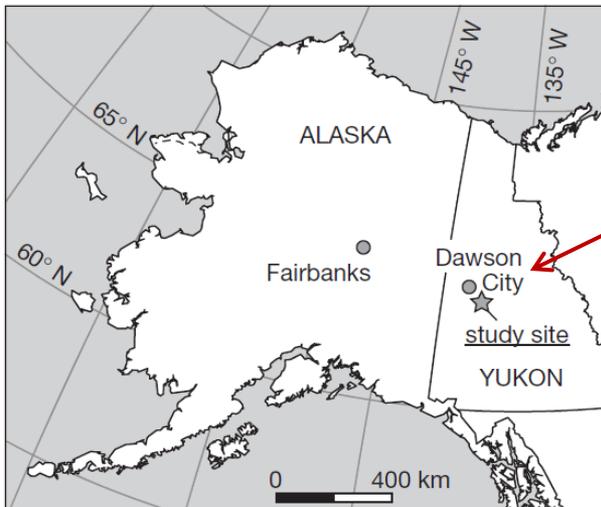
Schematisches Diagramm der phänotypischen Diversität von Antibiotikaresistenz bei Boden-Bakterien. Es gibt bereits Resistenzen gegen das breit wirksame Tigecyclin, das noch gar nicht therapeutisch eingesetzt wird.



From D`Costa et al.,
Antibiotic resistance is ancient,
Nature, 2011:477: 457.



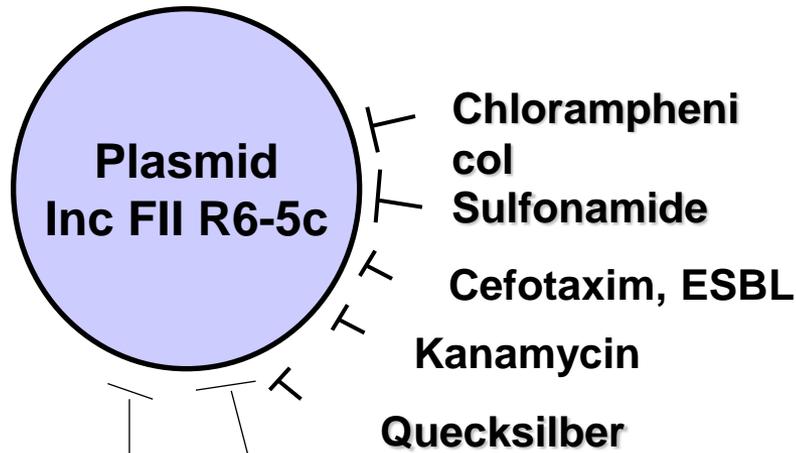
Dawson City



Metagenomic analysis of samples from permafrost soil in Alaska from a depth which corresponds to the age of ~ 27.000 years. demonstration and phylogenetic analysis of antibiotic – resistance genes

Mobile genetic elements containing antibiotic resistance genes

Plasmids



Transposons

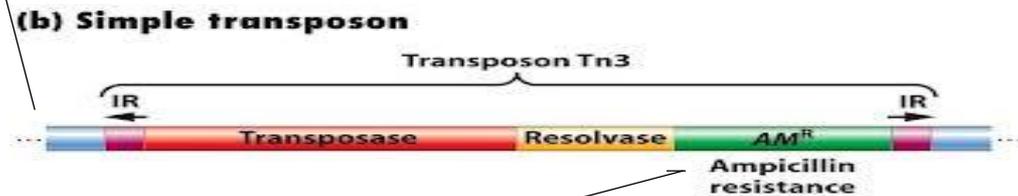
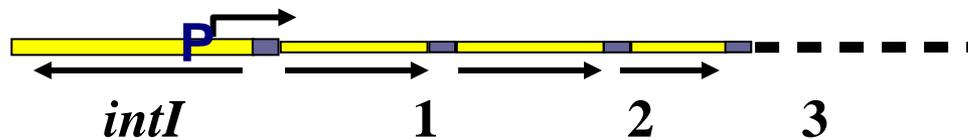
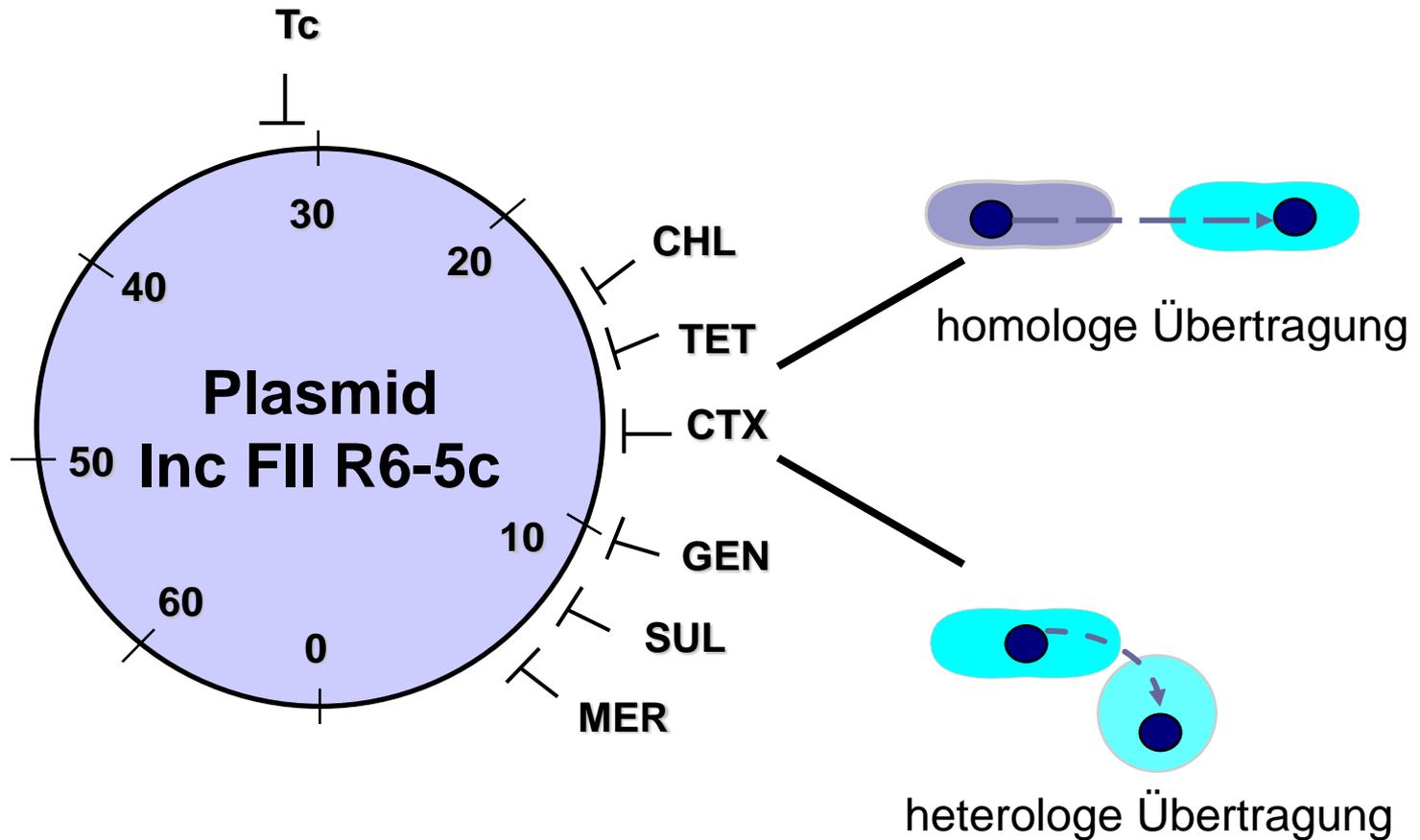


Figure 14-5
Introduction to Genetic Analysis, Ninth Edition
© 2008 W. H. Freeman and Company

Integrans





Location of resistance genes on a multiresistance plasmid and transfer to homologous and heterologous bacterial cells.

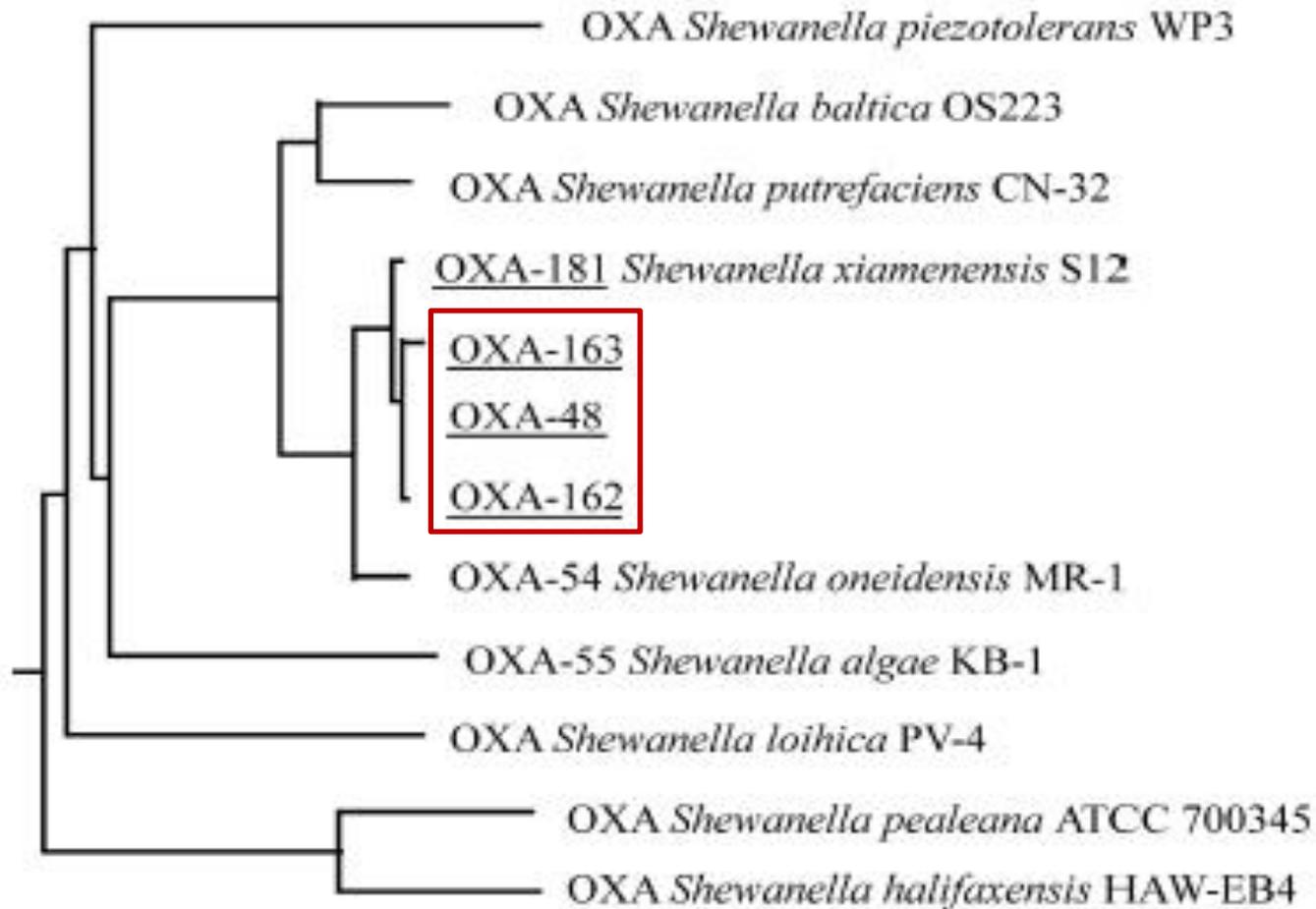
Resistenzgene: TET gegen Tetracyclin (Transportprotein), CHL gegen Chloramphenicol (Acetylase), CTX gegen Cephotoxim GEN gegen Gentamicin (Phosphorylase), SUL gegen Sulfonamide (Dihydropteroinsäure-Synthetase, MER gegen Quecksilbersalze (Hg-Reductase).

Classical examples for the acquisition of resistance genes by bacteria colonizing and infecting humans and other animals from environmental bacteria

1. Antibiotikc producers: (Julian Davies, Patrice Corvalin)
 - 23SrRNA methyltransferases and MLS –resistance , *erm* -genes
 - Aminoglykoside-modifying enzymes
(Acetyltransferases, Adenyltransferasen, Phosphotransferases)
2. Environmental bacteria
 - Carbapenemases (*Stenotrophomonas spp.*, *Stenotrophomonas spp.*)
 - ESBL of the CTX-M-type ,(*Kluyvera spp.*)

Relatedness of class-D-carbapenemases from enterobacterial species and from *Shewanella* spp.

Potron et al. AAC 53;9: 4405-7

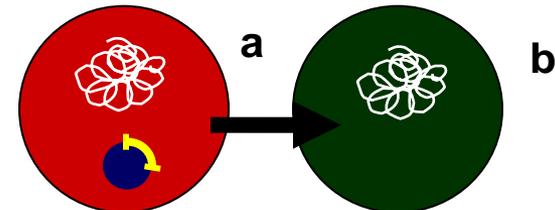


Spread of antibiotic resistance

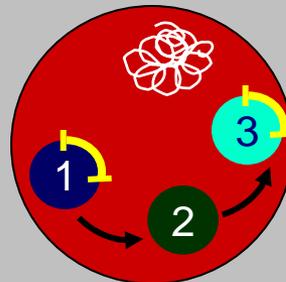
Clonal dissemination of resistant strains
(e.g., MRSA, resistant *S. pneumoniae*)

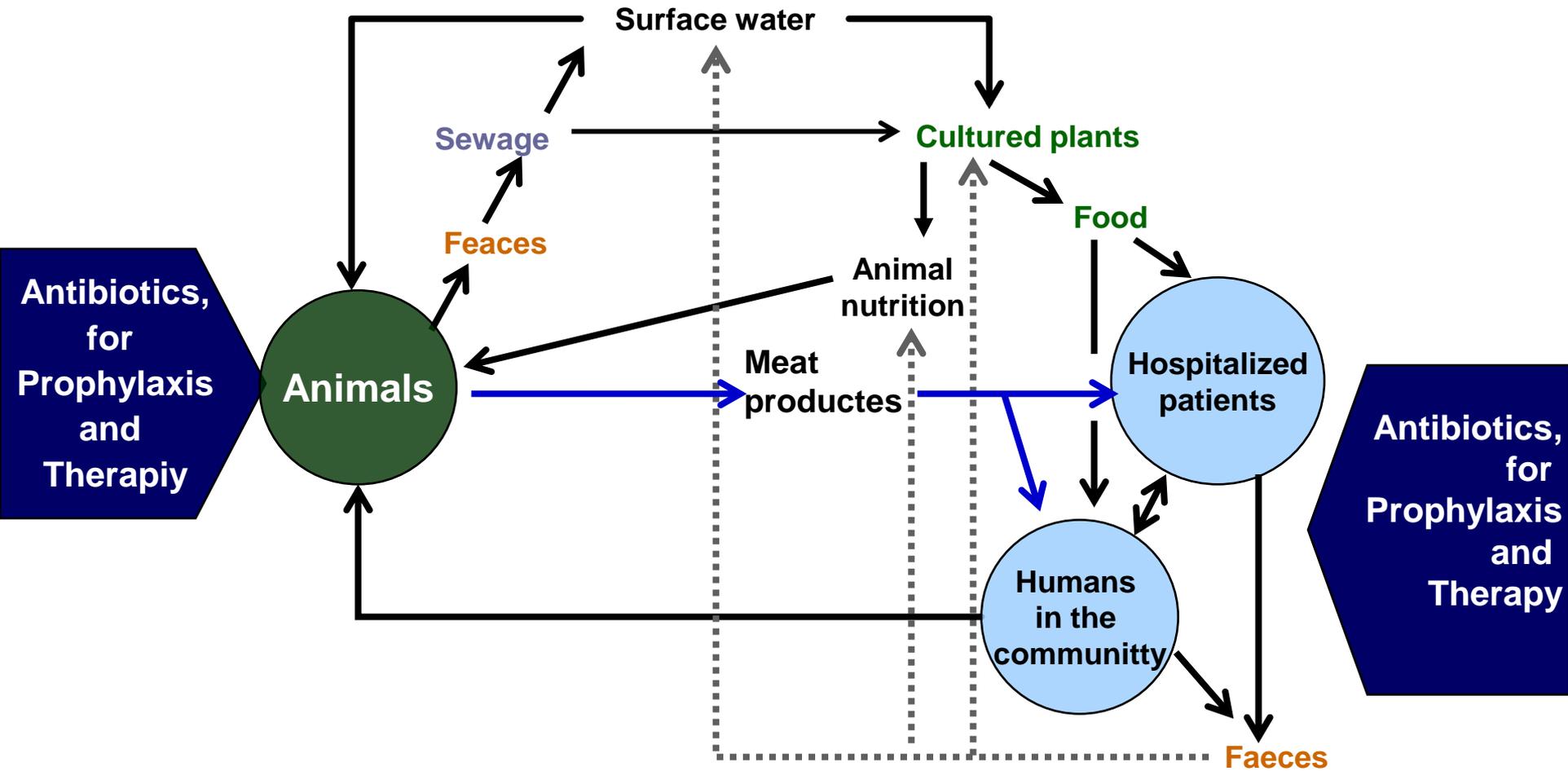


Horizontal spread of R-Plasmids
Between different strains



Horizontal spread of
resistance genes among
Different plasmids

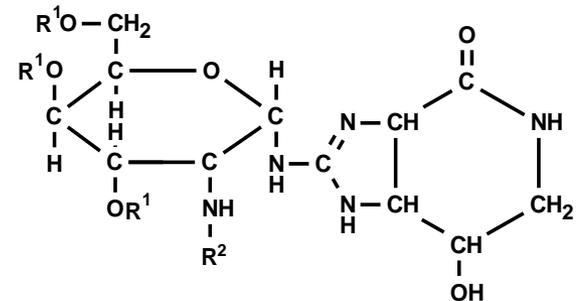




Witte, W., Science; 1998;279(5353):996-7.

Spread of transferable antibiotic resistance between different ecosystems

The antibiotic Nourseothricin as growth promoter for livestock



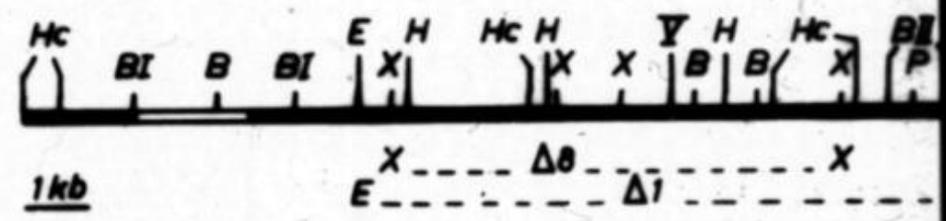
The streptothricin-antibiotic nourseothricin was exclusively used as growth promoter in conventional livestock from 1980 bis 1989 as replacement for oxytetracycline. There was no use for other purposes.

The emerging resistance mechanism (Acetyltransferase) did not confer cross resistance to other antibiotics.

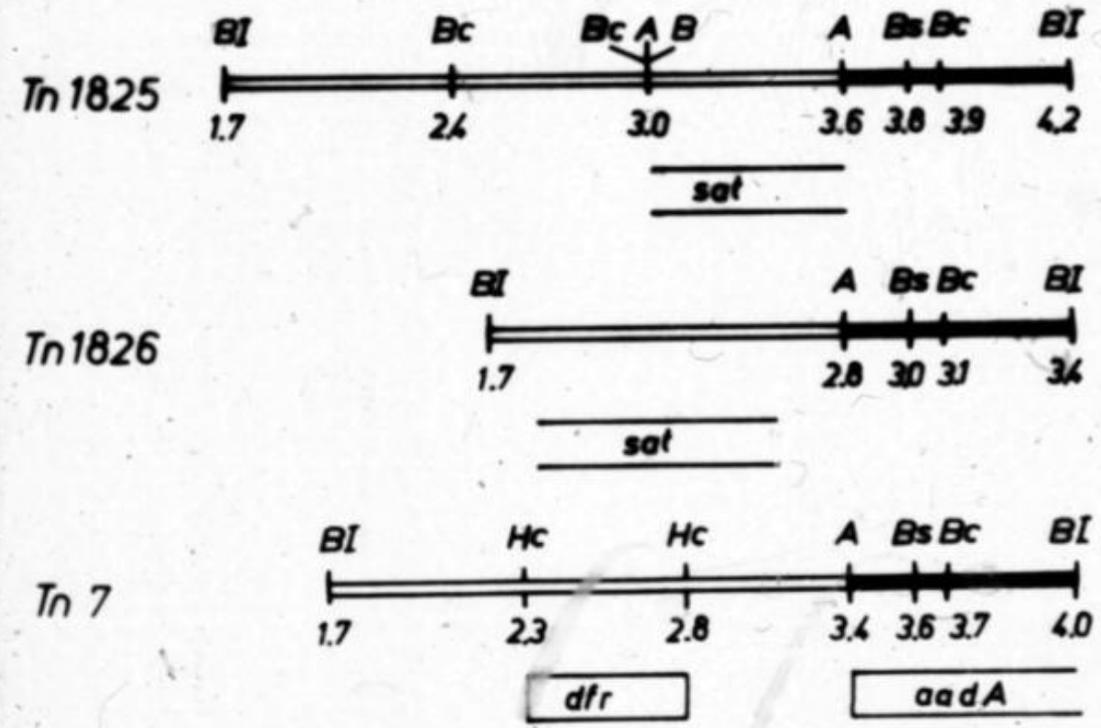
The resistance gene (*sat4*) is located at a transposon and transferable.

1a

St Sm/Sp ... Transposition ...



1b



Wide dissemination of sat-1 coded streptothricin resistance (sat-1 in a gene cassette on transposons of Tn7 family) in former East Germany

	1982	1983	1984	1985	1986	1987
<i>E. coli</i> , faecal flora of nourseothricin fed pigs	-	+	+	+	+	+
<i>E. coli</i> , faecal flora of pig from personnel	-	-	+	+	+	+
<i>E. coli</i> , faecal flora, family members of pig attendants	-	-	+	+	+	+
<i>E. coli</i> , gut flora of healthy adults (also in urban communities)	-	-	-	+	+	+
<i>E. coli</i> , urinary tract infections in humans	-	-	-	+	+	+
<i>Shigella sonnei</i> , diarrhoea in humans	-	-	-	-	-	+

Hummel R, Tschäpe H, Witte W., J Basic Microbiol. 1986;26(8):461-6.

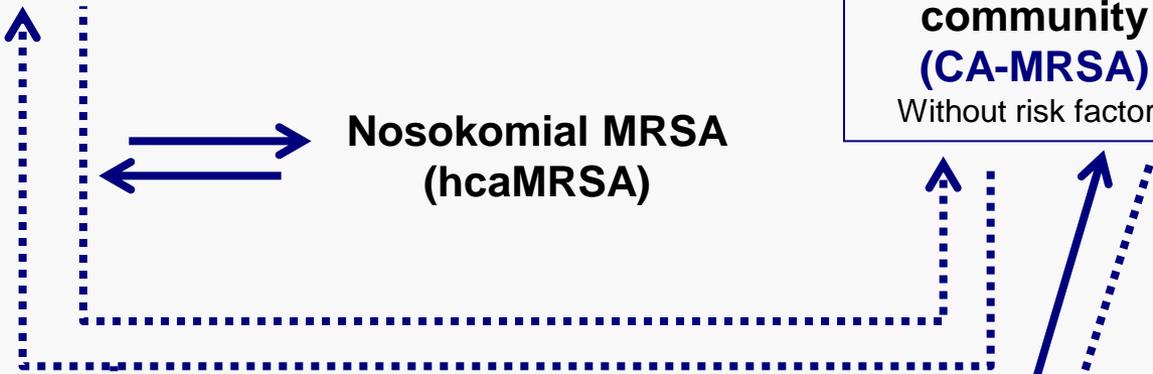
MRSA: definitions according to epidemiological origin

„Wenn die Begriffe nicht klar sind, breitet sich Unordnung aus“ Konfuzius

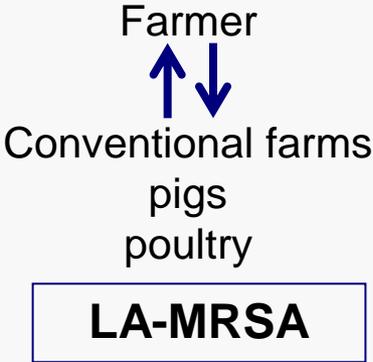
MRSA in humans:

**MRSA in hospitals
nosokomial MRSA
(HA-MRSA)**

**MRSA in the community
(CA-MRSA)**
Without risk factors



MRSA in animals:



Transmission of LA-MRSA to humans

Conventinal farm



Humans with occupational exposition
(farmers, vet`s)
70 – 86 % colonized



Familiar surroundigs

.....>
Family members
4 - 5% colonized)

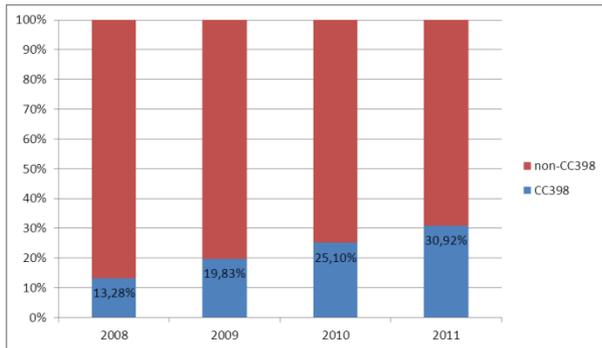
Humans in agricultural areas

Admission to hospitals
2,8% of all MRSA from nosocomial infections in DE)



Demonstration of LA-MRSA at hospital admission

Region Münsterland

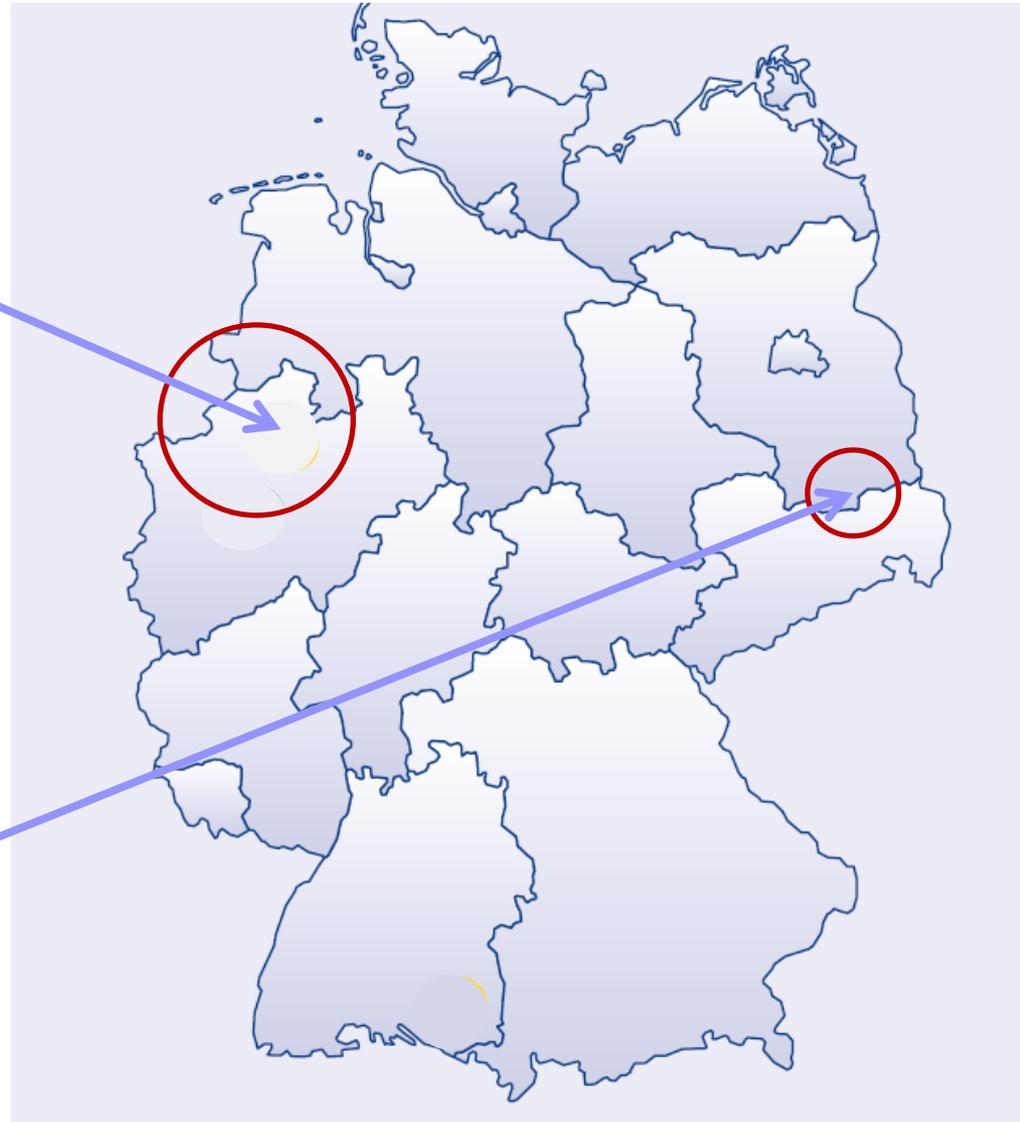


9414 Patienten,
 MRSA-Nachweise insgesamt : 1,6 %
 Anteil LA-MRSA: ~ 30 %
LA-Nachweise insgesamt: 0.48 %

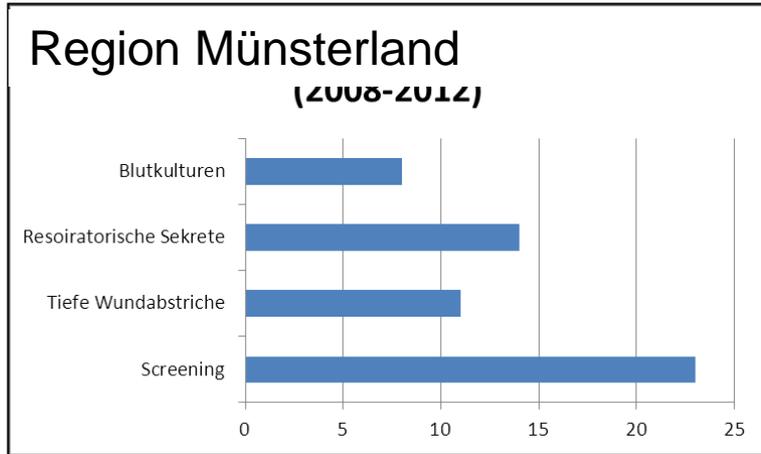
Köck et al., 2012, Plos One 2013
 Schaumburg JCM 2012;

Daten aus dem MRSA-Netzwerk Südbrandenburg (13855 Patienten)

MRSA Nachweise insgesamt: 0.78 %
 Anteil an LA-MRSA: 10.8 %
LA-MRSA-Nachweise insgesamt: 0.08 %



Proportion of LA-MRSA among all MRSA from nosocomial infections



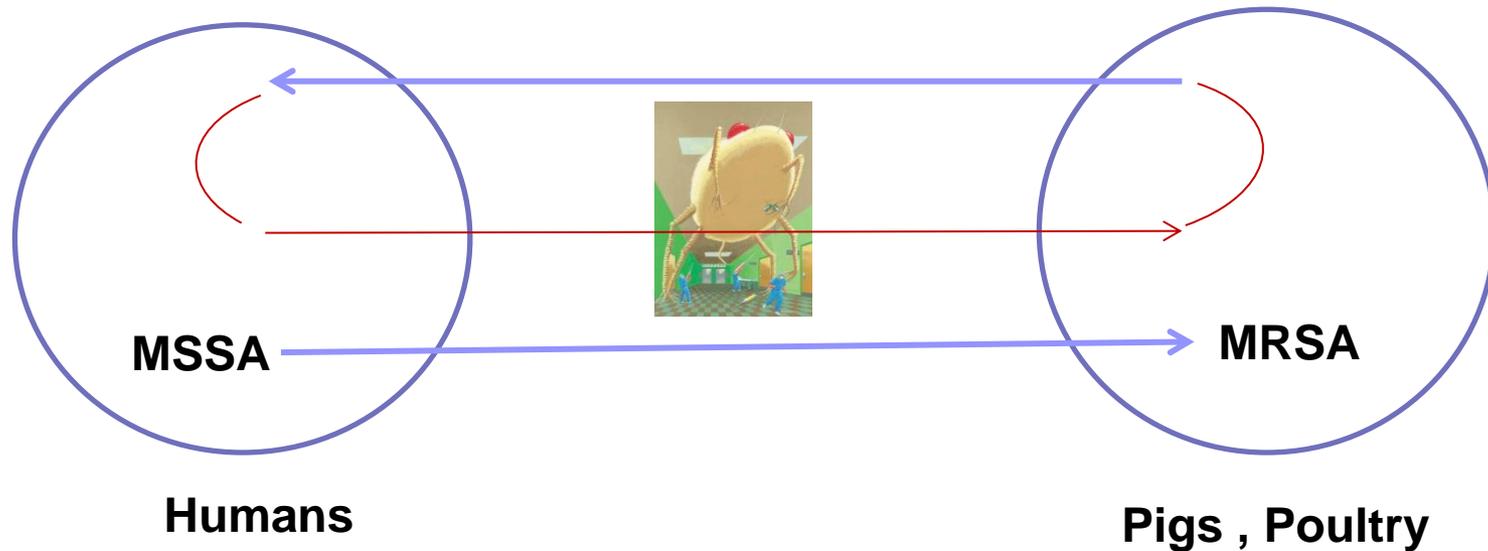
Köck; Plos One 2013
 Schaumburg JCM 2012;



Bundesrepublik Deutschland, insgesamt:
2 – 3%, dabei 1,8 % aus Blutkulturen
 NRZ f. Staphylokokken u. Enterokokken
 Layer et al., Epi.Bull., 2013

STAPHYLOCOCCUS AUREUS /MRSA FROM HUMANS TO ANIMALS AND BACK TO HUMANS

Acquisition of IEC, „readaptation“, 2011,
Further virulence genes ?, *luk-PV* ?



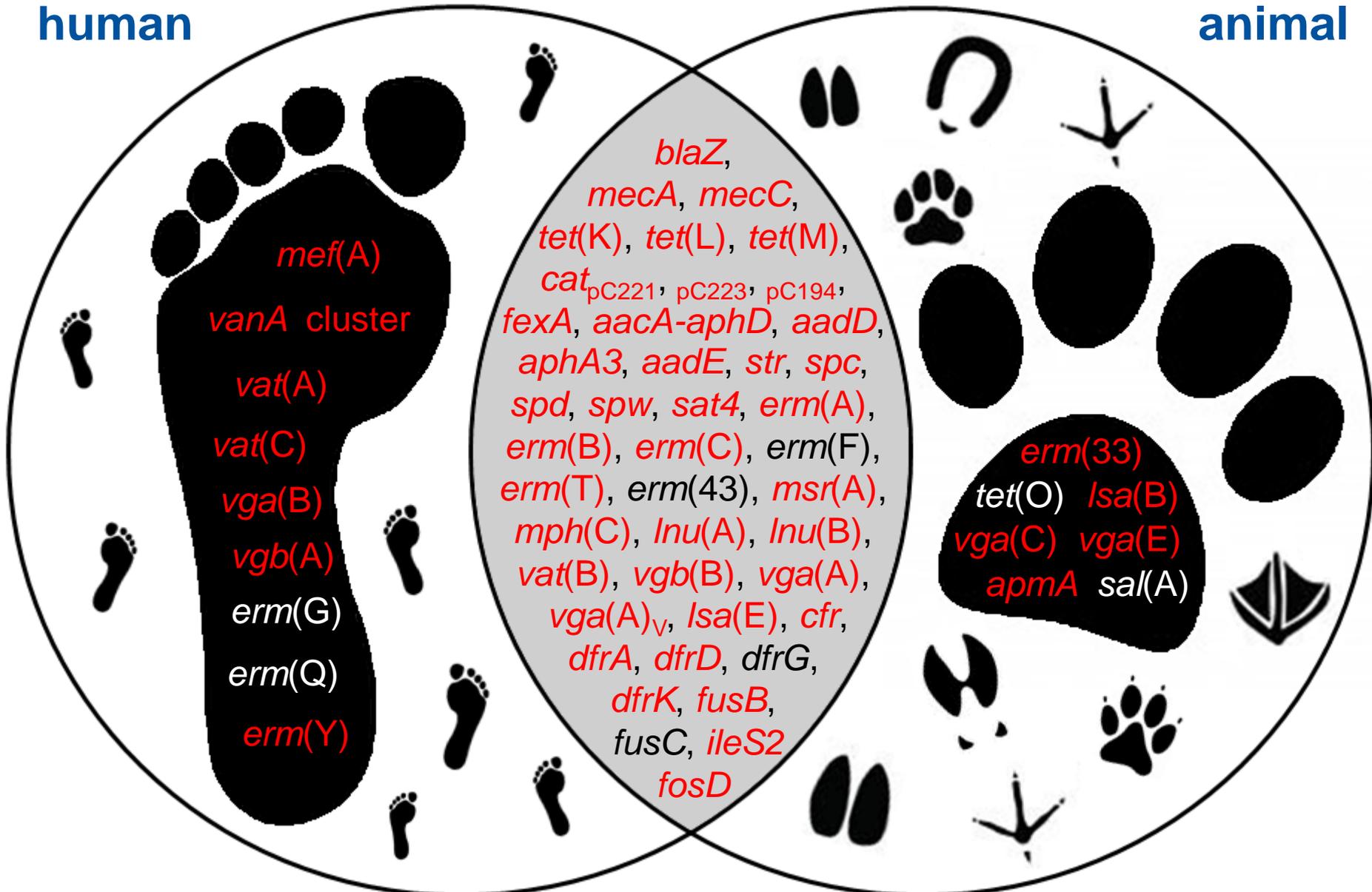
End 1990ties

Acquisition vof methicillin resistance
Linked to resistance against
 Cu^{2+} und Zn^{2+} , Loss of the
immun evasion gene clusters, IEC

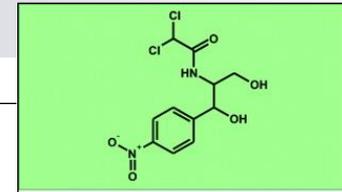
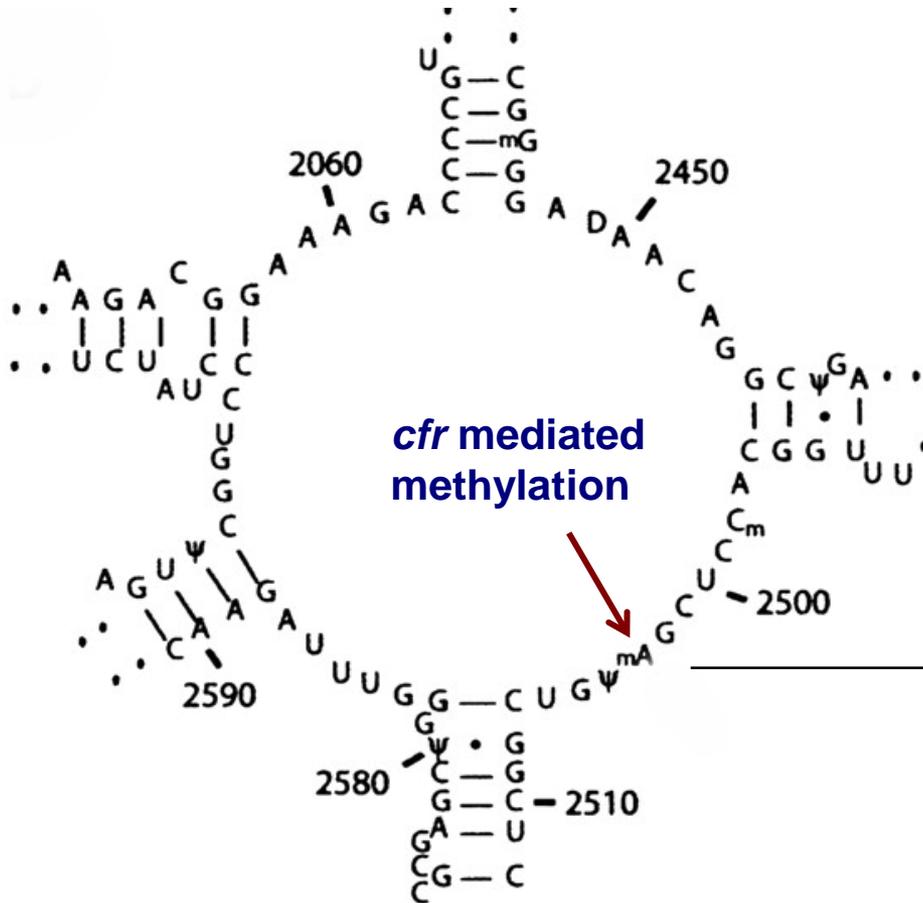
located on mobile genetic elements

human

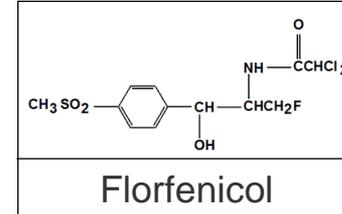
animal



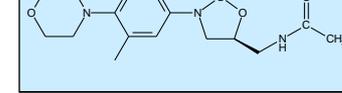
Methylation of A2504 by the *cfm* gene encoded methylase mediates cross resistance against several antibiotic classes



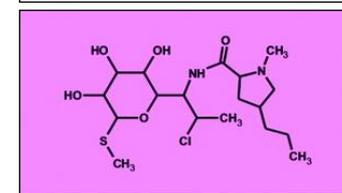
Chloramphenicol



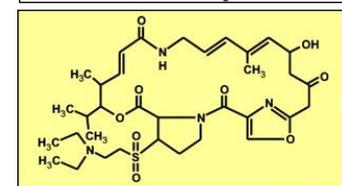
Florfenicol



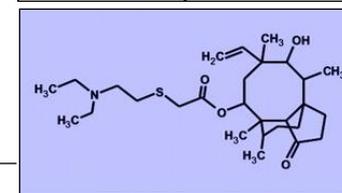
Linezolid



Clindamycin



Dalfopristin



Tiamulin

Veterinary medicine

Human medicine

Human medicine

Human medicine

Veterinary medicine

Resistance to linezolid in *Staphylococcus* spp.; demonstration of *cfr*, samples from Germany

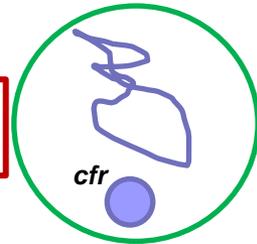
Origin	No. of individuals	
Pig farms, 3 among 8 positive	6 / 67 animals	<i>S. kloosii</i> , <i>S. cohnii</i> , <i>S. sciuri</i>
Farmers at these farms	0 / 39	
Veterinarians	4 / 344 (1.2 %)	<i>S. epidermidis</i> , <i>S. saprophyticus</i>
Horses		

The plasmid from *S. saprophyticus* was sequenced it is highly homologous (> 98%) to *cfr* containing plasmids from humans in China (*S.cohnii*), and in the USA (*S.epidermidis*, *S.aureus*)

Possibilities for dissemination of the *cfr*-gene mediated multiresistance against linezolid, pleuromutilines, lincosamidines

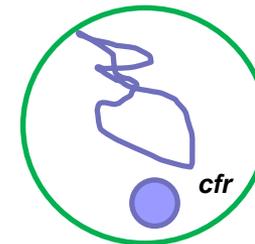
Nose, animal:

Selective pressure:
Tiamulin, Florfenicol

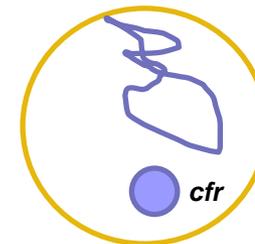


Koagulase-negative
Staphylococci from animals:
S. cohnii, *S. kloosii*, *S. sciurii*

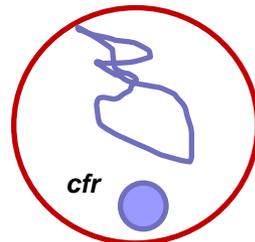
Nose, human:



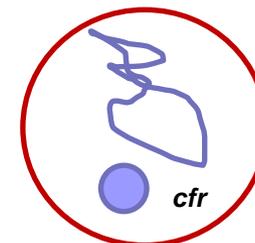
Selective pressure:
Linezolid
Retapamulin



S. epidermidis



S. aureus/LA-MRSA



S. aureus/MRSA



Linezolid resistant coagulase negative *Staphylococcus spp.* (CNS) from cattle, L (cooperation with Dr. Philippe Arnold, Echternsach)

Samples from 3 farms from 28 animals (nasal swabs)) 3 farms positive for CNS with independent upon previous treatment of the animals with florfenicol

Species- distribution :

S.lentus (4)

S.sciurii (3)

S.cohnii (1)

S.equorum (1)

Conjugation in *S.aureus* 8325-

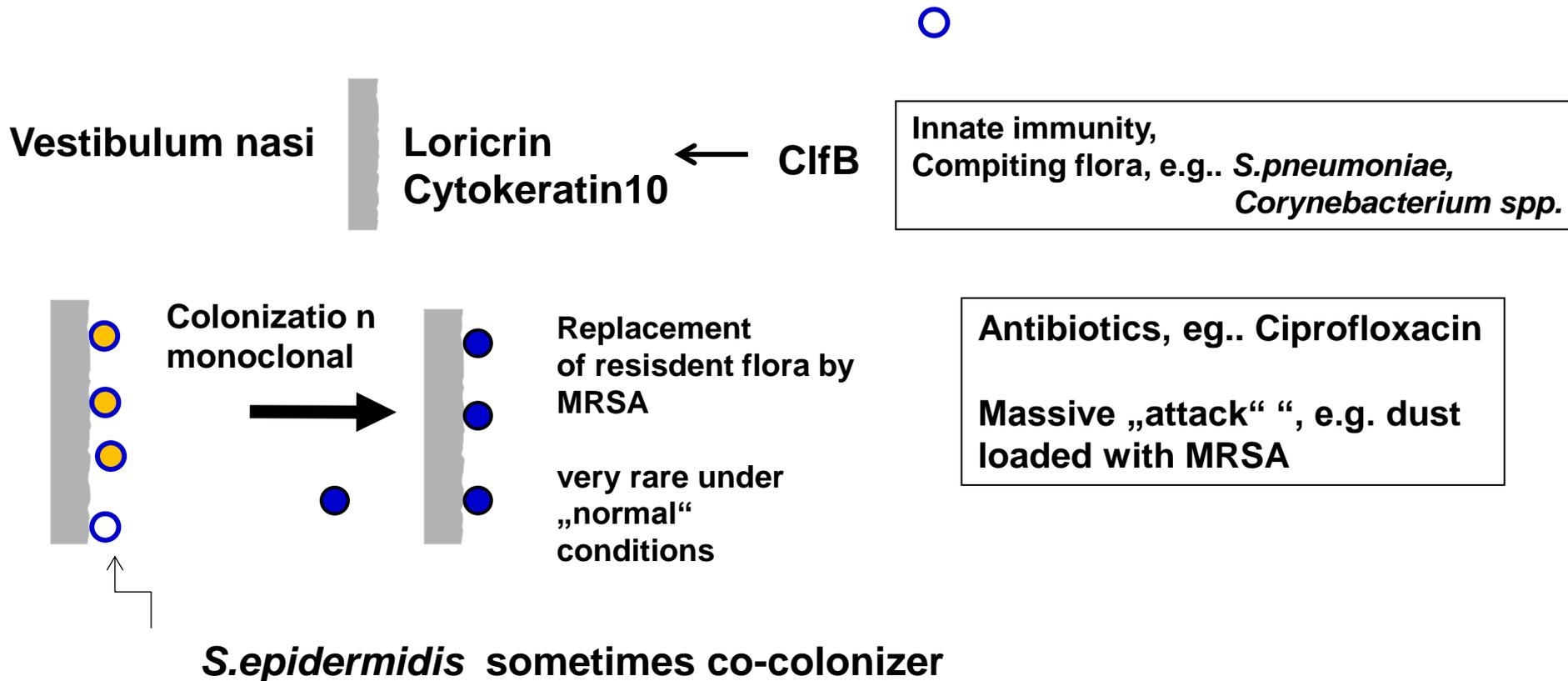
” ”

” ”

” ”

In a second step investigation (nasal swabs) of 10 humans living on these farms:
no *Staphylococcus spp.* with phenotypic resistance to florfenicol and *cfr*

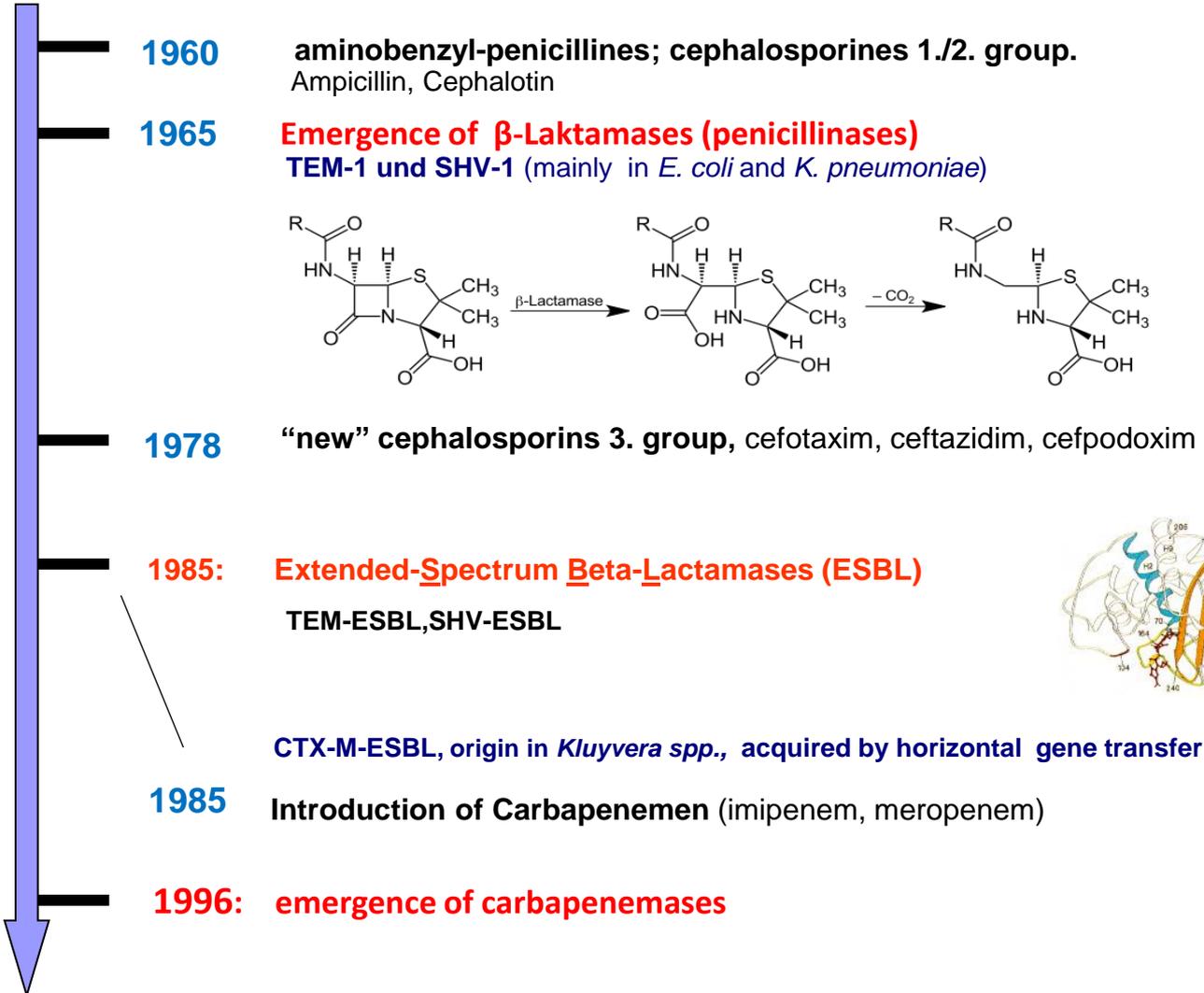
Colonization and infection with mainly susceptible *S. aureus* (●) and MRSA (●), and coagulase negative staphylococci (○)



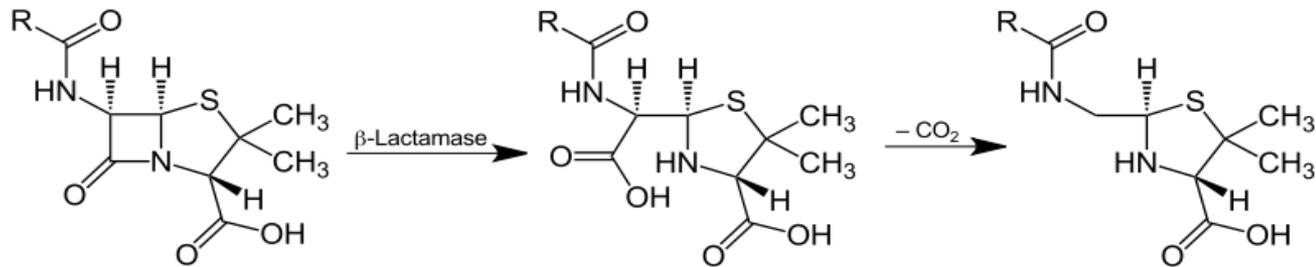
- Staphylococcus xylosus*
- Staphylococcus sciurii*
- Staphylococcus cohnii*
- Staphylococcus saprophyticus*
- Staphylococcus intermedius*

CNS from the nasal flora of livestock

Development of resistance against β -Laktamantibiotics in Enterobacteriaceae

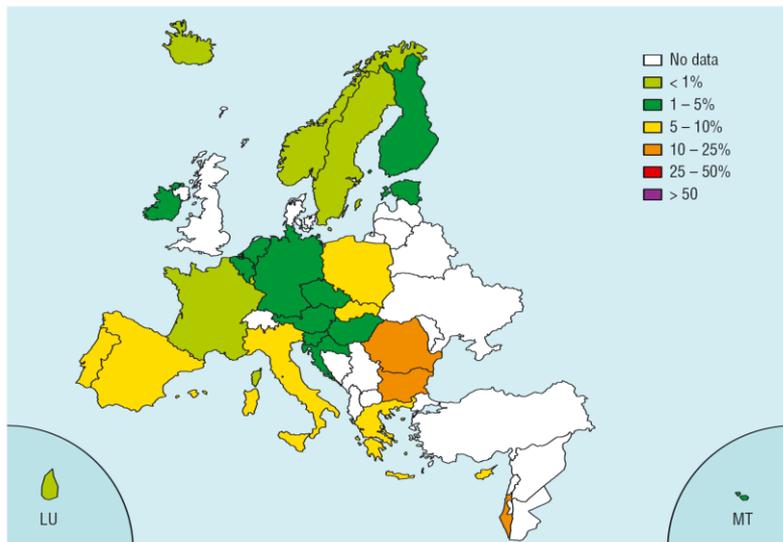


β-Laktamases in Gram-negative bacteria



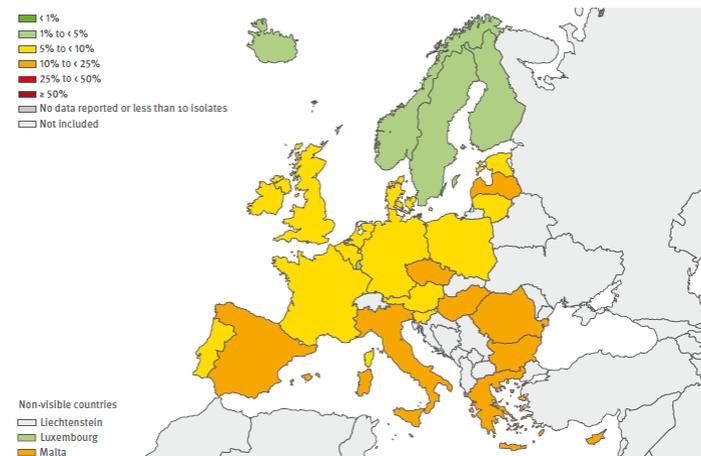
Proportion of *Escherichia coli* with resistance to cephalosporines of 3rd. generation (ESBL) (EARSS)

2004



2009

Figure 5.14: *Escherichia coli*: proportion of invasive isolates with resistance to third-generation cephalosporins in 2010



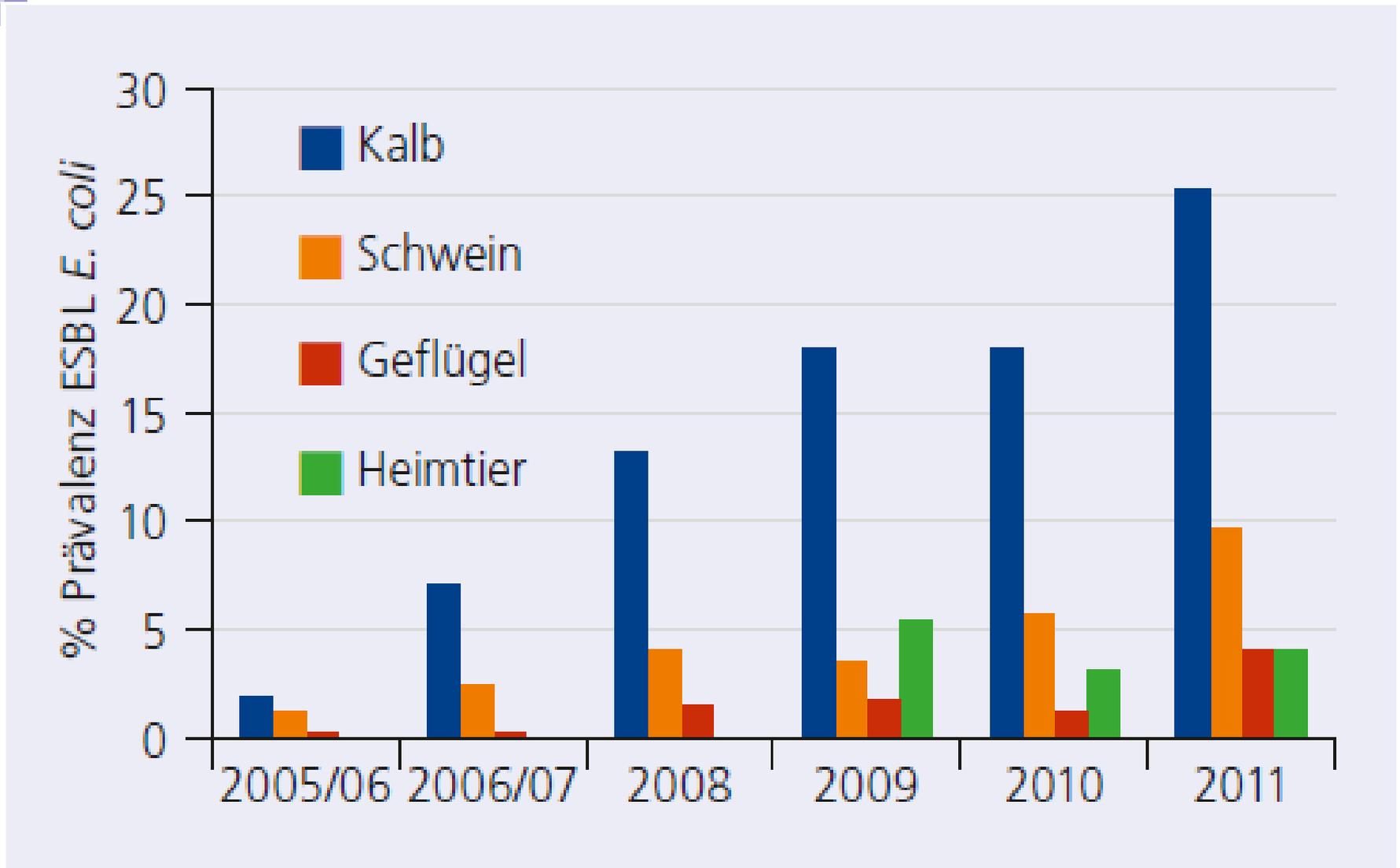
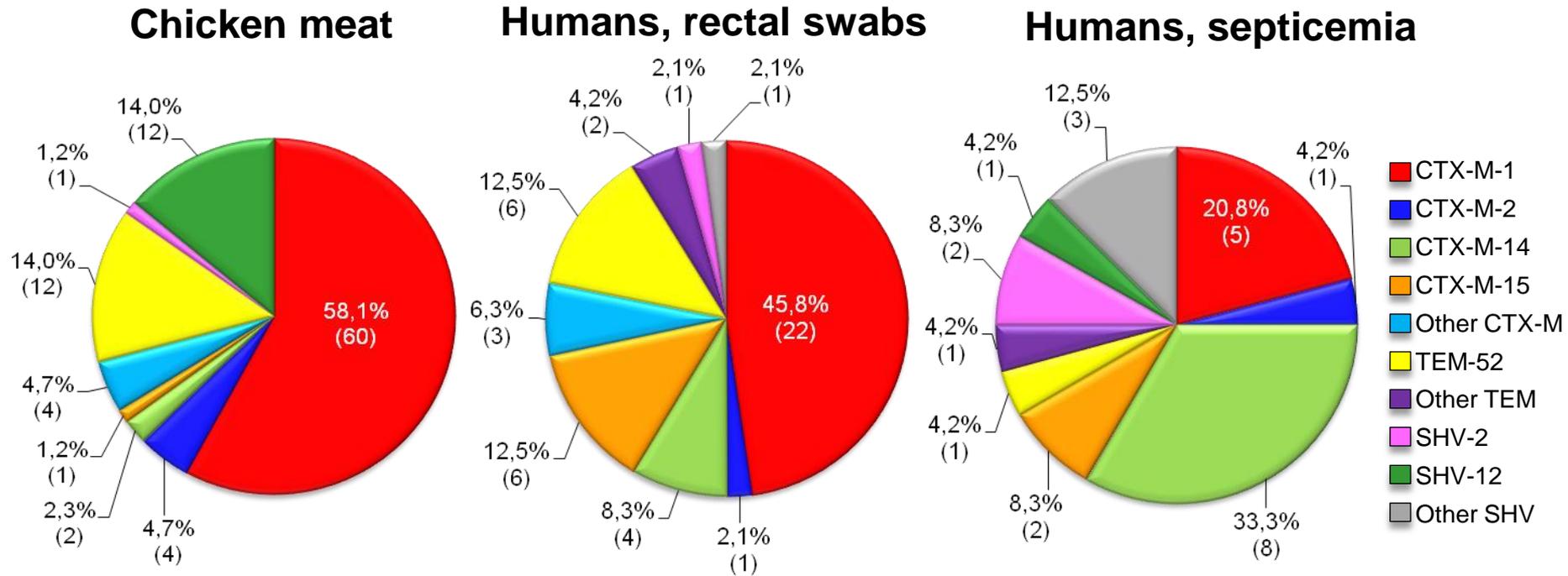


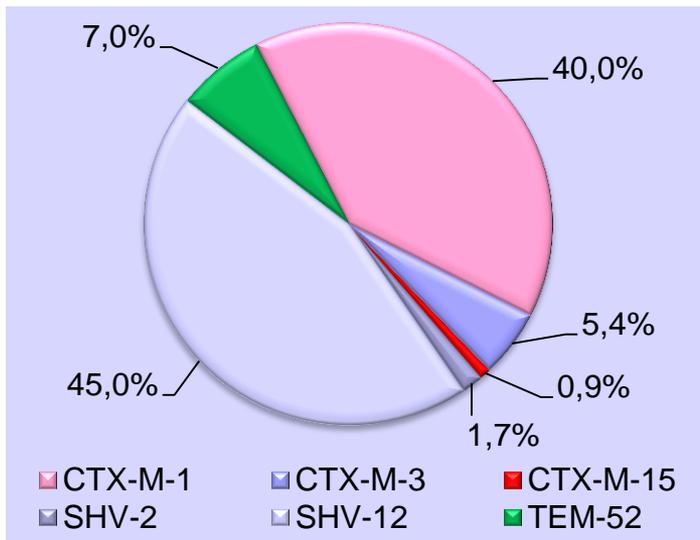
Abb. 1: Prävalenzdaten zu ESBL-bildenden *E.-coli*-Isolaten bei verschiedenen Tierarten, Deutschland 2005–2011

ESBL types in *Escherichia coli* of different origin

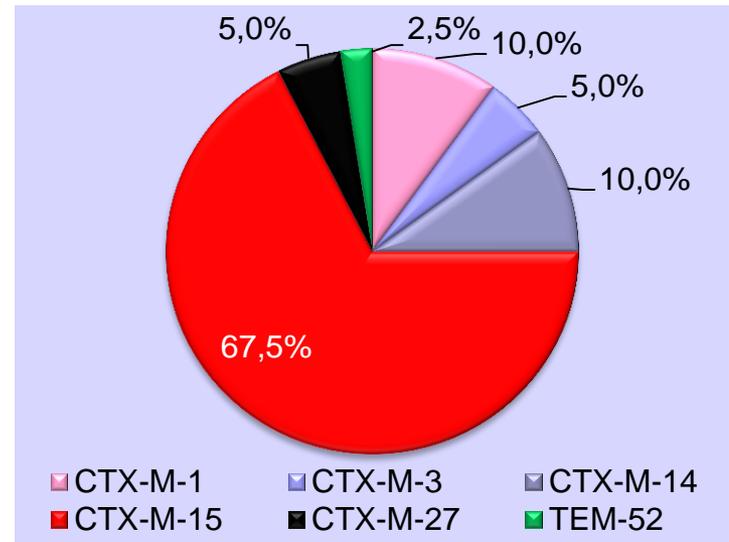
The Netherlands



Distribution of extended-spectrum β -lactamase genes in chicken meat (A), human rectal swabs (B), and human blood cultures (C), the Netherlands. Values in parentheses are no positive.

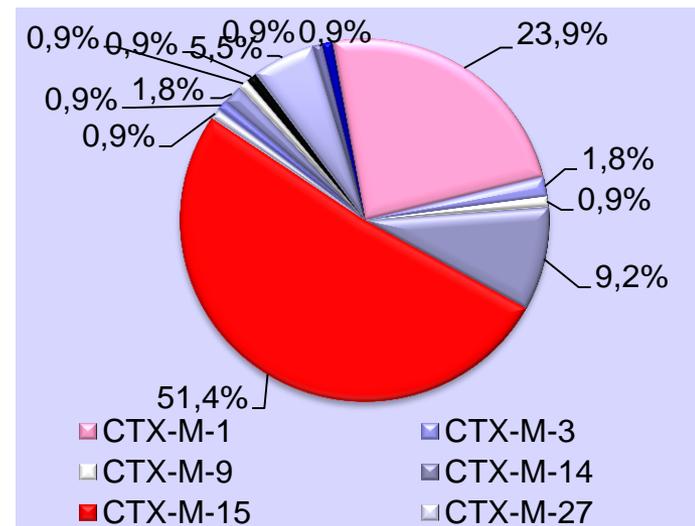


ESBL-types: poultry meat
(Kola et al.,2012)



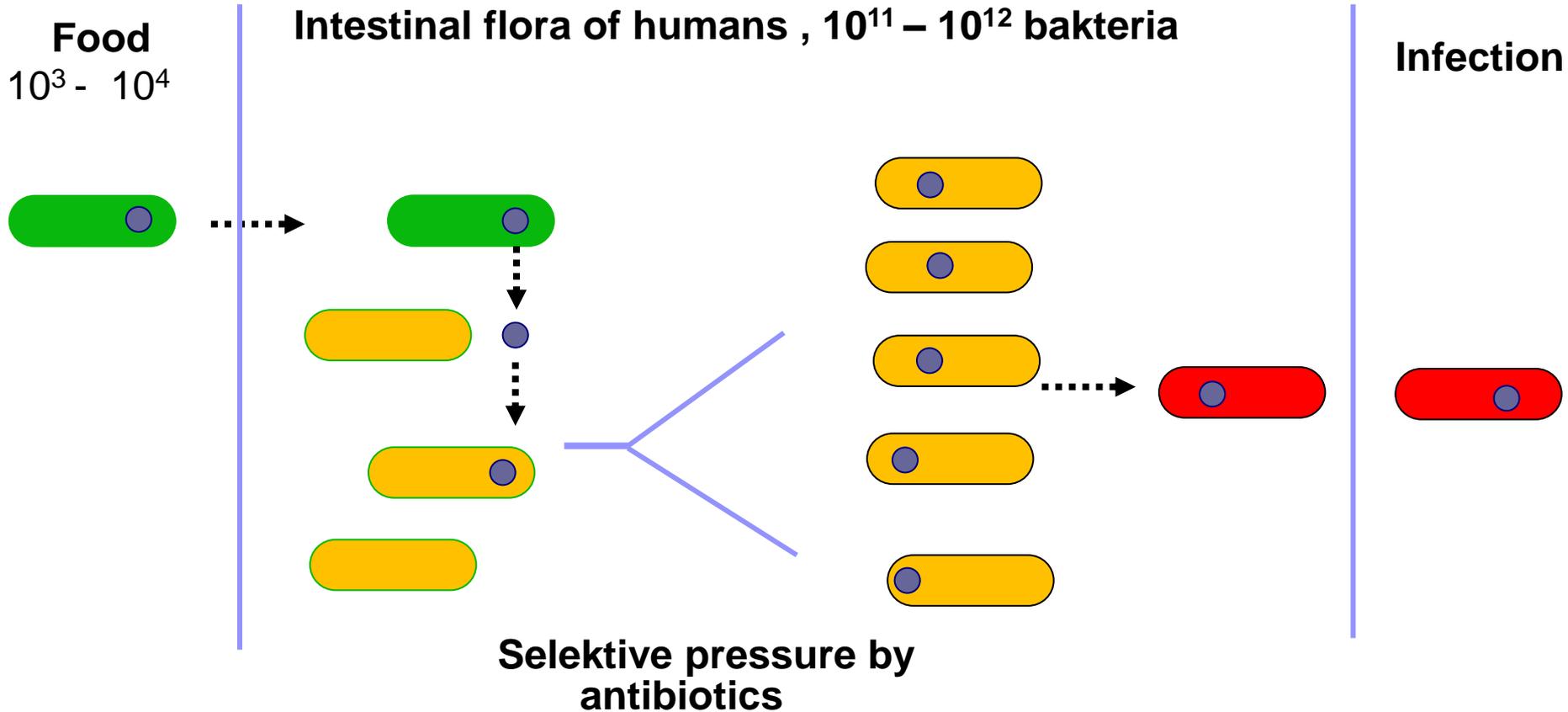
ESBL-types, humans, ambulatory care
(GERMAP, 2012)

Types of ESBL genes contained by *E.coli* of different origin Data from Germany



ESBLtypes,, humans nosocomial infections
(GERMAP, 2012)

Dissemination of *Escherichia coli* and of its resistance genes from contaminated food to humans as colonizer and as infectious agent



 *E.coli*, intestinal flora , animals
 *E.coli*, intestinal flora, humans

 *E.coli*, infectious agent humans

Acquisition of ESBL (*E. coli*) by travelling abroad

Study in the Netherlands, Paltansing et al., Emerg. Infect. Dis. 2013; 19: 1206-13

Rectal swabs immediately before and after return from 370 persons;
(average age: 33 years))

370 persons: 32 positive for ESBL before travel
 113 negativ before and positive after travel (30,5%)

Travel to: South-East Asia and China for 73% of the positive persons

Duration of travel: ~ 21 days

Most frequent ESBL CTX-M1; n = 22

 CTX-M15; n = 16

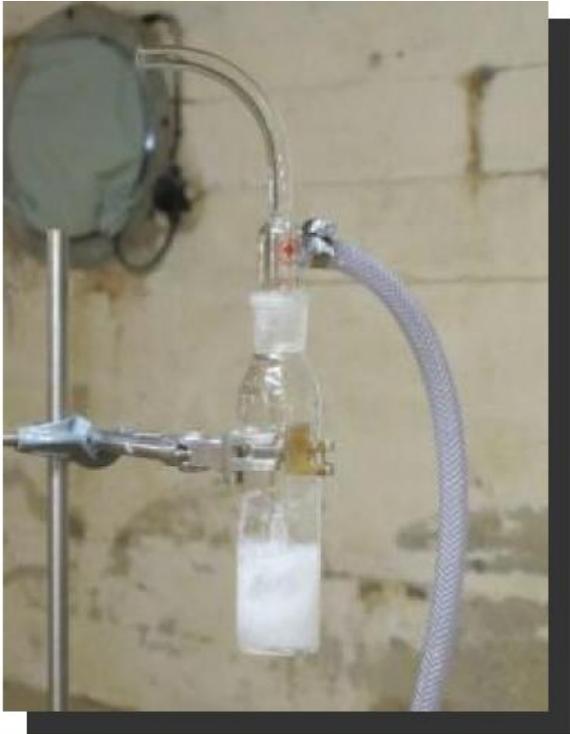
- no antibiotic usage before and during travel, ;
- no hospital stay abroad;
- besides one individual no travel associated diarrhoea .

Study in Sweden: Tängden et al., AAC, 2010

104 persons; negativ immediately before travel

25% positive at return from: Asia, Africa, Southern Europe

Sammeln von Staub in Tiermastanlagen und in ihrer Umgebung



„Immission“ of LA-MRSA from pig farms in DE

With exhausted air : demonstrated site still i 500 m distance down wind
(Schulz et al., ApplEnvironmMicrobiol, 20120)

Study on nasal Besiedlung colonization living near to pig farms

Distance of houses < 500 m, frequency of colonization: 1,5 %

Private „Farm-visits“, shopping in farm shops: 3,1 % consumers !

In the same sample: humans working in hospitals: 1,9 %

(Study in Lower Saxony Bisdorff et al., Epidemiol.Infect. 2012)

Results from a study in the Netherlands on colo-rectal colonization of humans with ESBL *Escherichia coli* in humans living on countryside in areas with high and low density of chicken farms

Colonization frequency ~ 5.1%, a bit lower (nonsignificant) in areas with low density

The only risk factor: possession of horses

Explanation by the authors: Owners of horses often have other home animals

Huijbers PM, et al. Clin Microbiol Infect. 2013 Jan 7. doi: 10.1111/1469-0691.12150. [Epub ahead of print]

Demonstration of ESBL- Enterobacteriace in dogs, cats, horses in NL

Dierikx et al. J Antimicrob Chemother 2012;67: 1368-74.

Demonstration of ESBL- *E.coli* in dogs

Switzerland: 7,4%, Huber et al. Vet Microbiol 2013;162: 992-6

Tyrol (AU): 5.3%, Franiek et al. Berl.Münch Tierärztl Wochenschr 2012;125: 469-75

Spread of ESBL *E.coli* by sewage sludge and manure

Demonstration in surface water, municipal sewage treatment plant, Styria, Austria Rheintaler et al. *Water.Res.* 2010;44: 1981-5

Spread of ESBL *E.coli* from cattle

Study in France , A.Hartmann et al., *Frontiers in Microbiology*,2012;3)

Demonstration of the same isolates (MLST) with the same CTX-M-types

In isolates - from cattle

- from manure

- from soil samples of manured pastures

- demonstration in soil one year after !

(dependend upon quantities of bacteria applied)

Antibiotic resistance gene in soil

Forsberg KJ, et al. [Bacterial phylogeny structures soil resistomes across habitats.](https://doi.org/10.1038/nature13377) Nature. 2014 May 21. doi: 10.1038/nature13377. [Epub ahead of print]

- Investigation of 18 samples (acre, pasture) on the presence of genes conferring resistance against 18 antibiotics
- 2895 resistance genes, mainly „new“ genes
- profile of resistance genes different in different samples
- resistance genes linked to particular taxa, horizontal resistance gene transfer in soil obviously rare
- Higher content of particular resistance genes in manured soil

Contamination of vegetables with ESBL *Escherichia coli*

Study in the Netherlands: [Reuland EA](#) et al. Prevalence of ESBL-producing Enterobacteriaceae in raw vegetables. EurJ Clin Microbiol Infect Dis, May, 2014

- Investigation of 110 samples from 15 different vegetables
- from this
 - 3 samples with *bla* CTX-M15 most frequent in humans
 - 1 sample with *bla* CTX-M1 in humans and livestock
 - 2 samples with *bla* CTX-M9 in humans and animals
 - 1 sample with *bla* SHV in humans and animals

Study in Germany: vegetarians are colonized with ESBL *E.coli* as humans who “omnivores”, Leistner, R. et al. Infect Drug Resist. 2014 Mar 13;7:57-62.

Demonstration of ESBL in 10% of faecal samples of rooks (*Corvus frugilegus*) in several European countries, also in DE, Literak et al., 2011-2012, Demonstration of MRSA and of ESBL in faecal samples of rooks in Austria Loncaric,I,et al.:[PLoS One](https://doi.org/10.1371/journal.pone.0084048). 2013 Dec 31;8(12):e84048. doi: 10.1371/journal.pone.0084048

Rooks are omnivores (seedlings, small animals in soil, in urban areas such as in parks also rests of food)

Their radius of action is up to 20 km

They often live in colonies



Spread of **ESBL *E.coli*** by surface water

Demonstration in the outlet of a sewage treatment plant as well as in rivers in Olsztyn, Poland

(TEM-K, CTX-M, OXA, SHV)

Korzeniewska et al. *Ecotoxicol Environm Saf*, 2013

Demonstration in the outlet of a sewage treatment plant as well as in the river in Barcelona, Spain

(beside others. *E.coli* ST131, CTX-M-15)

Colomer-Lluch *et al.*, *J. Antimicrob. Chemother.* 2013.

Demonstration in river Thame, West-London

Dhanij et al. *J. Antimicrob. Chemother.*, 2013

Demonstration in 21 from 58 rivers and lakes in Switzerland
(CTX-M-1, **CTX-X-M-15**, CTX-M-27)

Zurfluh et al., *Appl. Environm. Microbiol.* 2013



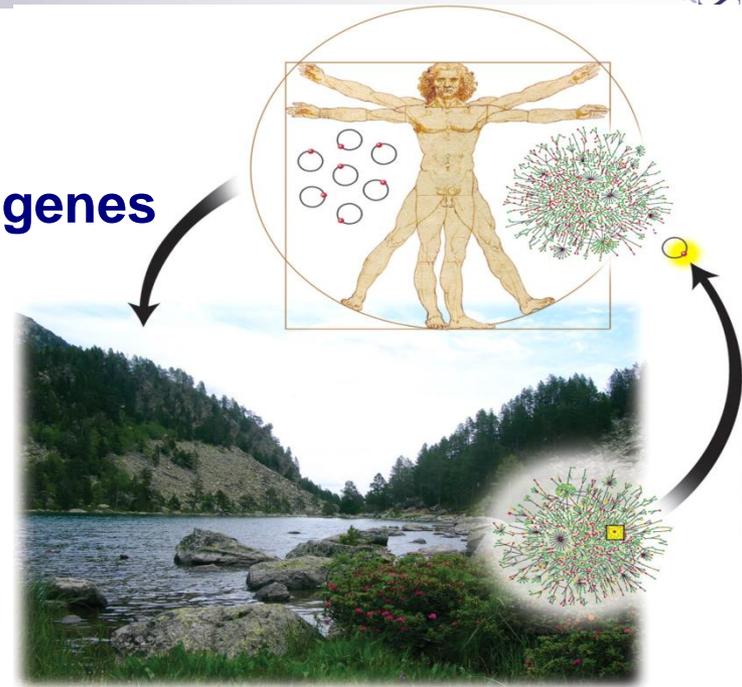
Spread by migrating birds

Crane , ESBL, Pacific area Raum
Kitadi et al. J.Vet.Sci.2012;74:395-7

Canada- goose , multiple resistant *E.coli*
Middleton & Ambrose, J.Wildlife Dis. 2005;41: 334-41

Demonstration of new antibiotic resistance genes in bacteria of the autochthonic microflora of rivers

rare so far



plasmid-located *qnr* in *Aeromonas punctata* and *Aeromonas media* from river Seine, Paris

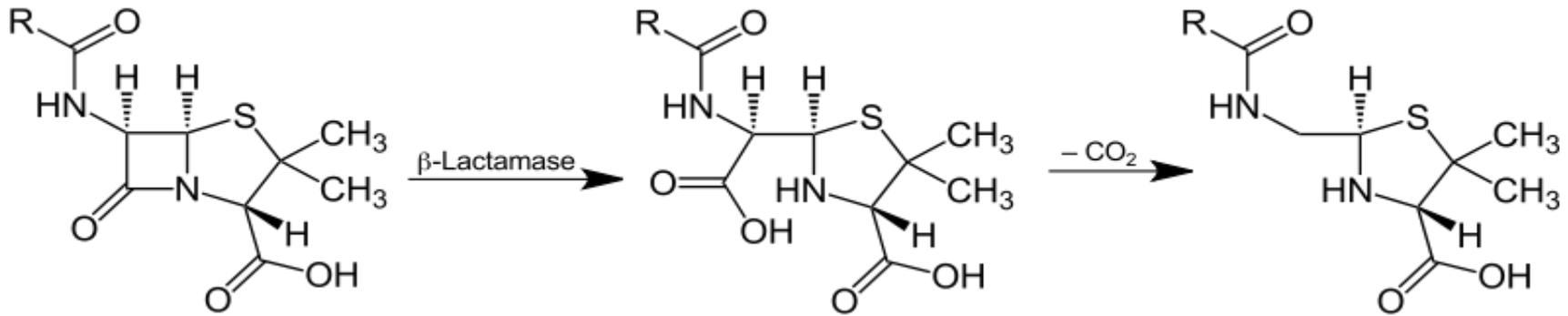
(Cattoir et al., *Emerg. Infect. Dis.* 2008; 14: 231-237).

Obviously horizontal transfer from *Enterobacteriaceae* to *Aeromonas* spp., (*qnr* mediates low level fluoroquinolone resistance by protection of the DANN-gyrase).

*bla*_{IMI-2} (Carbapenemase), located at a 65-kb-plasmid in *Enterobacter asubriae* in several rivers in the USA

(Aubron et al., *Emerg. Infect. Dis.* 2005; 11: 260-264)

β -Laktamases:



ESBL = **E**xtended **S**pectrum **b**eta-**L**aktamases

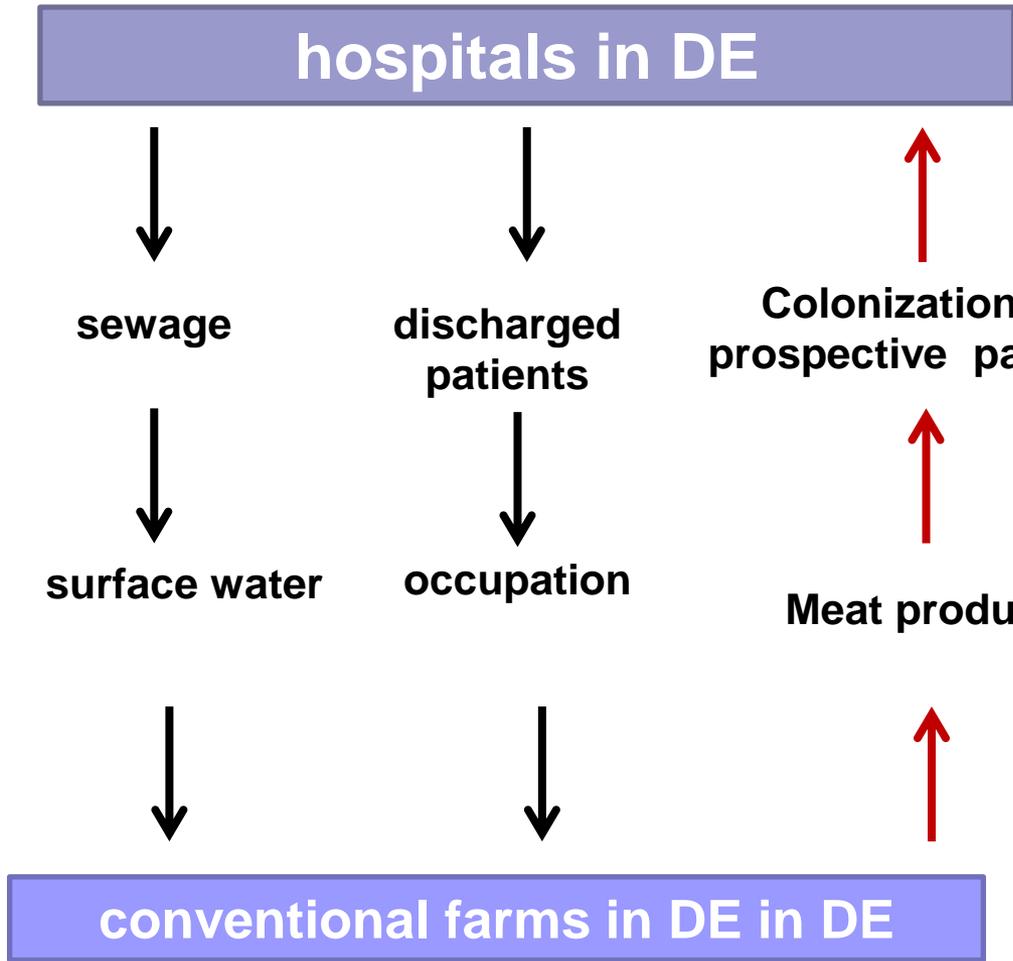
„Classical“ β -Laktamases hydrolyze aminopenicillines
and acylureidopenicillines

ESBL possess an extended substrate spectrum, they also hydrolyze cephalosporines of groups 3 and 4

ESBL originate from

- Mutations in genes of the classical enzymes
- Acquisition of **ESBL** by horizontal gene transfer from environmental bacteria

Emergence of carbapenemases



Demonstration of *E.coli* containing VIM-2 in 2 farms, and in the outlet of a sewage treatment plant



Non-visible countries
 Liechtenstein
 Luxembourg
 Malta



workers from countries with high prevalence of carbapenem resistant enterics

