

CHARACTERIZATION OF ESCHERICHIA COLI STRAINS ISOLATED FROM RAW VEGETABLES

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ABSTRACT

Vegetables are an important part of the human diet. Sometimes, contamination by pathogenic *Escherichia coli* can be underestimated; moreover there is a risk of antibiotic resistance spreading via the food chain. The purpose of this study was to examine the prevalence of *Escherichia coli* in fresh vegetables sold in retail market in the Czech Republic and to evaluate the risk to human health. Antibiotic resistance against 12 antibiotics, the presence of 12 virulence and 15 resistance genes were determined among 15 isolated strains. Most of tested strains belonged to B1 phylogenetic group, less frequently represented was B2 and D phylogroup. These results indicate that most strains are probably of human origin. All *E. coli* strains were resistant to at least one of twelve tested antibiotics. A multidrug resistance was observed in four strains. In this study, the presence of virulence factors *Einv* and *papC* and also genes encoding toxins (*CNF1*, *CNF2*) was detected. Nevertheless, none strain can be considered as STEC or EHEC. The widespread appearance of a growing trend associated with the prevalence of antibiotic resistance among enterobacterial isolates is undeniable and the possibility of transfer to humans cannot be ignored. Nevertheless, these results indicate that raw vegetables sold in the retail market can constitute a potential health risk for consumers.

Keywords: vegetables, *Escherichia coli*, virulence, resistance, safety

INTRODUCTION

Escherichia coli, a common inhabitant of intestinal tract of humans and animals, has been used as an indicator of fecal contamination in food. Fecal pollution can indicate the presence of enterobacterial pathogens. *E. coli* can be easily disseminated in different ecosystems through the food chain (Ryu et al., 2012). Raw vegetables can harbour many different pathogens including *Escherichia coli* and may become contaminated through animals, people, animal manures, and contaminated irrigation water (Harapas et al. 2010).

Escherichia coli strains can be assigned to one of the main phylogenetic groups: A, B1, B2 or D. These phylogroups apparently differ in their ecological niches, life-history and some characteristics, such as their ability to exploit different sugar sources, and their antibiotic-resistance profiles (Carlos et al., 2010). Strains from phylogroups B2 and D often contained more virulence factors than strains from the phylogroups A and B1. The extraintestinal pathogenic strains usually belong to groups B2 and D, the commensal strains to groups A and B1, whilst the intestinal pathogenic strains may belong to groups A, B1 and D. Fecal strains isolated from birds were assigned to groups D and B1; A and B1 were isolated from non-human mammals; and A and B2 were found in humans (Carlos et al., 2010). Clermont et al. (2005) have developed a PCR based method to characterize the

phylogroups using the genetic markers *chuA*, *yjaA* and the DNA fragment TspE4.C2.

The consumption of vegetables has risen over the last decades in many countries (Franz and van Bruggen, 2008). Lettuce, radish and salads are the most common causes of *E. coli* outbreaks, where vegetable was proved as a source of infection all over the world (ICMSF, 2005). A large epidemic caused by shigatoxigenic *E. coli* in spring 2011 in Germany resulted in reduction of trust in the health safety of raw vegetables and sprouted seeds. It has been found that the number of outbreaks of EHEC infections associated with the consumption of contaminated vegetables has increased over the last years (Tzschoppe et al., 2012). STEC and EHEC have been isolated from animal faeces, soil, water, sewage and manure and can persist in the environment over long periods of time (Fremaux et al., 2008). Vegetables can become contaminated with STEC and EHEC at all stages of food production. Unlike food of an animal origin, vegetables have rarely been examined as a possible source of human infections with EHEC (Tzschoppe et al., 2012).

The broad group of *E. coli* known as enterohemorrhagic *E. coli* (EHEC), including *E. coli* O157:H7, contain the LEE (locus of enterocyte effacement) encoded intestinal colonisation mechanism (*eae* gene). The *Einv* gene is responsible for encoding enteroinvasive mechanisms. The *Eagg* gene is known for its encoding enteroaggregative

mechanisms (Kaper and O'Brien, 1998). Cytonecrotic factors (CNF1, CNF2) are often produced by *E. coli* strains, which were isolated from intestinal and also extraintestinal infections of humans and animals. The *iss* (increased serum survival) gene and its protein product (ISS) of avian pathogenic *E. coli* (APEC) are important characteristics of resistance to the complement system. The *iss* gene is probably located in a conserved portion of some plasmids (Buchanan and Doyle, 1997). The *papC* gene encodes fimbrial adhesin. Genes encoding temperature-sensitive haemagglutinin (*tsh*), aerobactin (*iucD*), and serum resistance protein (*iss*) are known for their frequent or exclusive localization on large transmissible R plasmids in APEC (Buchanan and Doyle, 1997) and thus these genes are clearly associated with APEC strains (Yu and Kaper, 1992).

The major virulence factors of *E. coli* are Shiga toxins encoded by Shiga toxin genes *stx1* and *stx2*. The ability to produce Stx1 and/or Stx2 is a critical determinant of whether a bacterium can cause the clinical syndrome associated with STEC. Unlike O157:H7, most non-O157 STEC strain cannot be easily distinguished from non-pathogenic *E. coli* strains. The infection of non-O157 STEC in human beings is also considered to be underestimated (Li et al., 2016).

Apart from Shiga-toxin, epidemic strains can produce hydrolysing enzymes known as extended spectrum β -lactamases (ESBLs) causing resistance to several antimicrobial agents. Strains possessing ESBLs, have emerged in the last few decades as a global risk for human health and have been shown to contribute to increased morbidity and mortality (Said et al., 2015). Especially, when they also possess other resistance determinants represent these strains a growing public health threat (Tzschoppe et al., 2012). The high use of antibiotics not only in human medicine, but also in veterinary medicine or even in agriculture, could constitute a selective pressure for the spread of antibiotic resistant bacteria, including ESBL-Eb (Durso and Cook, 2014). ESBL-Eb could persist on the surface of plants or even reach their interior, and they could be transmitted to humans or animals. It is very important to highlight the potential role of consumption of uncooked vegetables in gastrointestinal bacteria acquisition (Hamilton-Miller and Shah, 2001). Future studies should be carried out to evaluate the real risk for human health of this potential transmission linked to the consumption of vegetables (Said et al., 2015).

Scientific hypothesis

The study was focused on the isolation of *E. coli* strains from fresh vegetables sold in the retail market in the Czech Republic. The main objective was to evaluate the presence of antibiotic resistance and virulence factors among these *E. coli* strains and determine a potential risk of fresh vegetables to human health.

MATERIAL AND METHODOLOGY

Samples and *E. coli* isolation

A total of 108 various fresh vegetable samples were bought in the Czech retail markets and investigated for the presence of *E. coli* during year 2015 and other 108 various fresh vegetable samples were investigated during 2016.

Ten grams of sample were homogenized in 90 ml of sterile saline solution, inoculated on the plates with the selective media for *E. coli* - Endo agar or Hi-chrome agar (Oxoid Ltd., United Kingdom) and incubated at 37 °C / 24 h.

Identification of strains

Suspected colonies were identified to the species level by using commercial identification microsystem ENTERotest24 (ErbaLachema Brno, Czech Republic). This test is designed for routine, definitive identification of important strains of family Enterobacteriaceae. The kit contains 24 biochemical tests (dehydrated substrates for biochemical reactions, e.g. IND, ONP), which are placed in microplate. Obtained data were evaluated by software TNW Lite 6.5 (ErbaLachema Brno, Czech Republic).

Bacterial isolates were cultivated on Nutrient Agar (beef extract 10 g, peptone 10 g, agar 15 g, NaCl 5 g, distilled water 1000 mL, pH 7,2) or on Mueller Hinton Agar. Subsequently, the strains were stored at -80°C in glycerol.

Phylogenetic group determination

A previously described multiplex PCR method was used for determination of phylogenetic groups according to presence of three genes (*chuA*, *yjaA*, *TspE4.C2*) (Clermont et al. 2000). A few colonies of each strain were solved in 100 μ L of 1x PCR buffer (ThermoPol Buffer, NEB, USA) and heated up to 95°C for 20 min. Supernatant after centrifugation (10.000 g/L min) was taken as DNA template for all PCR testing. The amplification products were visualized by 1% agarose gel electrophoresis and strains were assigned to the phylogenetic groups (Carlos et al., 2010).

Antibiotic resistance determination

Antimicrobial susceptibility testing to twelve antibiotics was performed by disc diffusion method according to EUCAST methodology (Matuschek et al., 2014). Antibiotic discs (Oxoid Ltd., United Kingdom): amoxicillin/clavulanic acid (AMC 30 μ g), ampicillin (AMP 10 μ g), ceftazidime (CAZ 10 μ g), cephalotine (CEF 30 μ g), ciprofloxacin (CIP 5 μ g), doxycycline (D 10 μ g), chloramphenicol (C 30 μ g), gentamicine (CN 10 μ g), sulbactam/cefoperazone (SCF 10 μ g), streptomycine (S 10 μ g), sulfamethoxazole/trimethoprim (SXT 25 μ g), and tetracycline (T 10 μ g) were used. The diameters of the inhibition zones were evaluated (susceptible, intermediate, resistant) according to EUCAST breakpoints.

Detection of virulence and resistance genes

Ten virulence genes (*stx1*, *stx2*, *tsh*, *CNF1*, *CNF2*, *papC*, *neuC*, *iss*, *iucD*, *EinV*, *Eagg* and *eaeA*) were assessed using PCR as was described previously (Holko et al., 2006; Ewers et al., 2007). The primer sequences of virulence genes, the expected size of their products, and the cycling conditions for the determination of the presence of selected ten genes are listed in Table 1.

The genes encoding antibiotic resistance: *qnrS*, *tet(A)*, *tet(B)*, *sul1*, *sul3* *qac*, *merA*, *qepA*, *int*, and the genes responsible for the ESBL phenotype (*blaTEM*, *blaSHV*, *blaOXA-1*, *blaOXA-7*, *blaPSE-4*, and *blaCTX-M-3*) were identified by polymerase chain reaction (PCR). The cycling conditions varied according to the specific gene determination (Table 1).

Table 1 Oligonucleotides sequences of primers used and PCR conditions for detection of virulence and resistance genes in *E. coli* strains.

Description	Virulence gene	Oligonucleotide sequence (5'-3')	Annealing temperature (°C)	Size of amplified product (bp)	Reference
temperature-sensitive haemagglutinin	<i>tsh</i>	ACTATTCTCTGCAGGAAGTC CTTCCGATGTTCTGAACGT	58	824	Ewers et al. 2007
cytotoxic necrotising factor	<i>CNF1</i>	GCGACAAATGCAGTATTGCT GACGTTGGTTGCGGTAATTTT	63	552	Holko et al. 2006
cytotoxic necrotising factor	<i>CNF2</i>	GTGAGGCTCAACGAGATTATG CCACGCTTCTTCTTCAGTTGT	63	839	
shiga toxin 1	<i>stx1</i>	TTTCCCCTCTTTTAGTCAGTCAACTG GGCAGGATTACAACAAAGTTTCACAG	63	160	Holko et al. 2006
shiga toxin 2	<i>stx2</i>	CCCCCTCTCTTTTGCACTTCTTTCC TGCTCCAGCAGTACCATCTCTAACCC	63	423	
pilus associated with pyelonephritis	<i>papC</i>	TGATATCACGCAGTCAGTAGC CCGGCCATATTCACATAAC	58	501	
K1 capsular polysaccharide	<i>neuC</i>	GGTGGTACATTCGGGATGTC AGGTGAAAAGCCTGGTAGTGT	58	670	Ewers et al. 2007
increased serum survival	<i>iss</i>	ATCACATAGGATTCTGCCG CAGCGGAGTATAGATCCCA	58	309	
aerobactin siderophore synthesis	<i>iucD</i>	ACAAAAAGTTCTATCGCTTCC CCTGATCCAGATGATCCTC	58	714	
enteroinvasive mechanisms	<i>EinV</i>	TTCTGATGCCTGATGGACCAG TGGAAAAACTGAGTGCCCTCTG	63	140	
enteroaggregative mechanisms	<i>Eagg</i>	AGACTCTGGCGAAAGACTGTA ATGGCTGTCTGTAATAGATGA	63	194	Holko et al. 2006
intimin	<i>eaeA</i>	TGAGCGGCTGGCATGAGTCAT TCGATCCCCATCGTCAACAGA	63	241	
resistance genes					
Beta-lactams	<i>bla_{TEM}</i>	GAGTATTCAACATTTTCGT ACCAATGCTTAATCAGTGA	50	857	Maynard et al. 2004
	<i>bla_{SHV}</i>	TCGCCTGTGTATTATCTCCC CGCAGATAAAATCACCACAATG	50	768	
	<i>bla_{OXA-1}</i>	GCAGCGCCAGTGCATCAAC CCGCATCAAATGCCATAAGTG	50	198	
	<i>bla_{OXA-7}</i>	AGTTCTCTGCCGAAGCC TCTCAACCCAACCAACCC	50	591	
	<i>bla_{PSE-4}</i>	CTGCTCGTATAGGTGTTTCC TCGCATCATTTTCGCTCTTC	50	705	
	<i>bla_{CTX-M-3}</i>	AATCACTGCGTCAGTTCAC TTTATCCCCCACAACCCAG	50	701	

Table 1 (Continue).

Resistance genes					
plasmid-mediated quinolone resistance	<i>qnrS</i>	ACGACATTCGTCAACTGCAA	58	600	Cattoir et al. 2007
		TAAATTGGCACCCCTGTAGGC			
tetracycline	<i>tet(A)</i>	GGCCTCAATTCCTGACG	55	372	Guillaume et al. 2000
		AAGCAGGATGTAGCCTGTGC			
	<i>tet(B)</i>	GAGACGCAATCGAATTCGG	55	228	
		TTTAGTGGCTATTCTTCCTGCC			
sulphonamides	<i>sul1</i>	CGGCGTGGGCTACCTGAACG	63	433	Perreten, Boerlin, 2003
		GCCGATCGCGTGAAGTTCCG			
	<i>sul3</i>	GAGCAAGATTTTTGGAATCG	55	880	
quarternary ammonium compounds	<i>qac</i>	GCCCTTCCGCCGTTGTCATAATC	63	250	Johnson et al. 2012
		CGGCCCTCCGACGCGACTTCC			
mercury resistant genes	<i>merA</i>	GATCCGCGCCGCCATATCGCCCATCTG	60	250	
		CACGCGCTCGCCGCCGTCGTTGAGTTG			
plasmid-mediated gene responsible for reduced fluoroquinolones	<i>qep</i>	GCAGGTCCAGCAGCGGGTAG	60	199	Yamane et al. 2008
		CTTCTGCCCGAGTATCGTG			
integron mediated antibiotic resistance	<i>int</i>	GGGTCAAGGATCTGGATTTCG	60	483	Mazel et al. 2000

Statistical analysis

The results of antibiotic resistance and virulence factors were evaluated by Pearson's correlation coefficient between the measured variables. The analysis was performed using statistical software STATISTICA CZ (StatSoft, Inc. 2007).

RESULTS AND DISCUSSION

The prevalence of *Escherichia coli* in various raw vegetables bought in Zlín region (Czech Republic) is shown in Table 2. *E. coli* was detected in 15 out of 108 samples bought in 2015 (13.9%). In contrast, among 108 fresh vegetable samples bought in 2016, there was found no *Escherichia coli* strain. Thus, the prevalence of *E. coli* strains in vegetable during two years is 15 out of 216 (6,9%). In 2013, the incidence of *E. coli* in raw vegetable in the Czech Republic was 26.4% (Skočková et al., 2013). This study proves a decreasing trend in the occurrence of *E. coli* in retail market in the Czech Republic. In comparison, data from Canada reported 8.2% of *E. coli* recovered from fresh produce (lettuce, spinach, carrots, and green onions), which represents low levels of enteric pathogen contamination in vegetables sold in North America (Bohaychuk et al., 2009). On the other hand, a total of 90 samples of raw salad vegetables (parsley, lettuce, radish) were collected in Lebanon and *E. coli* was present in almost half (45.5%) of samples (Faour-Klingbeil et al., 2016).

All positive samples in this study came from European countries (Table 2). The most commonly contaminated vegetable samples were mung sprouts (4/12), radish (2/7), tomatoes (2/10), and spring onion (2/4). The occurrence of *E. coli* in the other types of vegetable was less frequent.

Skočková et al. (2013) indicated leafy vegetable and sprouted seeds as the most common sources of *E. coli*.

Mukherjee et al. (2004) who analysed fresh fruits and vegetables produced by organic and conventional farmers in Minnesota have shown *E. coli* prevalence rates of 1.6 and 9.7%, respectively. Tzschoppe et al. (2011) have detected *E. coli* in five (12.5%) of 40 salad and sprouted seed samples. Lower prevalence of *E. coli* may also be a result of a different methodology of detection with no enrichment (Skočková et al., 2013).

Phylogenetic groups

In this study, the most *E. coli* strains (73.3%) belonged to B2 phylogroup, much less of them was assigned into B1 (13.3%) and D (13.3%) phylogroup. None of the strains can be determined as A phylogroup. It is known (Carlos et al., 2010) that B2 phylogroup *E. coli* strains are highly probably human extraintestinal pathogenic strains. On the other hand, *E. coli* strains isolated from chicken meat mostly belong to A, less to B1 phylogroup (Pavličková et al., 2015). This study is also in accordance with the statement that strains from phylogroups B2 and D contained more virulence factors than strains from the phylogroups A and B1 (Carlos et al., 2010).

Antibiotic resistance

All 15 strains (100.0%) isolated from raw vegetables in this work were resistant to at least one antibiotic, even more 4 of these strains (26.7%) were multiresistant (3 or more). The most frequent antibiotic resistance is ampicillin resistance (93.3%) and resistance to cephalotine (53.3%) and ceftazidime (40.0%). Also, resistance against gentamicine (13.3%) and streptomycine (6.7%) were

Table 2 Prevalence of *E. coli* in raw vegetable samples sold in retail market.

Vegetable	Country of origin	Number of samples positive for <i>E. coli</i> /number of samples
mung sprouts	Czech Republic, Italy	4/12
lentils sprouts	Czech Republic	0/1
alfalfa sprouts	Czech Republic	0/1
broccoli	Spain	0/4
strawberry	Spain	0/4
carrot	Czech Republic	1/4
zucchini	Spain	1/3
spinach	Italy, Spain	0/3
ice lettuce	Italy	0/3
cucumber	Slovakia	0/6
mix of lettuces	Hungary, Italy	0/9
tomato	Morocco	2/10
eggplant	Italy	0/3
chickpeas sprouts	Italy	0/1
baby carrot	Czech Republic, Netherlands	1/3
leek	Czech Republic	0/1
radish	Czech Republic, Italy	2/7
spring onion	Germany	2/4
pepper	Poland	0/2
lettuce little gem	Netherlands	1/2
rucola	Italy	0/3
lettuce	Czech Republic	0/1
lamb's lettuce	Italy	0/1
wallflower	Netherlands	0/1
celery	Spain	0/1
champignon	Poland	0/1
parsley	Czech Republic	1/2
avocado	unknown	0/1
beet	Czech Republic	0/1
turnip	unknown	0/1
cauliflower	Czech Republic	0/1
green beans	unknown	0/1
potato	Czech Republic	0/1

present. High prevalence of resistance to aminopenicillins is also proved by presence of *bla* genes (Table 3).

ESBL-Eb that contaminates vegetables can be transmitted to human consumers via the food chain. In the work of Said et al. (2015), ESBL-Eb were detected in 4 of 45 vegetable samples of market origin tested and in 3 of 13 markets. ESBL-Eb positive isolates were also detected among vegetables samples in the Netherlands (Reuland et al., 2013).

Fluoroquinolone antibiotics inhibit two bacterial enzymes, DNA gyrase and topoisomerase IV, both of which play essential roles in DNA replication. Resistance to quinolone is often linked to amino acid substitutions in the quinolone-resistance-determining regions of DNA gyrase and DNA topoisomerase IV subunits, leading to target modification (Rezazadeh et al., 2016). However, recent reports indicate that quinolone resistance can also be mediated by mobile genetic elements such as plasmids.

Table 3 Characterization of *E. coli* strains isolated from fresh vegetable.

Isolate	Source	Country of origin	Resistance phenotype	Resistance genes	β -lactamase genes	Virulence genes	PG
F10	mung sprouts	Italy	CAZ, AMP	-	<i>blaOXA-1</i>	<i>EinV</i>	B2
F52	mung sprouts	Czech Republic	S, CEF, AMP	<i>qac</i>	<i>blaTEM, blaSHV, blaOXA-1, blaPSE-4, blaCTX-M-3</i>	<i>CNF1, EinV</i>	B2
F53	mung sprouts	Czech Republic	CEF, AMP	<i>qac</i>	<i>blaTEM, blaOXA-1</i>	<i>papC, EinV</i>	D
F77	spring onion	Czech Republic	CAZ, AMP	<i>sul1</i>	<i>blaTEM</i>	<i>EinV</i>	B2
F78	tomato	Morocco	CAZ, AMP	-	-	<i>papC, EinV</i>	B2
F81	lettuce little gem	Italy	AMP	<i>tetA, int, sul1, sul3, mer</i>	<i>blaTEM</i>	<i>EinV</i>	B1
F84	baby carrot	Netherlands	CEF, AMP	<i>qnrS, qac</i>	<i>blaTEM, blaSHV, blaOXA-1, blaCTX-M-3</i>	<i>papC, CNF1, EinV</i>	B2
F87	mung sprouts	Czech Republic	CAZ, CEF, AMP	<i>qnrS, qac, mer</i>	<i>blaTEM, blaSHV, blaOXA-1, blaPSE-4, blaCTX-M-3</i>	<i>EinV</i>	B2
F94	tomato	Czech Republic	AMP	<i>sul1</i>	-	<i>CNF1, EinV</i>	B2
F103	parsley	Czech Republic	AMP	<i>qnrS, qac</i>	<i>blaOXA-1</i>	<i>EinV</i>	B2
F104	radish	Czech Republic	CAZ, CEF, AMP	<i>qnrS, qac</i>	<i>blaOXA-1</i>	<i>papC, EinV</i>	B2
F105	carrot	Czech Republic	AMP	<i>tetB</i>	<i>blaTEM, blaCTX-M-3</i>	<i>EinV</i>	B2
F106	radish	Czech Republic	CEF, CN	<i>qac</i>	<i>blaOXA-1</i>	<i>papC, CNF2, EinV</i>	D
F107	spring onion	Czech Republic	CAZ, CEF, AMP, CN	<i>tetB</i>	<i>blaTEM</i>	<i>EinV</i>	B1
F108	zucchini	Spain	CEF, AMP	<i>qac</i>	<i>blaTEM, blaSHV, blaOXA-1, blaPSE-4, blaCTX-M-3</i>	<i>papC, CNF2</i>	B2

Note: AMP – ampicillin; CAZ – ceftazidime; CEF – cephalotine; CN – gentamycine; S – streptomycine; PG – phylogroup.

Plasmid-mediated quinolone resistance is mediated by the genes (*qnr*) encoding proteins that protect DNA gyrase and topoisomerase IV against quinolone compounds. The three major groups of *qnr* determinants are *qnrA*, *qnrB*, and *qnrS*.

The first plasmid-mediated quinolone-resistance gene (*qnrA*) was identified in a clinical strain of *Klebsiella pneumoniae* isolated in Alabama in 1998. The other two determinants of *qnr* (*qnrB* and *qnrS*) have subsequently been observed in other enterobacteria including *E. coli*, *Enterobacter*, *Salmonella*, and *Klebsiella pneumoniae* (Rezazadeh et al., 2016).

It is of interest to remark that vegetables containing ESBL-Eb of market origin are commonly eaten uncooked, and the possibility of transfer to humans cannot be ignored. Different authors also indicate the potential problems derived from these uncooked food samples containing antibiotic resistant bacteria (Hamilton-Miller and Shah, 2001; Veldman et al., 2014). In fact,

foodborne outbreaks due to ESBL-positive *E. coli* isolates related to vegetables have been previously reported (Reuland et al., 2013). Obviously, the widespread appearance of a growing trend associated with the prevalence of antibiotic resistance among enterobacterial isolates is undeniable.

Detection of virulence factors

In this study, 15 out of 15 isolates (100.0%) possessed some virulence factor and 2 of these strains (13.3%) were even multivirulent (more than 3 factors). The most frequently found virulence factors were *EinV* gene (93.3%) and *papC* (40.0%). The *EinV* gene is responsible for encoding enteroinvasive mechanisms (EIEC) and *papC* gene encodes an adhesin. Presence of these two factors much more resemble origin in wildlife (Pavličková et al., 2017) than in e.g. poultry meat (Pavličková et al., 2015). Moreover, five strains were positive for cytotoxic necrotizing factors CNF toxins (20.0% *CNF1*; 13.3%

CNF2). These results may represent potential threat to human health. CNF1 is a major virulence factor of UPEC strains and it was found in bacteria isolated from meningitis affected children. Moreover, CNF1 is produced in some extraintestinal *E. coli* (ExPEC). There are hints that CNF1 may be involved in cancer development: CNF1 induces the expression of cyclooxygenase-2 (COX-2), activates nuclear factor-kappa B (NF-κB), increases cell motility and inhibits apoptosis. CNF2 has been demonstrated in *E. coli* isolated in calves and lambs with diarrhoea (Knust and Schmidt, 2010).

Plasmid-mediated resistance is of growing clinical concern as they may transfer resistance genes to other species via horizontal gene transfer. Resistance of *eaeA*-positive STECs to fluoroquinolones constitute health threat to consumers, where resistance determinants can spread among non-pathogenic bacteria in the gastrointestinal tract due to plasmid mobility (Khalil and Gomaa, 2016). Moreover, the simultaneous presence of extended-spectrum beta-lactamases (ESBLs), AmpC, and *qnr* genes on the same plasmid has been well documented and this highlights the complexity of determinants involved in plasmid-mediated resistance among the enterobacterial isolates (Rezazadeh et al., 2016). It can be observed that at least four strains isolated in this study represent plasmid mediated resistance (Table 3). Fortunately, neither *eaeA*-positive strains (EHEC) nor STEC strains were proved among *E. coli* strains found in the Czech raw vegetable, thus it can be summarised that vegetables sold in the Czech Republic are not enteropathogenic/shigatoxigenic.

In this work, statistically significant correlation ($p < 0.05$) was not proved between presence of antibiotic resistance and virulence factors.

CONCLUSION

It can be concluded that presence of *Escherichia coli* on raw vegetables sold in retail market in the Czech Republic is decreasing. In 2015 it was found 13.9% positive samples and a year later there were no *E. coli* strain among 108 samples. It was observed that all 15 *E. coli* isolates were resistant at least to one antibiotic, especially against aminopenicillins and cephalosporines. Four strains carry resistance to three or more antibiotics. Furthermore, all strains also encode at least one of virulence factors – *Einv*, *papC* and even *CNF1/CNF2*, which are toxins and may represent pathogenic bacteria. In contrast, neither STEC nor EHEC were determined. There exists a possibility of antibiotic resistance transfer from enterobacteria to humans and it should not be ignored, as well as there is a small hazard of intestinal infection. These results indicate that raw vegetables sold in the retail market can represent a potential health risk for consumers.

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