

Introduction

Recent studies indicated that some highly resistant strains of *E. coli* can be common contaminants of broiler meat, and resistance determinants can be of importance for the food production and human health. However, much less is known about their virulence determinants, and detailed genetic analyses of antimicrobial resistance and virulence are especially missing in *E. coli* from newly hatched broiler chicks.

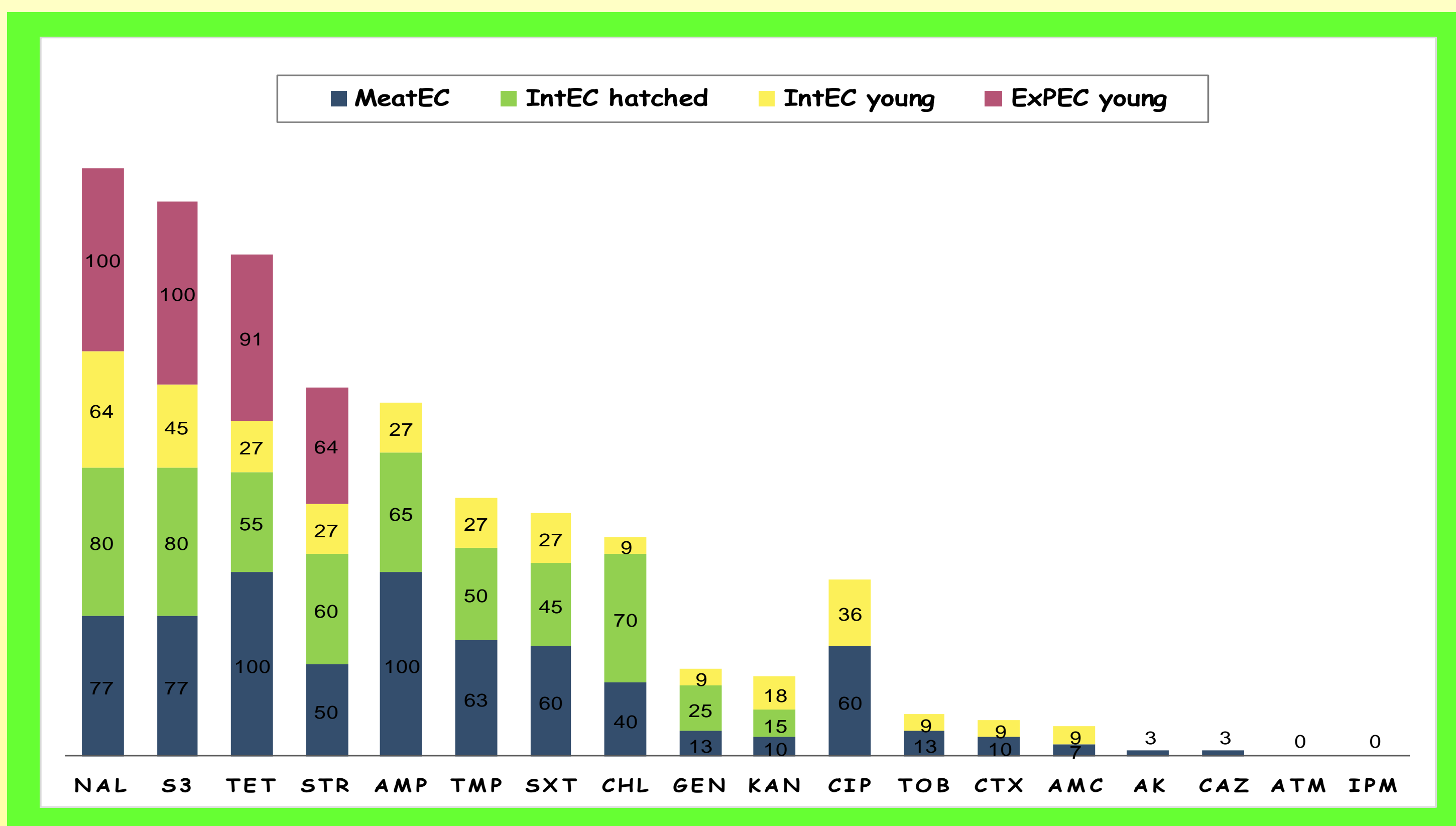
Main objective

To provide a first **comparative characterization** of antimicrobial resistance and virulence traits of *E. coli* strains isolated from **young chicks** from farms and from **fresh broiler meat** in relation to those from **newly hatched chicks**.

Comparative studies on antimicrobial resistance phenotypes and genotypes of commensal and pathogenic *E. coli* from chicken

- multiresistance was a common characteristic of *E. coli* strains regardless of the source of origin and pathotype (Fig. 1)

Fig. 1. Differing distribution (%) of antimicrobial resistance phenotypes among *E. coli* strains from different chicken sources



- the association between nalidixic acid-sulfonamide-tetracycline-streptomycin (Nal-S3-Tet-Str) was frequently found
- commensal *E. coli* from meat (MeatEC) carried resistance at different extent against the majority of antimicrobials tested
- the antimicrobial resistance genotype of MeatEC showed the highest similarity with the intestinal strains from newly hatched chicks (Table 1)

Table 1. Distribution (%) of the most prevalent antimicrobial resistance genes according to the sample sources

Function	Gene	MeatEC	IntEC hatched	IntEC young	ExPEC young
Integron related	intI1	40	75	55	100
	aadA1-like	33	30	36	91
	aadA2-like	10	20	9	18
	sul1	20	75	45	100
β-lactams	blaTEM-1	97	60	27	9
Tetracyclines	tetA	47	25	27	82
	tetB	67	20	0	27
Phenicol	catA1	20	65	18	9
	floR	17	15	0	0
Sulfonamides	sul2	57	45	18	0
Aminoglycosides	strA	23	0	9	0
	strB	43	30	18	9
Trimethoprim	dfr12	0	20	0	9
	dfrA1	37	0	18	0
	dfrA14	7	30	0	0
	dfrA17	17	0	0	0

Materials and methods

***E. coli* strains.** A total of 70 *E. coli* strains characterized derived from different poultry sources: **raw poultry meat** (28), **young chicks** from farms (represented by 11 intestinal- and 11 extraintestinal strains) and 20 *E. coli* isolates from **newly hatched chicks**.

Resistance and virulence genotyping was performed using high throughput PCR-microarray systems, AMR05 and Ec03 respectively (Identibac).

Comparative studies on virulence genotypes of *E. coli* from chicken

- the general predominance of the virulence genes in the extraintestinal *E. coli* (ExpEC) strains was not surprising (Table 2)
- virulence genes involved in serum resistance (*iss*), iron transport (*iroN*) and some toxin genes (*tsh*, *astA*) showed high prevalence also in commensal isolates from newly hatched/young chick and from the meat

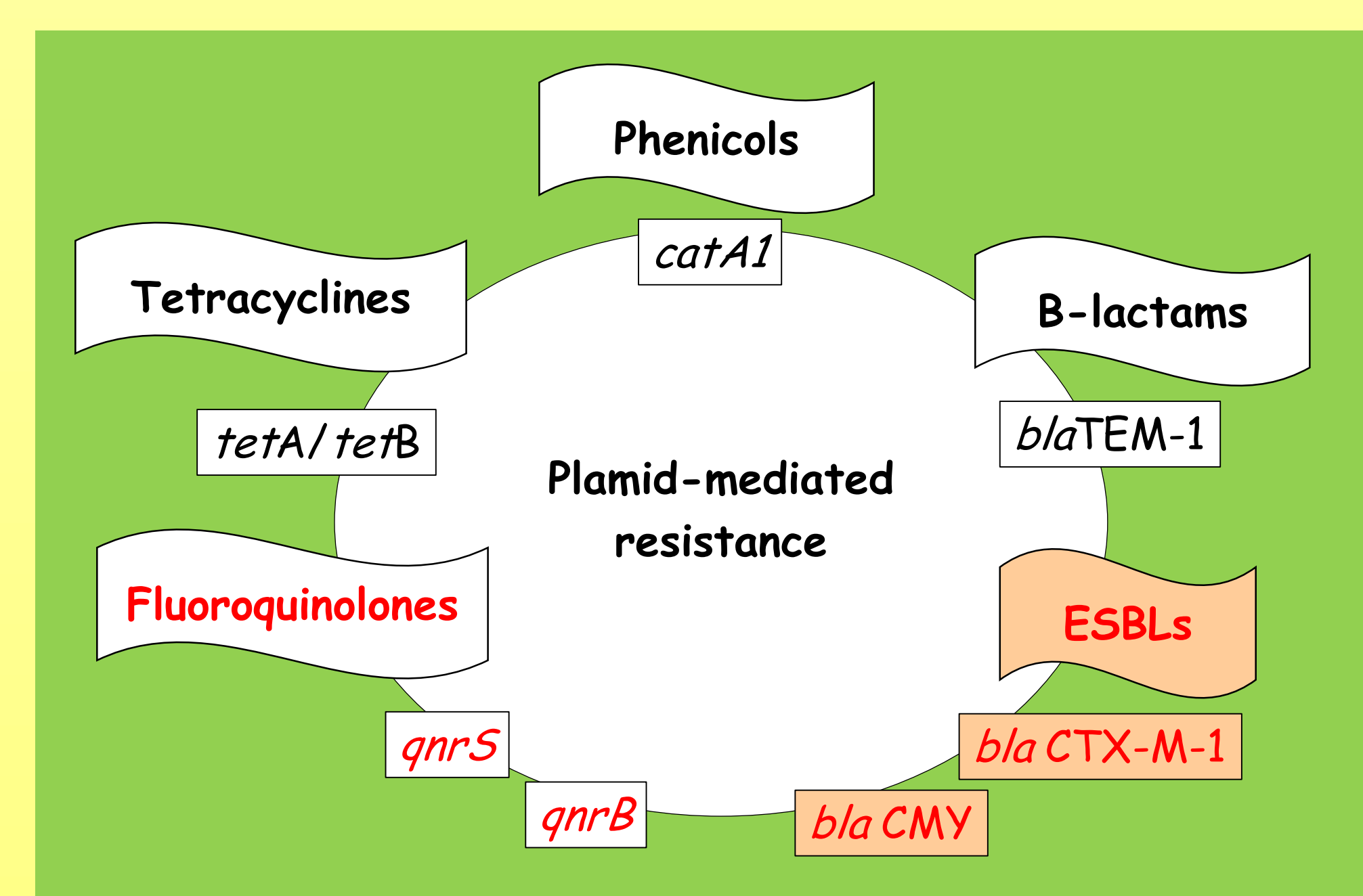
Table 2. Distribution (%) of the most prevalent virulence genes according to the sample sources

Function	Gene	MeatEC	IntEC hatched	IntEC young	ExPEC young
Serum resistance	iss	87	65	73	100
Fimbriae/adhesins	lpfA	47	35	82	91
	prfB	3	5	9	45
Siderophore receptors	iroN	57	30	64	91
SPATE elements	tsh	37	40	36	91
Enterotoxins	astA	30	30	0	36
Colicins/bacteriocins	mchF	40	25	45	82
	cma	40	30	9	36
	cba	13	30	0	36

EPEC-related virulence genotype in MeatEC
eae, *espAFJ*, *tir*, *tccP*, *nleAB*

- chicken meat may represent a source for contamination with pathogenic *E. coli*
- the prevalence of antimicrobial resistance and virulence genes related to the flexible genome suggests the commonly high distribution of certain mobile genetic elements (i.e. plasmids) in poultry *E. coli* (Fig. 2)

Fig. 2. Plasmid-mediated „conventional” and „emerging type” resistance genes in chicken commensal *E. coli*



Conclusion

Results indicate that *E. coli* from newly hatched chicks may represent an important reservoir for multiresistance and virulence for both pathogenic and commensal *E. coli* strains of young chicks and of poultry meat.

Acknowledgement

This work was supported by EU FP7 Collaborative Project PROMISE. Ama Szmolka is a holder of János Bolyai Research Fellowship of the Hungarian Academy of Sciences.