



Министарство пољопривреде, шумарства и водопривреде

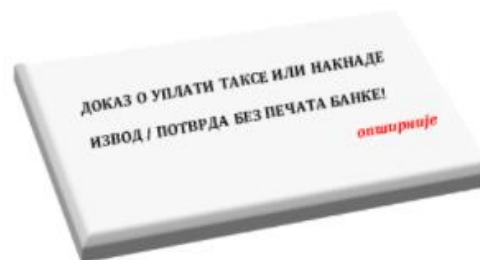
Управа за ветерину



Почетна Организација Пројекти Програми Вести О нама Контакти Документи Линкови Регистри

ПРЕСТАНАК ВАКЦИНАЦИЈЕ СВИЊА ПРОТИВ КЛАСИЧНЕ КУГЕ СВИЊА У РЕПУБЛИЦИ СРБИЈИ ОД 15.12.2019.ГОДИНЕ

Престанак вакцинације свиња против класичне куге свиња у Републици Србији.

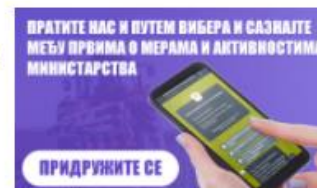


АКТ О БЕЗБЕДНОСТИ ИНФОРМАЦИОНО-КОМУНИКАЦИОНОГ СИСТЕМА УПРАВЕ ЗА ВЕТЕРИНУ

четвртак, 14 октобар 2021 12:32

Дана 13.10.2021.године Управа за ветерину усвојила је акт о безбедности информационо-комуникационог система који можете преузети овде.

Последње ажурирано четвртак, 14 октобар 2021 12:40



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Show all X

- i. ОДЕЉЕЊЕ за здравствену заштиту, добробит и следљивост животиња
 - ii. - за ветеринарско јавно здравство
 - iii. - ветеринарске инспекције
 - iv. - граничне ветеринарске инспекције
 - v. - за међународни промет и сертификацију



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FOOD SECURITY vs FOOD SAFETY

-
- The World Health Organization defines **veterinary public health** as, “The sum of all contributions to the complete physical, mental and social well-being of humans through an understanding and application of veterinary medical science.
 - THE COMPONENTS OF VETERINARY PUBLIC HEALTH
 - 1 Food production and safety.
 - 2 Zoonosis control.
 - 3 Environmental contamination.
 - 4 Role of animals in society.



БОЛЕСТИ ПРЕНОСИВЕ ХРАНОМ/FOOD_BORNE DISEASE

проф. др Снежана Булајић
УНИВЕРЗИТЕТ У БЕОГРАДУ, ФВМ, КАТЕДРА ЗА ХИГИЈЕНУ И ТЕХНОЛОГИЈУ
ХРАНЕ ЖИВОТИЊСКОГ ПОРЕКЛА

The goal of the food safety professional should be to create a food safety culture, not a food safety program.

Frank Yiannas

Author of Food Safety Culture: Creating a Behavior-Based Food Safety Management System



Reference: <http://foodsafetyquotes.com/>

www.magnattackglobal.com

APPROVED: 11 November 2022

doi: 10.2903/j.efsa.2022.7666

The European Union One Health 2021 Zoonoses Report

European Food Safety Authority
European Centre for Disease Prevention and Control

Abstract

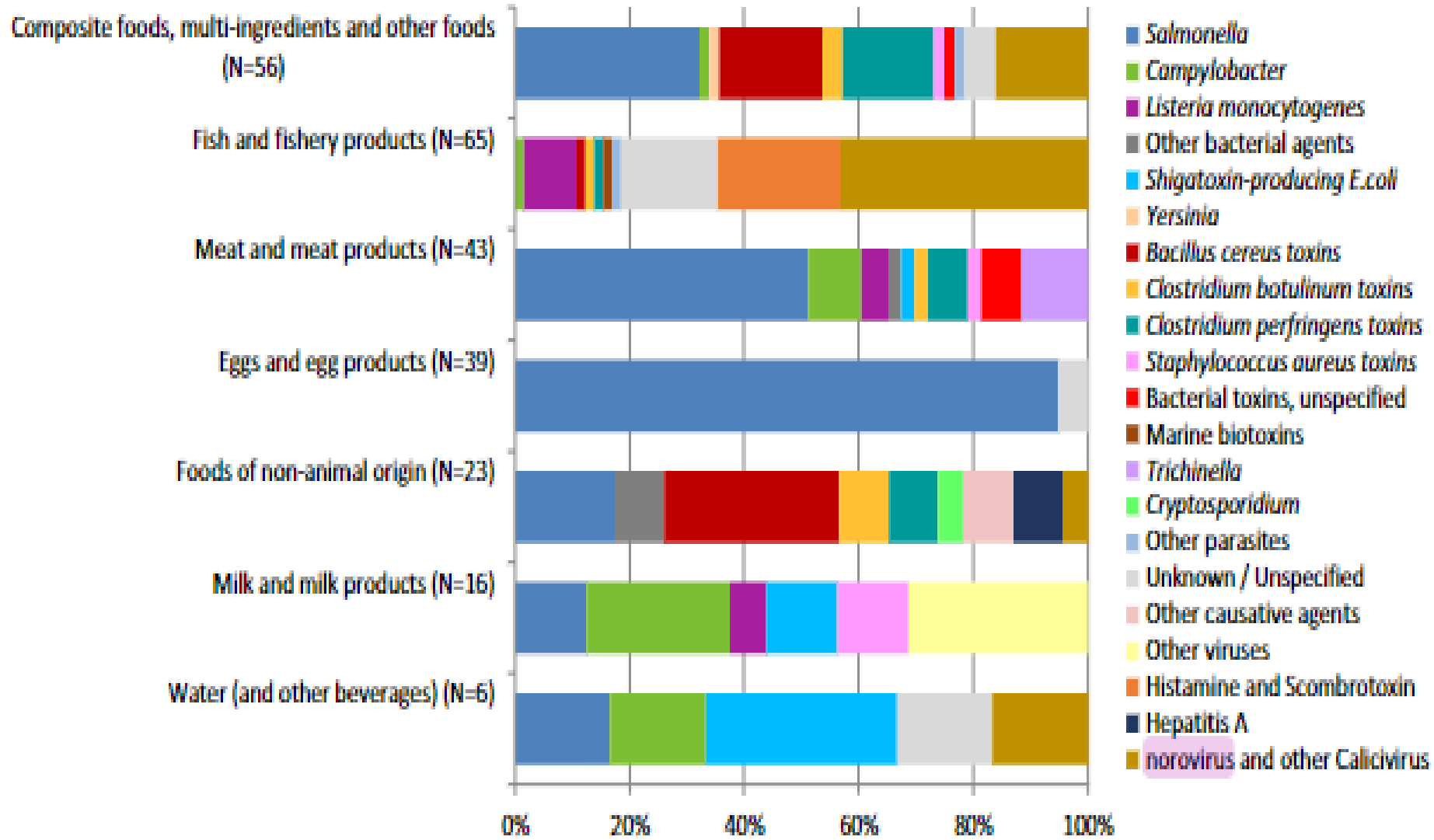
This report of the European Food Safety Authority and the European Centre for Disease Prevention and Control presents the results of zoonoses monitoring and surveillance activities carried out in 2021 in 27 MSs, the United Kingdom (Northern Ireland) and nine non-MSs. Key statistics on zoonoses and zoonotic agents in humans, food, animals and feed are provided and interpreted historically. In 2021, the first and second most reported zoonoses in humans were campylobacteriosis and salmonellosis, respectively. Cases of campylobacteriosis and salmonellosis increased in comparison with 2020, but decreased compared with previous years. In 2021, data collection and analysis at the EU level were still impacted by the COVID-19 pandemic and the control measures adopted in the MSs, including partial or total lockdowns. Sixteen MSs and the United Kingdom (Northern Ireland) achieved all the established targets in poultry populations for reduction in *Salmonella* prevalence for the relevant serovars. *Salmonella* samples from carcasses of various animal species and samples for *Campylobacter* quantification from broiler carcasses were more frequently positive when performed by the competent authorities than when own-checks were conducted. Yersiniosis was the third most reported zoonosis in humans, followed by Shiga toxin-producing *Escherichia coli* (STEC) and *Listeria monocytogenes* infections. *L. monocytogenes* and West Nile virus infections were the most severe zoonotic diseases, with the most hospitalisations and highest case fatality rates. Overall, MSs reported more foodborne outbreaks and cases in 2021 than in 2020. *S. Enteritidis* remained the most frequently reported causative agent for foodborne outbreaks. *Salmonella* in 'eggs and egg products' and in 'mixed foods' were the agent/food pairs of most concern. Outbreaks linked to 'vegetables and juices and products thereof' rose considerably compared with previous years. This report also provides updates on brucellosis, *Coxiella burnetii* (Q fever), echinococcosis, rabies, toxoplasmosis, trichinellosis, tuberculosis due to *Mycobacterium bovis* or *M. caprae*, and tularaemia.

© 2022 European Food Safety Authority and European Centre for Disease Prevention and Control.

Keywords: *Campylobacter*, foodborne outbreaks, *Listeria*, monitoring, parasites, *Salmonella*, zoonoses

Requestor: European Commission

Question number: EFSA-Q-2021-00762

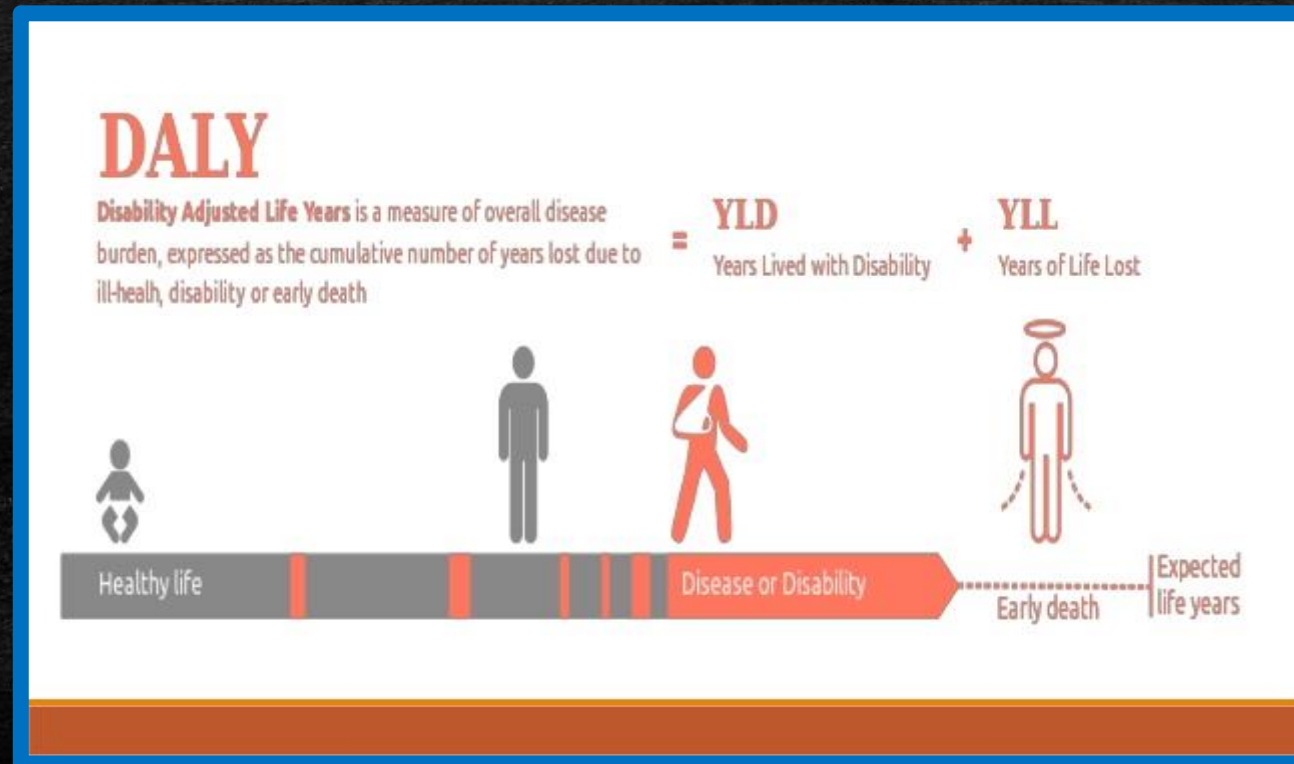


Contributing factors in strong-evidence foodborne outbreaks

- Information on factors contributing to food contamination and outbreaks was available for a minority of foodborne outbreaks . Risk factors were documented in 152 strong-evidence outbreaks (47.4% of strong-evidence 'general' outbreaks).
1. **Contamination by 'food handlers'** - norovirus FBO and *Bacillus cereus*
 2. **Cross-contamination** - *Salmonella* and *L. monocytogenes*
 3. **Inadequate heat treatment**
 4. **Time/temperature storage** - *C. perfringens* toxins
 5. **Inadequate chilling** - food poisoning by bacterial agents

WHO, 2022

- An estimated 600 million – almost 1 in 10 people in the world – fall ill after eating contaminated food and 420 000 die every year, resulting in the loss of 33 million healthy life years (DALYs).



БОЛЕСТИ ПРЕНОСИВЕ ХРАНОМ

- **ИНФЕКЦИЈЕ** - *Salmonella* spp., *Listeria monocytogenes*, *Campylobacter jejuni*, *Yersinia enterocolitica*
- **ТОКСОИНФЕКЦИЈЕ** - *Shigella* spp., Shiga toxin-producing *Escherichia coli*, *Clostridium perfringens*, *Bacillus cereus* (дијареични синдром)
- **ИНТОКСИКАЦИЈЕ** - *Clostridium botulinum*, *Staphylococcus aureus*, *Bacillus cereus* (еметични синдром)
- **ЕПИДЕМИЈЕ/СПОРАДИЧНИ СЛУЧАЈЕВИ**

Bolest	Izvor infekcije		
	Čovek	Mleko životinja	Sredina
Virusne bolesti			
Infekcije adenovirusima	x		
Infekcije enterovirusima (poliovirus i <i>Coxsackie virus</i>)	x		
Slinavka i šap		x	
Infektivni hepatitis	x		
Krpeljski encefalomijelitis		x	
Bakterijske bolesti			
Antraks		x	x
Botulizam		x	
Bruceloza		x	
Q groznica		x	
Koli infekcije (enterovirulentne <i>E. coli</i>)		x	
Infekcije sa <i>Cl. perfringens</i>			x
Difterija	x		
Leptospiroza		x	
Listerioza		x	
Paratifus	x	x	
Mišja groznica			x
Salmoneloza	x	x	
Šigeloza	x		
Stafilokokna enterotoksemija	x	x	
Streptokokne infekcije	x	x	
Tuberkuloza	x		
Tifus	x		
Protozoe			
Toksoplazmoza		x	

ТАБЕЛА 29. Болести које се путем млека преносе на људе

ТИФУС, ДИФТЕРИЈА, САЛМОНЕЛОЗА, СТРЕПТОКОКОЗЕ (ШАРЛАХ), Q ГРОЗНИЦА, БРУЦЕЛОЗА И ТУБЕРКУЛОЗА

Escherichia coli, *L. monocytogenes*, *Campylobacter* врсте, *Yersinia enterocolitica*



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International Dairy Journal

journal homepage: www.elsevier.com/locate/idaairy



Review

A review of the microbiological hazards of dairy products made from raw milk



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БИОЛОШКИ ХАЗАРД У СИРОВОМ МЛЕКУ

Bacillus cereus, *Campylobacter coli*, *Campylobacter jejuni*, enterotoxin-producing *Staphylococcus aureus*, verocytotoxin-producing *Escherichia coli* (VTEC), *Yersinia*, *Leptospira*, *Listeria monocytogenes*, *Salmonella* spp., *Streptococcus agalactiae*, *Streptococcus equi* subsp. *zooepidemicus*, *Clostridium botulinum*, *Brucella* spp., *Mycobacterium bovis*

ХИПОТЕТИЧКИ : није потврђено патогено деловање на људе -*Mycobacterium avium* subsp. *paratuberculosis*; MAP)

SCIENTIFIC OPINION

**Scientific Opinion on the public health risks related to the consumption of
raw drinking milk¹**

EFSA Panel on Biological Hazards (BIOHAZ)^{2,3}

European Food Safety Authority (EFSA), Parma, Italy

This scientific output, published on 8 May 2015, replaces the earlier version published on 13 January 2015.*

EFSA Panel on Biological Hazards (EFSA BIOHAZ Panel, 2015)

Јасна веза између конзумације сировог млека и обољења људи - *Campylobacter spp.*, *Salmonella spp.*, *STEC*, *Brucella melitensis*, *Mycobacterium bovis* и вирус крпељног енцефалитиса - tick-borne encephalitis virus (TBEV)

According to the EFSA Panel on Biological Hazards, there were **27 reported** outbreaks in the EU involving raw milk between 2007 and 2012. Of these, 21 were associated with ***Campylobacter spp.*** (primarily *C. jejuni*), one with *Salmonella Typhimurium*, two with *STEC* and three with TBEV.

No case of *L. monocytogenes* transmission to humans from raw milk was reported between 2007 and 2012.

According to this report, about 85% of outbreaks were due to raw milk from cows, and the rest of them occurred after consumption of caprine raw milk. Interestingly, raw donkeys' milk generally seems to be free of foodborne pathogens.

Based on the limited data available and expert opinion, microbiological hazards which are not regarded as main hazards with respect to raw milk consumption in the EU were: *Bacillus cereus*, *Brucella abortus*, *L. monocytogenes*, *S. aureus*, *Y. enterocolitica*, *Y. pseudotuberculosis*.

ВИРУСНЕ БОЛЕСТИ КОЈЕ СЕ ПРЕНОСЕ МЛЕКОМ

- Adenovirusi, Poliovirusi, Coxsacki вирус и вирус инфективног хепатитиса - вирулентни за људе, извор контаминације млека - човек
- Вирус крпељног енцефалитиса, вирус слинавке и шапа, вирус крављих богиња – вирулентни за људе и животиње, извор контаминације млека – обољеле животиње



Contents lists available at ScienceDirect

International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro



Review

Foodborne viruses: Detection, risk assessment, and control options in food processing



Albert Bosch^a, Elissavet Gkogka^b, Françoise S. Le Guyader^c, Fabienne Loisy-Hamon^d, Alvin Lee^e, Lilou van Lieshout^{f,*}, Balkumar Marthi^{g,h}, Mette Myrmelⁱ, Annette Sansom^j, Anna Charlotte Schultz^k, Anett Winkler^l, Sophie Zuber^m, Trevor Phisterⁿ

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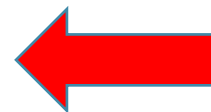
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ⁿ PepsiCo Europe, Beaumont Park 4, Leycroft Road, LE4 1ET Leicester, United Kingdom

CDC – Centar for Disease Control and Prevention: 2009-2019 - у 48% случајева болести преносивих храном, као узрочник препознаје се *Norovirus*; зелено поврће, свеже воће и шкољке

Table 2Viruses documented to be found in the human gastrointestinal tract.^b

Genus	Genome	Popular name	Disease caused
<i>Enterovirus</i>	ssRNA	Poliovirus Coxsackie A, B virus	Paralysis, meningitis, fever Herpangina, meningitis, fever, respiratory disease, hand-foot-and-mouth disease, myocarditis, heart anomalies, rash, pleurodynia, diabetes ^a
		Echovirus	Meningitis, fever, respiratory disease, rash, gastroenteritis
<i>Hepatovirus</i>	ssRNA	Hepatitis A virus	Hepatitis
<i>Kobuvirus</i>	ssRNA	Aichi virus	Gastroenteritis
<i>Parechovirus</i>	ssRNA	Human parechovirus	Respiratory disease, gastroenteritis, CNS infection
<i>Orthoreovirus</i>	segmented dsRNA	Human reovirus	Unknown
<i>Rotavirus</i>	segmented dsRNA	Human rotavirus	Gastroenteritis
<i>Norovirus</i>	ssRNA	Human norovirus	Gastroenteritis
<i>Sapovirus</i>	ssRNA	Human sapovirus	Gastroenteritis
<i>Hepevirus</i>	ssRNA	Hepatitis E virus	Hepatitis
<i>Mamastrovirus</i>	ssRNA	Human astrovirus	Gastroenteritis, CNS infection
<i>Flavivirus</i> ^c	ssRNA	Tick-borne encephalitis virus	Encephalitis, meningitis
<i>Coronavirus</i>	ssRNA	Human coronavirus	Gastroenteritis, respiratory disease, SARS, MERS
<i>Orthomyxovirus</i>	segmented ssRNA	Avian influenza virus	Influenza, respiratory disease
<i>Henipavirus</i>	ssRNA	Nipah virus, Hendra virus	Encephalitis, respiratory disease
<i>Parvovirus</i>	ssDNA	Human parvovirus	Gastroenteritis
<i>Mastadenovirus</i>	dsDNA	Human adenovirus	Gastroenteritis, respiratory disease, conjunctivitis
<i>Polyomavirus</i>	dsDNA	Polyomavirus	Progressive multifocal leukoencephalopathy, diseases of urinary tract
<i>Alphatorquevirus</i>	ssDNA	TT (Torque Teno) virus	Unknown, hepatitis ^a , respiratory disease ^a haematological Disorders ^a , cancer ^a

^a Uncertain whether the disease is caused by the virus.^b Any virus in the gastrointestinal tract could potentially be transmitted via food.^c Has been found in food (milk) but not in gastrointestinal tract.

FOOD-BORNE VIRUSES

- viral GE – 10^{13} вирусних партикула /g фецеса
- Низак ниво контаминације – хетерогена дистрибуција – процедура изолације и детекције
- индикатори фекалне контаминације – *Escherichia coli* – непоуздани показатељи присуства ентеричних вируса
- PCR – методологија – детекција вирусне нуклеинске киселине – инфективност вируса
- КОНТРОЛНЕ МЕРЕ - *@growth is not a concern, whereas survival or maintaining infectivity is KEY*
- > 90°C/ 90 sek (инактивација норовируса у шкољкама)

Review

Food-Borne Transmission of Tick-Borne Encephalitis Virus—Spread, Consequences, and Prophylaxis

Alicja M. Buczek¹, Weronika Buczek¹, Alicja Buczek^{1,*} and Joanna Wysokińska-Miszczuk²

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Abstract: Tick-borne encephalitis (TBE) is the most common viral neurological disease in Eurasia. It is usually transmitted via tick bites but can also occur through ingestion of TBEV-infected milk and dairy products. The present paper summarises the knowledge of the food-borne TBEV transmission and presents methods for the prevention of its spread. The incidence of milk-borne TBE outbreaks is recorded in central, eastern, and north-eastern Europe, where *Ixodes ricinus*, *Ixodes persulcatus*, and/or *Dermacentor reticulatus* ticks, i.e., the main vectors of TBEV, occur abundantly. The growing occurrence range and population size of these ticks increases the risk of infection of dairy animals, i.e., goats, sheep, and cows, with viruses transmitted by these ticks. **Consumers of unpasteurised milk and dairy products purchased from local farms located in TBE endemic areas are the most vulnerable to alimentary TBEV infections.** Familial infections with these viruses are frequently recorded, mainly in children. Food-transmitted TBE can be monophasic or biphasic, and some of its neurological and psychiatric symptoms may persist in patients for a long time. Alimentary TBEV infections can be effectively prevented by consumption of pasteurised milk and the use of TBEV vaccines. It is recommended that milk and dairy products should be checked for the presence of TBE viruses prior to distribution. Protection of dairy animals against tick attacks and education of humans regarding the epidemiology and prophylaxis of TBE are equally important.

Keywords: tick-borne encephalitis virus; TBE outbreaks; food-borne transmission; milk-borne infections; alimentary infection



Citation: Buczek, A.M.; Buczek, W.; Buczek, A.; Wysokińska-Miszczuk, J. Food-Borne Transmission of Tick-Borne Encephalitis Virus—Spread, Consequences, and Prophylaxis. *Int. J. Environ. Res. Public Health* **2022**, *19*, 1812. <https://doi.org/10.3390/ijerph19031812>



Approximately 10,000–13,000 cases of this disease are registered each year, and the highest TBE incidence (>10/100,000 population) is reported in the Baltic countries, the Czech Republic, Slovakia, Russia, and Slovenia.

According to estimates, approximately 1% of all human TBEV infections are acquired through consumption of infected unpasteurised milk or dairy products from infected livestock.



Short communication

Tick-borne encephalitis outbreak following raw goat milk consumption in a new micro-location, Croatia, June 2019

[Maja Ilic](#)^{a,b}  , [Ljubo Barbic](#)^c, [Maja Bogdanic](#)^b, [Irena Tabain](#)^b, [Vladimir Savic](#)^d, [Mirjana Lana Kosanovic Licina](#)^e, [Bernard Kaic](#)^b, [Andreja Jungic](#)^d, [Marko Vucelja](#)^f, [Vlado Angelov](#)^g, [Marinka Kovacevic](#)^h, [Dobrica Roncevic](#)^h, [Samira Knezevic](#)ⁱ, [Vladimir Stevanovic](#)^c, [Irena Slavuljica](#)^{i,j}, [Danijela Lakoseljac](#)^h, [Ninoslava Vickovic](#)^k, [Marina Bubonja-Sonje](#)^{i,j}, [Lisa Hansen](#)^{a,l}, [Tatjana Vilibic-Cavlek](#)^{b,m}

SURVEILLANCE AND OUTBREAK REPORT

A cluster of two human cases of tick-borne encephalitis (TBE) transmitted by unpasteurised goat milk and cheese in Germany, May 2016

SO Brockmann¹, R Oehme², T Buckenmaier³, M Beer⁴, A Jeffery-Smith⁵, M Spannenkrebs⁶, S Haag-Miltz⁷, C Wagner-Wiening², C Schlegel¹, J Fritz¹, S Zange⁸, M Bestehorn⁹, A Lindau⁹, D Hoffmann⁴, S Tiberi⁵, U Mackenstedt⁹, G Dobler^{8,9}

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-
- The highest number of food-borne TBE infections is noted in Slovakia, where as many as 17% of all recorded human TBE cases are associated with the consumption of contaminated unpasteurised milk .
 - As many as 24 of the 30 countries with the highest consumption of milk and dairy products per capita are European countries . They are represented by the Baltic countries (Finland, Sweden, Denmark, Norway, Lithuania, Estonia) as well as central (Switzerland, Austria, Germany) and south-eastern (Slovenia, Croatia, Greece) European countries, where an increase in the TBE incidence is reported.

Table 1. Examples of tick-borne encephalitis (TBE) outbreaks in Europe related to milk and cheese consumption.

Country	Years/Months	Number of Ill/Exposed People/Outbreaks	The Source of the Infection (Number/% of Hospitalized Patients)	References
Slovak Republic	2012–2016/ April–November, the most outbreaks from April to June	110/714/13	goat's milk, cheese (41 /37.3%) sheep's milk, cheese (67/60.9%) cow's milk, cheese (2/1.8%)	Dorko et al. 2018 [101]
Czech Republic	1997–2008	64/nd/nd	goats' milk (36/56.3%) sheep's milk, cheese (21/32.8%) dairy milk (7/10.9%)	Kriz, Benes and Daniel 2009 [36]
Hungary	2007 / August 2011/September–October	25/154/1 30/nd/nd	goat milk cow milk	Bologh et al. 2010 [107] Caini et al. 2012 [113]
Slovenia	2012/May	3/5/1	goat milk	Hudopisk et al. 2013 [108]
Croatia	2015/ April–May 2019/ June	7/10/1 5/nd/1	goat milk or cheese goat milk	Markonovović et al. 2016 [109] Ilic et al. 2020 [111]
Austria	2008	6/nd/1	self-made cheese from mixture of goat milk and cow milk	Holzmann et al. 2009 [106]
Germany	2016/May–June	2/3/1	goat milk, cheese	Brockmann et al. 2018 [39]
Poland	2017/June	4/nd/1	goat milk	Król et al. 2019 [110]
Estonia	2005/ May–June	27/nd/nd	goat milk	Kerbo et al. 2004 [33]

ВИРУС – ИНАКТИВАЦИЈА НТСТ ПАСТЕРИЗАЦИЈА

КРПЕЉНИ ЕНЦЕФАЛИТИС

- Далекоисточни или руски пролећно – летњи енцефалитис, централно европски крпељни енцефалитис, биундулантни менингоенцефалитис, дифазична млечна болест
- ARBOVIRUSI групе В; genus FLAVIVIRUS
- Субтипови: европски (TBEV-Eu), сибирски (TBEV-Sib), далекоисточни (Far Eastern (TBEV-FE))
- there are two TBEV variants, which are probably new subtypes, i.e., Baikalian (TBEVBkl) and Himalayan (TBEV-Him)
- симптоми: инкубација 3-4 дана (7-14 дана након уједа крпеља)- грозница, општа слабост, главобоља – АСИМПТОМАТСКИ ПЕРИОД (2-10 дана) – енцефалитис, менингитис, мијелитис

Tick-Borne Encephalitis Virus Seropositivity among Tick Infested Individuals in Serbia

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 † Equal contribution.



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Abstract Tick-borne encephalitis (TBE), caused by the TBE virus (TBEV), is a life-threatening disease with clinical symptoms ranging from non-specific to severe inflammation of the central nervous system. Despite TBE is a notifiable disease in Serbia since 2004, there is no active TBE surveillance program for the serologic or molecular screening of TBEV infection in humans in the country. This prospective cohort study aimed to assess the TBEV exposure among tick-infested individuals in Serbia during the year 2020. A total of 113 individuals exposed to tick bites were recruited for the study and screened for anti-TBEV antibodies using a commercial indirect fluorescent antibody test (IFA) test. Blood samples from 50 healthy donors not exposed to tick bites were included as a control group. Most of the enrolled patients reported infestations with one tick, being *I. ricinus* the most frequent tick found in the participants. The TBEV seroprevalence was higher (13.27%, 15 total 113) in tick-infested individuals than in healthy donors (4%, 2 total 50), although the difference was not significant. Notably, male individuals exposed to tick bites showed five times higher relative risk (RR) of being TBEV-seropositive than healthy donors of the same gender (RR= 5.1, CI = 1.6–19; $p = 0.007$). None of the seropositive individuals developed clinical manifestations of TBE, but the first clinical-stage of Lyme borreliosis (i.e., erythema migrans) was detected in seven of them. Potential TBEV foci were identified in rural areas, mostly in proximity or within the Fruška Gora mountain.

Novi Sad dobio dva mlekomata

25. septembra 2022.



Foto: <https://nsuzivo.rs/>

ignorantia juris non excusat

"Током 2016-2017. године играо сам рукомет у Аустрији и тада сам се по први пут сусрео са млекомотима. Изненадио сам се што је млеко које сам ту куповао имало потпуно другачији, пунији и лепши укус. Одговарало ми је и то што је млеко на млекомотима доступно 24 сата, па сам, рецимо, могао да га купим у 10 увече када се вратим са тренинга", рекао овај млади предузетник за "Пољопривредник".

Лист подсећа да држава однедавно издваја бесповратна средства газдинствима и предузетницима за куповину ових апарата што је додатни подстицај за све оне који желе да избегну посреднике у продаји млека.

БАКТЕРИЈСКЕ БОЛЕСТИ КОЈЕ СЕ ПРЕНОСЕ МЛЕКОМ

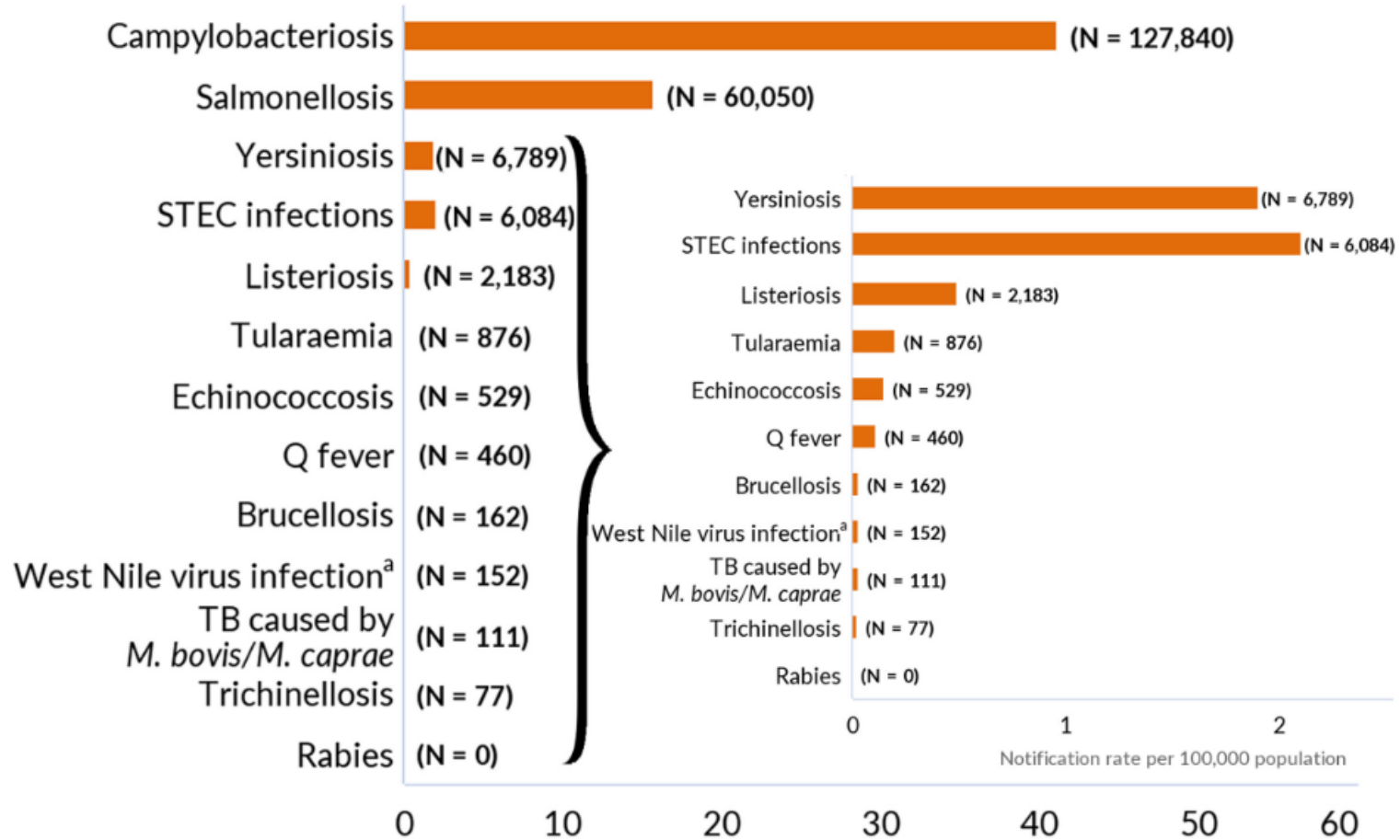
- Q – ГРОЗНИЦА
- ТУБЕРКУЛОЗА
- БРУЦЕЛОЗА
- ПАРАТУБЕРКУЛОЗА
- САЛМОНЕЛОЗА
- АНТРАКС
- ЛЕПТОСПИРОЗА
- ЛИСТЕРИОЗА
- КАМПИЛОБАКТЕРИОЗА

- ИНТОКСИКАЦИЈЕ ЕНТЕРОТОКСИНИМА СТАФИЛОКОКА
- БАЦИЛАРНА ТРОВАЊА ХРАНОМ
- ОБОЉЕЊА ИЗАЗВАНА ЕНТЕРОВИРУЛЕНТИМ *E. coli*



EU One Health Zoonoses Report 2021

With regard to foodborne outbreaks (FBOs), *Salmonella*, Norovirus and *Campylobacter* accounted for the highest number of outbreaks and cases.



GLOBAL TUBERCULOSIS REPORT

2022



GLOBAL TUBERCULOSIS REPORT 2022

TB SITUATION AND RESPONSE

- Tuberculosis (TB) is contagious and airborne.
- TB is the second leading infectious killer after COVID-19 and the 13th leading cause of death worldwide. It is also the leading killer of people with HIV and a major cause of deaths related to antimicrobial resistance

TB BURDEN

- In 2021, an estimated 10.6 million (95% confidence interval 9.9-11 million) people fell ill with TB worldwide, of which 6.0 million were men, 3.4 million were women and 1.2 million were children. People living with HIV accounted for 6.7% of the total.
- The TB incidence rate (new cases per 100 000 population per year) rose by 3.6% between 2020 and 2021, reversing declines of about 2% per year for most of the past 2 decades.
- Globally, the estimated number of deaths from TB increased between 2019 and 2021, reversing years of decline between 2005 and 2019. In 2021, 1.6 million people died from TB, including 187 000 people with HIV.
- Eight countries accounted for more than two thirds of the global total: India, Indonesia, China, the Philippines, Pakistan, Nigeria, Bangladesh and the Democratic Republic of the Congo.

GLOBAL
TUBERCULOSIS
REPORT

2022



World Health
Organization



THE COVID-19 PANDEMIC HAS
REVERSED YEARS OF PROGRESS
MADE IN THE FIGHT TO END TB

It continues to have a damaging
impact on access to TB services



1.6 MILLION TB DEATHS
INCLUDING 187 000 TB DEATHS
AMONG PEOPLE WITH HIV

TB is one of the top infectious killers
worldwide.

TB is also the leading cause of deaths among people
with HIV and a major cause of antimicrobial resistance
related deaths

74 MILLION LIVES SAVED (2000 - 2021)

Tuberculosis (TB) causing organisms include *M. tuberculosis sensu stricto* and *M. africanum*, causing the majority of human disease. A number of other organisms from the *M. tuberculosis* complex (MTBC), present in animals and the environment, can cause zTB, these include *M. canetti*, *M. bovis*, *M. caprae*, *M. microti*, *M. pinnipedii*, *M. mungi*, and *M. orygis* (*M. orygis* seems to be the major pathogen in Indian cattle, *Bos indicus*).

The detection of *M. orygis* in both humans and animals presents three possible scenarios: 1) the infection is endemic in animals, which are a source of transmission to humans; 2) humans are the principal maintenance host of *M. orygis* and spill over occurs to other species during close contact; or 3) the infection is endemic in both humans and animals. The absence of clarity in this regard has been highlighted by others.

Mycobacteria forming so-called *Mycobacterium tuberculosis* (MTB) complex that is currently comprising ten species (*Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium canettii*, *Mycobacterium caprae*, *Mycobacterium microti*, *Mycobacterium mungi*, *Mycobacterium orygis*, *Mycobacterium pinnipedii*, *M. tuberculosis sensu stricto* and *Mycobacterium suricattae*)

Genomic analysis of *Mycobacterium tuberculosis* variant *bovis* strains isolated from bovine in the state of Mato Grosso, Brazil

[Taís Ramalho dos Anjos](#), ¹ [Vinícius Silva Castro](#), ² [Edson Silva Machado Filho](#), ³ [Philip Noel Suffys](#), ^{3,*} [Harrison Magdinier Gomes](#), ³ [Rafael Silva Duarte](#), ⁴ [Eduardo Eustáquio de Souza Figueiredo](#), ⁵ and [Ricardo César Tavares Carvalho](#) ^{1,*}

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Associated Data

► [Supplementary Materials](#)

► [Data Availability Statement](#)

Abstract

[Go to:](#) ►

The species *Mycobacterium tuberculosis* variant *bovis* (*M. tuberculosis* var. *bovis*) is associated with tuberculosis, mainly in cattle and buffaloes. This pathogen has the potential to infect other mammals, including humans. Tuberculosis caused by *M. tuberculosis* var. *bovis* is a zoonosis clinically identical to tuberculosis caused by *Mycobacterium tuberculosis*, and the recommended treatment in humans results in the use of antibiotics. In this study, we used the whole genome sequencing (WGS) methodology Illumina NovaSeq 6000 System platform to characterize the genome of *M. tuberculosis* var. *bovis* in cattle circulating in Mato Grosso, identify mutations related to

Phylogenomic analysis of the species of the *Mycobacterium tuberculosis* complex demonstrates that *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*, *Mycobacterium microti* and *Mycobacterium pinnipedii* are later heterotypic synonyms of *Mycobacterium tuberculosis*

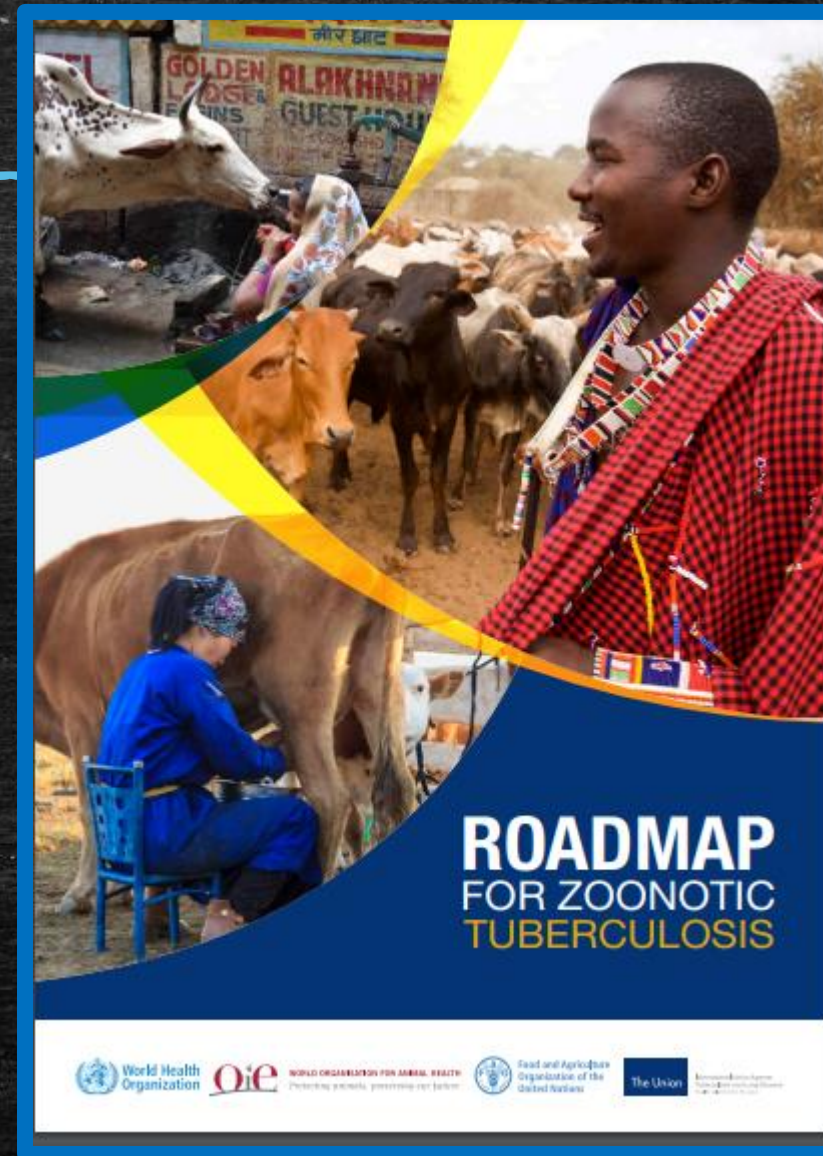
Marco A. Riojas,^{1,*} Katya J. McGough,^{1,2} Cristin J. Rider-Riojas,³ Nalin Rastogi⁴ and Manzour Hernando Hazbón¹

Abstract

The species within the *Mycobacterium tuberculosis* Complex (MTBC) have undergone numerous taxonomic and nomenclatural changes, leaving the true structure of the MTBC in doubt. We used next-generation sequencing (NGS), digital DNA–DNA hybridization (dDDH), and average nucleotide identity (ANI) to investigate the relationship between these species. The type strains of *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*, *Mycobacterium microti* and *Mycobacterium pinnipedii* were sequenced via NGS. Pairwise dDDH and ANI comparisons between these, previously sequenced MTBC type strain genomes (including '*Mycobacterium canettii*', '*Mycobacterium mungi*' and '*Mycobacterium orygis*') and *M. tuberculosis* H37Rv^T were performed. Further, all available genome sequences in GenBank for species in or putatively in the MTBC were compared to H37Rv^T. Pairwise results indicated that all of the type strains of the species are extremely closely related to each other (dDDH: 91.2–99.2 %, ANI: 99.21–99.92 %), greatly exceeding the respective species delineation thresholds, thus indicating that they belong to the same species. Results from the GenBank genomes indicate that all the strains examined are within the circumscription of H37Rv^T (dDDH: 83.5–100 %). We, therefore, formally propose a union of the species of the MTBC as *M. tuberculosis*. *M. africanum*, *M. bovis*, *M. caprae*, *M. microti* and *M. pinnipedii* are reclassified as later heterotypic synonyms of *M. tuberculosis*. '*M. canettii*', '*M. mungi*', and '*M. orygis*' are classified as strains of the species *M. tuberculosis*. We further recommend use of the infrasubspecific term 'variant' ('var.') and infrasubspecific designations that generally retain the historical nomenclature associated with the groups or otherwise convey such characteristics, e.g. *M. tuberculosis* var. *bovis*.

Of 10 million people currently with new active TB, 140,000 (range, 69,800–235,000) are estimated to be new cases of zTB (1.4%) of which an approximately 11,400 (8.1%, range 4,470-21,600) died ([WHO, 2020a](#)).

- The OIE, the World Health Organization (WHO), the Food and Agriculture Organization of the UN (FAO) and the International Union Against Tuberculosis and Lung Disease (The Union) jointly launched the first-ever [roadmap to tackle zoonotic TB](#) in October 2017. It is based on a [One Health](#) approach recognising the interdependence of human and animal health sectors for addressing the major health and economic impacts of this disease.



10 PRIORITIES FOR ZOO NOTIC TB

Ten priority areas have been identified for tackling zoonotic TB in people and bovine TB in animals. These fall under three core themes: improving the scientific evidence base, reducing transmission at the animal-human interface, and strengthening intersectoral and collaborative approaches.

„The maintenance function represents the capacity to maintain the pathogen within the ecosystem. A maintenance host is a host population (single population) or multiple populations in which the pathogen persists even in the complete absence of transmission from other hosts”

The role of wildlife

Domestic cattle are the principal hosts of *M. bovis*. However, other domestic livestock and wildlife are also susceptible to infection. Some wildlife species are considered “maintenance” hosts, acting as important sources of infection for livestock. This can be due to their inherent susceptibility to the pathogen or the habitat they occupy in relation to livestock. These include European badgers (*Meles meles*) in the United Kingdom and Ireland; brushtail possums (*Trichosurus vulpecula*) in New Zealand; wild boar (*Sus scrofa*) in the Iberian peninsula; African buffalo (*Syncerus caffer*) in South Africa; and elk (*Cervus canadensis*) and white-tailed deer (*Odocoileus virginianus*) in the United States. Other wildlife species can be considered “spillover” hosts, meaning that they can be infected but do not necessarily play a role in transmission to livestock. Multi-sectoral research efforts are needed to improve understanding of the role of wildlife in the dynamics of *M. bovis* infection in livestock and to develop sustainable control strategies.

6. Reduce the risk to people

Identify key populations and risk pathways for transmission of zoonotic TB

Preventing disease in people requires reducing the risk of exposure and transmission at the human-animal interface. While the principal routes of transmission are known, more information is needed about the underlying sociocultural and economic reasons for practices that facilitate transmission to people, and how to promote safer alternatives. Determinants of progression from exposure to infection, and from infection to disease, should be explored. The use of sequencing technologies and phylogenetic analyses may play a role in characterising transmission mechanisms, identifying sources of infection and investigating drug resistance. Groups at risk of disease need to be better defined but can include:

- communities living in close contact with livestock and where access to safe food, healthcare, veterinary services may be poor, including rural communities or semi-nomadic/nomadic pastoralist populations;
- people with an occupational exposure to livestock, including farmers, veterinarians and other animal health workers, abattoir workers, butchers and livestock traders;
- children and those more likely to consume unpasteurized milk and dairy products; and
- immunocompromised people, such as those living with HIV/AIDS.

Cultural practices can influence **food consumption behaviours**. In many parts of the world, dairy systems often lack specialized equipment for collecting, treating and processing milk, which may be influenced by cultural and/or economic factors. For example, groups such as the Fulani in West and Central Africa or the Maasai in East Africa rely on livestock for their livelihoods and commonly consume milk and other dairy products without heat treatment. This places these communities at risk of contracting foodborne diseases, including zoonotic TB. In some African countries, butchers may eat the parts of the cows' lungs with visible TB lesions in order to convince potential buyers that the meat is safe.

In high-income countries, zoonotic TB may still pose a risk to some groups. In the United States of America, Hispanic communities bear the majority of the burden of zoonotic TB. This is linked to the practice of consuming fresh cheese made from untreated milk (queso fresco), often sourced from areas in Latin America where bovine TB is endemic.

INTERFACE

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Research



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Life Sciences–Mathematics interface

Characterizing reservoirs of infection and the maintenance of pathogens in ecosystems

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We use a previously published compartmental model of the dynamics of pathogens in ecosystems to define and explore the concepts of maintenance host, maintenance community and reservoir of infection in a full ecological context of interacting host and non-host species. We show that, contrary to their current use in the literature, these concepts can only be characterized relative to the ecosystem in which the host species are embedded, and are not ‘life-history traits’ of (groups of) species. We give a number of examples to demonstrate that the same (group of) host species can lose or gain maintenance or reservoir capability as a result of a changing ecosystem context, even when these changes primarily affect non-hosts. One therefore has to be careful in designating host species as either maintenance or reservoir in absolute terms.

Terms in use include maintenance host, maintenance community, reservoir host/species and reservoir community, where the first two relate directly to the persistence of the pathogen (i.e. indefinite presence). The latter two terms relate to the ability of the pathogen to persist and to act as a sustained source of transmission (reservoir) of that pathogen to a specified (target) host species of concern (for example, humans, farm animals, agricultural crops, plant or animal species of conservation interest).

A maintenance host/community is essential for the persistence of a pathogen, whether or not such a host/ community can also transmit the pathogen to a specified target species of concern.

Reverse zoonoses or zoonoanthroposes have been recorded in studies from Africa and India (Duffy et al., 2020).

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Zoonotic Tuberculosis – The Changing Landscape

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In India, *M. tuberculosis* (MANU strain) was found to be more prevalent in cattle than *M. bovis*. *M. tuberculosis* MANU1 strain infection in cattle is likely due to spillover from humans in TB endemic areas and demonstrates the potential for MDR-TB strains to acquire an animal reservoir that could then pose a future risk to human TB control. Reverse zoonoses with *M. tuberculosis* has also been reported in zoo animals especially in elephants, primates and felines.

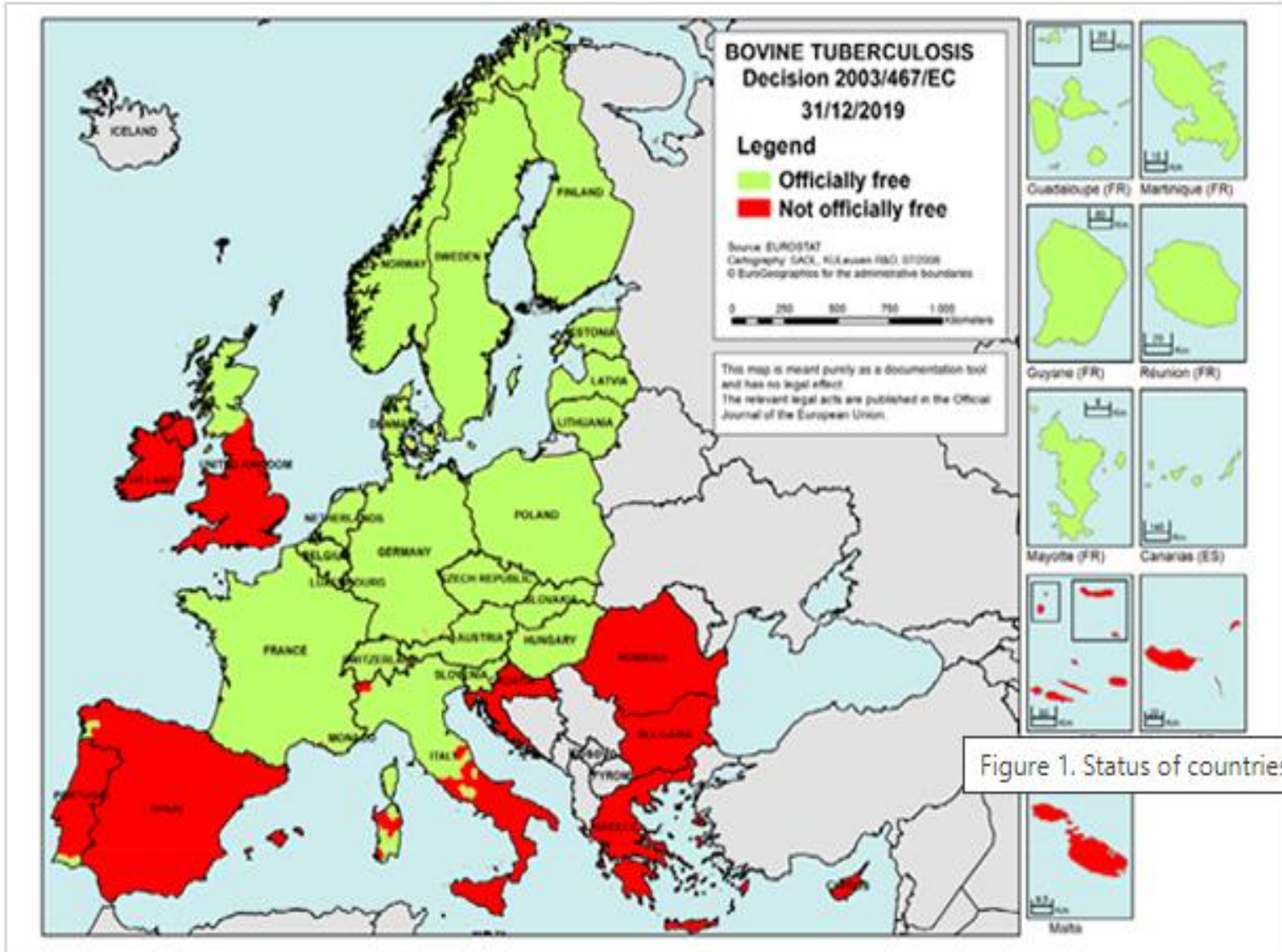


Figure 1. Status of countries on TB in bovine animals, 2019 (EFSA, 2021)

Figure 1. Status of countries on TB in bovine animals, 2019 (EFSA, 2021) (2):

▪ ТУБЕРКУЛИНИЗАЦИЈА – ТЕРМИЧКА ОБРАДА

- У промет се може ставити сирово млеко од крава или биволица, које припадају стаду, слободном од туберкулозе, у складу са посебним прописом којим се уређују мере за откривање, спречавање ширења, сузбијања и искорењивања заразне болести туберкулозе, или колострум, као и млеко женки других врста животиња, које припадају стадима која се, ако се ради о врстама које су пријемчиве на туберкулозу, редовно контролишу на присуство те болести у оквиру програма мера здравствене заштите животиња. Ако се козе држе заједно са кравама, такве козе морају бити прегледане и испитане на присуство туберкулозе.
- Млеко које потиче од животиња које нису реаговале позитивно на тестове прописане за туберкулозу и, које не показују симптоме те болести, а које припадају стаду у коме је дијагностикована туберкулоза, након издвајања оболелих и животиња код којих је утврђена позитивна туберкулинска реакција, се може користити после топлотне обраде након које је реакција алкалне фосфатазе негативна.

САЛМОНЕЛОЗА

- Свежи сиреви, меки сиреви произведени слатком коагулацијом, млеко у праху
- Производне партије сира, маслаца и павлаке, произведених од сировог млека, партије млека у праху, сурутке у праху и сладоледа уколико садрже *Salmonella* spp. у 25 г или мл узорка, представљају опасност по здравље људи и не могу се ставити у промет, а ако се налазе у промету, производна партија се мора опозвати или повући из промета.

САЛМОНЕЛОЗА

Salmonella у различитим категоријама хране:

- задовољавајућа, ако све вредности указују на одсуство бактерије,
- незадовољавајућа, ако је присуство бактерије откривено у било којој јединици узорка.

Правилник о општим и посебним условима хигијене хране у било којој фази производње, прераде и промета: 72/2010-14, 62/20

Претрага по приказаном тексту							
	елиминисхе ризик од салмонеле						употребе
1.8.	Производи од меса живине, намењени за јело после кувања	<i>Salmonella</i>	5	0	Не сме бити у 25 g	EN ISO 6579	Производ у промету током његовог рока употребе
1.9.	Желатин и колаген	<i>Salmonella</i>	5	0	Не сме бити у 25 g	EN ISO 6579	Производ у промету током његовог рока употребе
1.10.	Сиреви, маслац и павлака произведени од сировог млека или млека које је обрађено температуром нижом од температуре пастеризације ⁽¹⁰⁾	<i>Salmonella</i>	5	0	Не сме бити у 25 g	EN ISO 6579	Производ у промету током његовог рока употребе
1.11.	Млеко у праху и сурутка у праху	<i>Salmonella</i>	5	0	Не сме бити у 25 g	EN ISO 6579	Производ у промету током његовог рока употребе
1.12.	Сладолед ⁽¹¹⁾ , изузимајући производе код којих процес производње или састав производа елиминисхе ризик од салмонеле	<i>Salmonella</i>	5	0	Не сме бити у 25 g	EN ISO 6579	Производ у промету током његовог рока употребе

САЛМОНЕЛОЗА

TABLE 7 Salmonellosis outbreaks traced back to milk and dairy products consumption occurred from 2000 to 2019

Serotype	Country	Year	Food	Number of cases	References
<i>S. Typhimurium</i>	USA (Pennsylvania and New Jersey)	2000	Milk contaminated after pasteurization	93	Olsen et al., 2004
<i>S. Enteritidis</i>	France	2001	Cantal cheese made from raw milk	215	Haeghebaert et al., 2003
<i>S. Stanley</i>	Switzerland	2006 to 2007	Local soft cheese	82	Pastore et al., 2008
<i>S. Typhimurium</i>	France	2008	Unpasteurized goat's cheese	25	van Cauteren et al., 2009
<i>S. Montevideo</i>	France	2006	Soft cheese made with raw milk from cows	23	Dominguez et al., 2009
<i>S. Newport</i>	USA (Illinois)	2006 to 2007	Unpasteurized Mexican-style aged cheese	85	Austin et al., 2008
<i>S. Agona</i>	France	2005	Powdered infant formula	141	Brouard et al., 2007
<i>S. Typhimurium</i>	USA (multistate)	2002	Raw milk	62	Mazurek et al., 2004
<i>S. Typhimurium</i>		2006 to 2007	Ripened hard cheese made from raw milk	224	Van Duynhoven et al., 2009
<i>S. Typhimurium</i>	USA (Pennsylvania)	2007	Raw milk and raw milk cheese	29	Lind et al., 2007
<i>S. Give</i>	France	2008	Infant milk formula	6	Jourdan et al., 2008
<i>S. Enteritidis</i>	USA (multistate)	2012	Mexican-style fast food restaurant chain (77% of the ill people reported eating cheese)	68	CDC, 2012
<i>S. Dublin</i>	France	2012	Saint-Nectaire (bovine raw-milk cheese)	103	Ung et al., 2019
<i>S. Stanley</i>	USA (multistate)	2013 to 2014	Raw Cashew Cheese	17	CDC, 2014
<i>S. Dublin</i>	France	2015	Reblochon (bovine raw-milk cheese)	34	Ung et al., 2019
<i>S. Agona</i>	France, Spain and Greece	2017	Infant formula	39	EFSA & ECDC, 2018
<i>S. Poona</i>	France	2018 to 2019	Infant formula	33	Jones et al., 2019



Potrošački kutak »

OBAVIJESTI ZA POTROŠAČE



Opoziv proizvoda – SARAJEVSKA PLJESKAVICA 900g

14. listopada 2021.

OBAVIJEST ZA POTROŠAČE

Opoziv proizvoda

SARAJEVSKA PLJESKAVICA 900g

Državni inspektorat Republike Hrvatske obavještava potrošače o opozivu proizvoda SARAJEVSKA PLJESKAVICA 900g, smrznuti proizvod, LOT broja 22321, upotrijebiti do 13.08.2022., radi utvrđene bakterije iz roda *Salmonella* spp.

Proizvod nije u skladu s Uredbom (EZ) br. 2073/2005 od 15. studenoga 2005. o mikrobiološkim kriterijima za hranu.

Detaljnije informacije o opozivu proizvoda dostupne su na stranicama subjekta u poslovanju s hranom <https://stanic.hr/obavijest-za-kupce-opoziv-proizvoda-sarajevska-pljeskavica-900-g/>

Podaci o proizvodu:

Proizvođač: SZTR "Đurđević", Subotičke-Pečinci, Srbija

Stavlja na tržište: STANIĆ d.o.o., Kerestinec, Hrvatska

Obavijest se odnosi isključivo na proizvod sa gore navedenim podacima

"опозив"
(*engl. recall*) и "повлачење" (*engl. withdrawal*) прехранбених производа

Под опозивом се подразумева уклањање небезбедне хране из дистрибутивних ланаца и укључује повлачење производа продатих крајњим потрошачима.

Под повлачењем производа се подразумева уклањање небезбедних производа из дистрибутивних ланаца, али не укључује повлачење производа продатих потрошачима.

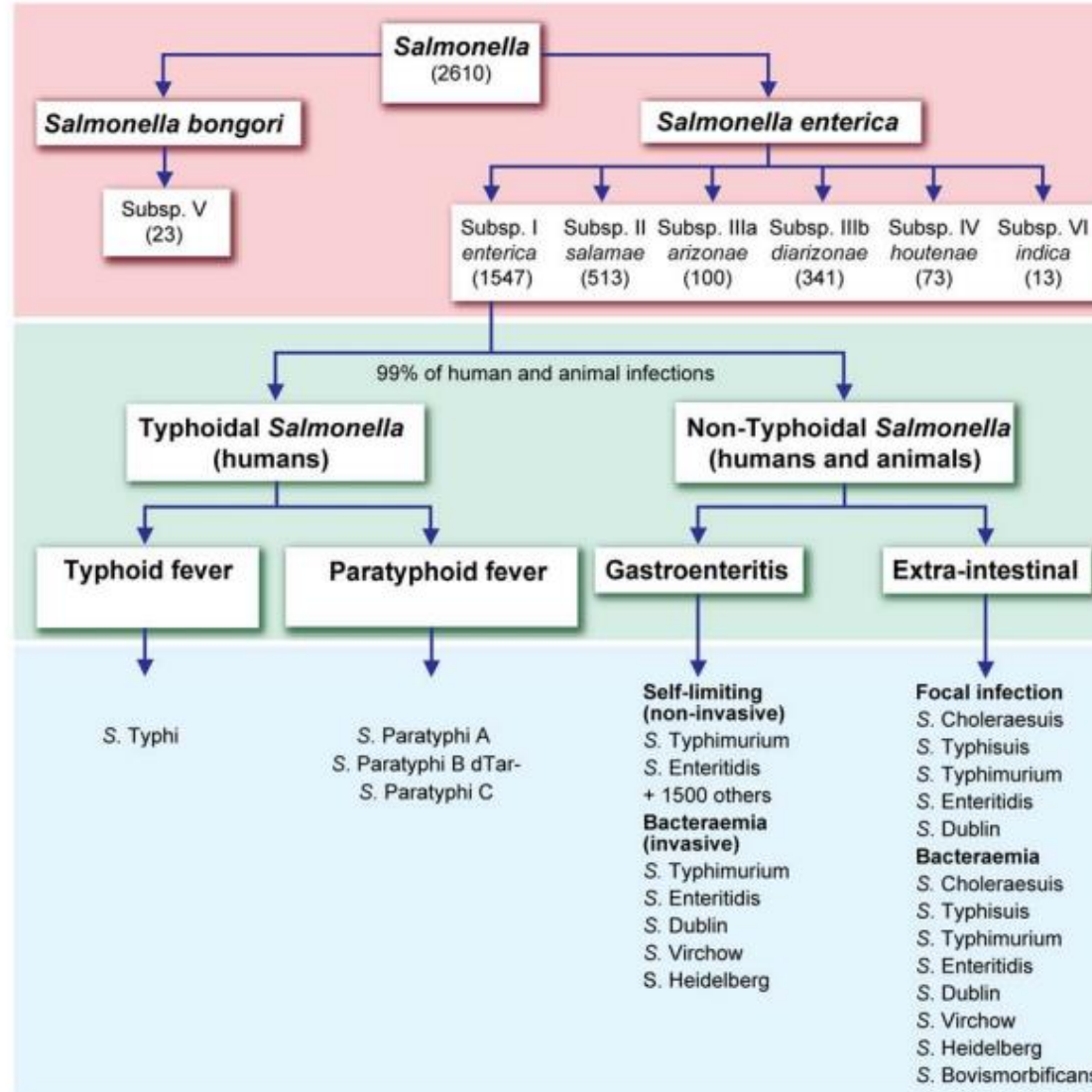
2023.7069	Milk and milk products	food	Detection of listeria monocytogenes in cheese	17 OCT 2023		 France	information notification for attention	serious	Details >>
2023.6730	Milk and milk products	food	Undeclared allergen lactose in cheese spread, from the Netherlands.	4 OCT 2023		 Netherlands	alert notification	serious	Details >>
2023.6355	Milk and milk products	food	Staphylococcal enterotoxin in raw milk cheese from Switzerland	19 SEP 2023		 Germany	alert notification	serious	Details >>
2023.6318	Milk and milk products	food	Listeria detected in cheese	18 SEP 2023		 France	alert notification	serious	Details >>
2023.5921	Milk and milk products	food	Listeria monocytogenes in cheese from France	31 AUG 2023		 Germany	alert notification	serious	Details >>
2023.5884	Milk and milk products	food	Suspected contamination with Listeria monocytogenes in soft cheese from Germany	30 AUG 2023		 Germany	alert notification	serious	Details >>
2023.5859	Milk and milk products	food	Suspicion of E.coli O103 and O26 in cheese made from raw goat's milk	29 AUG 2023		 France	alert notification	serious	Details >>
2023.5782	Milk and milk products	food	Metal particles in cheese from Spain	25 AUG 2023		 Switzerland	alert notification	potentially serious	Details >>
2023.5769	Milk and milk products	food	Shigatoxin-producing Escherichia coli (STEC) in goat cheese from France	25 AUG 2023		 Germany	alert notification	potentially serious	Details >>
2023.5764	Milk and milk products	food	Shigatoxin-producing Escherichia coli (STEC) in goat cheese from France	25 AUG 2023		 Germany	alert notification	serious	Details >>

ТИФОИДНЕ *Salmonella* spp.

слабост, главобоља,
анорексија и конгестија
мукозних мембрана горњег
респираторног тракта –
бактеријемија у 1. недељи –
развојем болести симптоми
артритиса (2%); стопа
морталитета 10%

НЕТИФОИДНЕ *Salmonella* spp.

“self-limiting” ГЕ; инкубација
12-36 сати; абдоминални
грчеви, грозница, дијареја,
понекад повраћање; трајање
1-7 дана



Species and subspecies were originally defined by DNA-DNA hybridisation, confirmed by MLEE and MLST and are currently differentiated by biochemistry and serology.

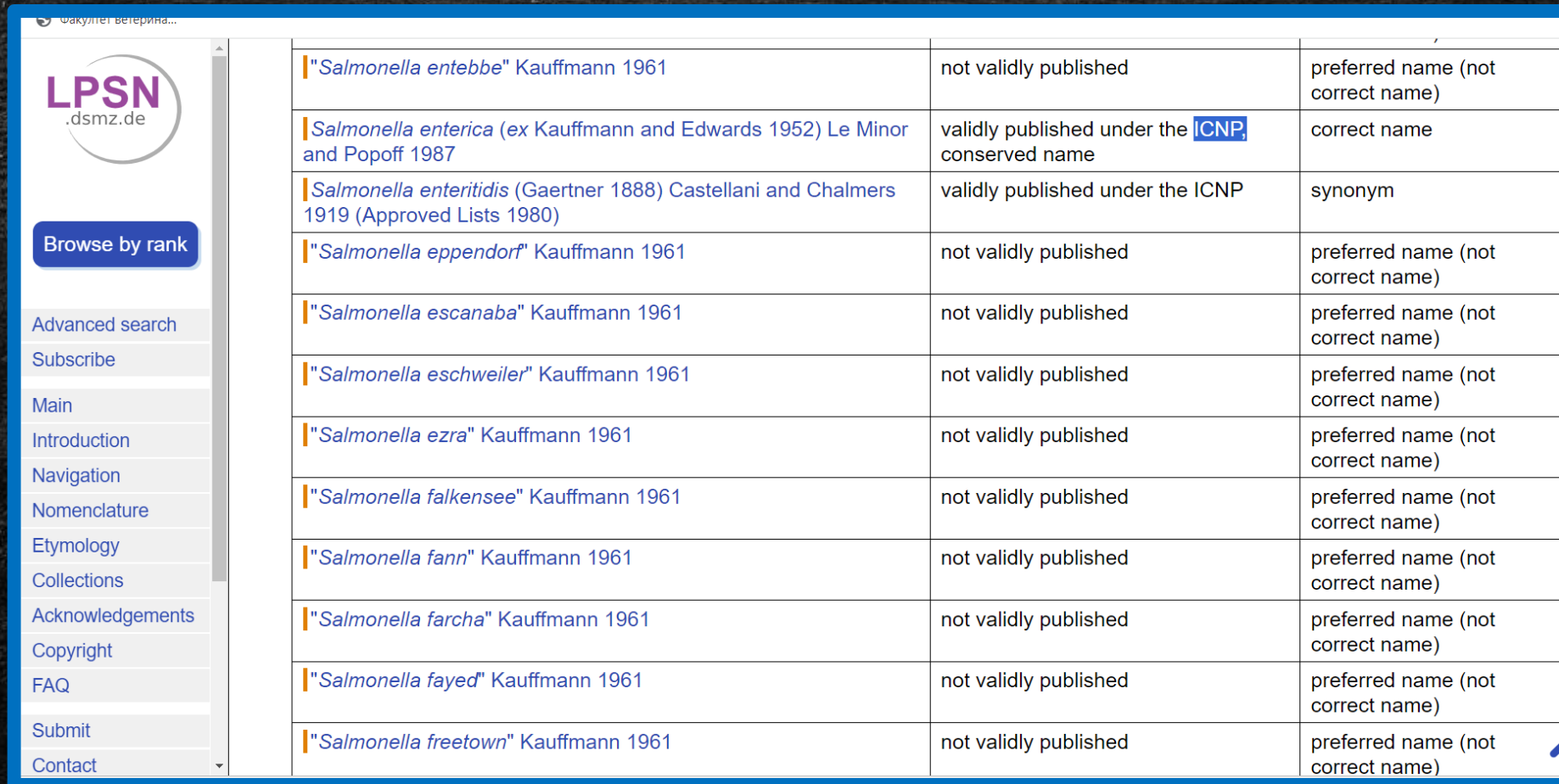
The split in typhoidal and non-typhoidal is based on the disease syndrome. Typhoid and paratyphoid fever is prolonged, whilst extra-intestinal infection is usually acute and metastatic. Gastroenteritis is characterised by diarrhoea.

Differentiation of serovars is by agglutination with specific antisera against LPS (O), two phases of flagella (H1 and H2). There are 46 O, 85 H and 1 capsule (Vi) antigen which have been described in about 1,500 combinations within subspecies I.

Figure 1. General overview of the current classification of *Salmonella enterica*.

doi:10.1371/journal.ppat.1002776.g001

<https://lpsn.dsmz.de/genus/salmonella>



The screenshot shows the LPSN website interface. On the left is a navigation menu with the LPSN logo and various links. The main content area displays a table of Salmonella species. The table has three columns: the species name and author, the publication status, and the nomenclature status.

" <i>Salmonella entebbe</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
<i>Salmonella enterica</i> (ex Kauffmann and Edwards 1952) Le Minor and Popoff 1987	validly published under the ICNP, conserved name	correct name
<i>Salmonella enteritidis</i> (Gaertner 1888) Castellani and Chalmers 1919 (Approved Lists 1980)	validly published under the ICNP	synonym
" <i>Salmonella eppendorf</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella escanaba</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella eschweiler</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella ezra</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella falkensee</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella fann</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella farcha</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella fayed</i> " Kauffmann 1961	not validly published	preferred name (not correct name)
" <i>Salmonella freetown</i> " Kauffmann 1961	not validly published	preferred name (not correct name)

Together We Can

Take on Typhoid

Getting it right with *Salmonella* nomenclature

Patricia I. Fields, PhD, Division of Foodborne, Waterborne, and Environmental Diseases, US Centers for Disease Control and Prevention
John A. Crump, MB ChB, MD, DTM&H, McKinlay Professor of Global Health, Co-Director, Otago Global Health Institute, University of Otago



? What are the *Salmonella* species and subspecies that I need to know?

There are two species of *Salmonella*:

Salmonella enterica

Salmonella bongori

Within *Salmonella enterica*, there are six subspecies which are commonly abbreviated by Roman numerals:

Salmonella enterica subspecies *enterica* (subspecies I)

Salmonella enterica subspecies *diarizonae* (subspecies IIIb)

Salmonella enterica subspecies *salamae* (subspecies II)

Salmonella enterica subspecies *hautena* (subspecies IV)

Salmonella enterica subspecies *arizonae* (subspecies IIIa)

Salmonella enterica subspecies *indica* (subspecies VI)

Most human infections are associated with *Salmonella enterica* subspecies *enterica*.

? How should I abbreviate *Salmonella* serovars?

Main point: Clearly define abbreviation before using it, i.e. *Salmonella enterica* serovar Typhi (*Salmonella* Typhi)

Other points: The White-Kauffman-Le Minor Scheme recommends against abbreviating genus unless species is also provided. For example:

✗ *S. Typhi* is discouraged

✓ *Salmonella* Typhi is acceptable

✓ *S. enterica* serovar Typhi is acceptable

'Serovar Typhi' is particularly useful for multiple serovars, e.g., 'serovars Typhi, Paratyphi A, and Paratyphi B'

→ And remember, there is no such thing as '*Salmonella* Paratyphi'; rather, *Salmonella* Paratyphi A, *Salmonella* Paratyphi B, and *Salmonella* Paratyphi C. These can also be abbreviated as *Salmonella* serovars Paratyphi A, Paratyphi B, and Paratyphi C.

? What are appropriate collective terms for serovars?

Typhoidal *Salmonella* refers to serovars that cause typhoid or paratyphoid fever.

Nontyphoidal *Salmonella* (NTS) refers to all other serovars.

→ 'Serotype' is a widely used alternative to 'serovar,' 'serotyping' is the process of determining serovars.

? What are the appropriate terms for the diseases caused by *Salmonella*?

- **Typhoid fever** is caused by *Salmonella* Typhi.
- **Paratyphoid fever** is caused by *Salmonella* Paratyphi A, *Salmonella* Paratyphi B, or *Salmonella* Paratyphi C.
- **Enteric fever** is the collective noun for typhoid and paratyphoid fevers.
- **Nontyphoidal *Salmonella* (NTS)** are important causes of enterocolitis*, and may cause bloodstream infections and other extraintestinal infections of normally sterile sites. Some serovars and sequence types of NTS cause extraintestinal infections more frequently than others relative to diarrhea.

*Anatomically and pathologically speaking, NTS cause predominately enterocolitis rather than gastroenteritis.

? Where can I find out more?

These website provide an excellent overview of the history and current status of *Salmonella* taxonomy and nomenclature:

- o <http://www.bacterio.net/salmonella.html>
- o <http://www.bacterio.net/~salmonellanom.html>
- o https://www.pasteur.fr/sites/default/files/veng_0.pdf

Learn more and join the effort at www.takeontyphoid.org

#TakeOnTyphoid

TyVAC

Typhoid Vaccine
Advisory Committee



a program of the
Sabin Vaccine Institute

OPEN *Salmonella* nomenclature in the genomic era: a time for change

Marie A. Chattaway¹✉, Gemma C. Langridge² & John Wain^{2,3}

Salmonella enterica nomenclature has evolved over the past one hundred years into a highly sophisticated naming convention based on the recognition of antigens by specific antibodies. This serotyping scheme has led to the definition of over 2500 serovars which are well understood, have standing in nomenclature and, for the majority, biological relevance. Therefore, it is highly desirable for any change in naming convention to maintain backwards compatibility with the information linked to these serovars. The routine use of whole genome sequencing and the well-established link between sequence types and serovars presents an opportunity to update the scheme by incorporating the phylogenetically relevant sequence data whilst preserving the best of serotyping nomenclature. Advantages include: overcoming the variability in antibody preparations; removing the need to use laboratory animals and implementing a truly universal system. However, the issue of trying to reproduce the phenotyping gold standard needs to be relaxed if we are to fully embrace the genomic era. We have used whole genome sequence data from over 46,000 isolates of *Salmonella enterica* subspecies *enterica* to define clusters in two stages: Multi Locus Sequence Typing followed by antigen prediction. Sequence type—serotype discrepancies were resolved using core SNP clustering to determine the phylogenetic groups and this was confirmed by overlaying the antigenic prediction onto the core SNP clusters and testing the separation of clusters using cgMLST Hierarchical Clustering. This allowed us to define any major antigenic clusters within an ST—here called the MAC type and written as ST-serovar. Using this method, 99.96% of *Salmonella* isolates reported in the UK were assigned a MAC type and linked to a serovar name taken from the Kauffmann and White scheme. We propose a change for reporting of *Salmonella enterica* sub-types using the ST followed by serovar.

ЛИСТЕРИОЗА

- *Listeria monocytogenes* преживљава у различитим хабитатима (природни – земљиште, површинске воде, трулежна вегетација; фарма и окружење фарме и процесно окружење), али се препознаје и као узрочник инфекција људи и животиња
- Извештај о зоонозама (EFSA, ECDC, 2021)- на подручју Европске уније у 2019. години - 2 621 потврђен случај инвазивне листериозе људи, уз високу стопу морталитета (17,6%).
- Из контаминиране хране изолују се хипервирулентни сојеви *Listeria monocytogenes*

-
- 4 главне филогенетске линије (лозе) (I-IV) (енгл. *lineages*), више од 14 серотипова и 4 PCR серогрупе (мултиплекс ланчана реакција полимеразе за амплификацију 4 специфична маркер гена; добра корелација са серотиповима *Listeria monocytogenes*)
 - Серотипови линије III и IV ретко се изолују из хране и углавном се доказују код преживара
 - Већина изолата који се доказују у случајевима листериозе људи припада 4b (највећи број клиничких изолата), 1/2a (највећи број изолата пореклом из процесног окружења) и 1/2b серотиповима.

Могући сценарио трансмисије *Listeria monocytogenes* на фарми музних крава

- Иницијална контаминација усева и земљишта путем водотокова, дивљих животиња, птица, коришћењем стајњака за ђубрење култивисаних површина
- Фармске животиње могу бити директно изложене *Listeria monocytogenes* из земљишта и усева током паше, ипак, у овом случају, ради се о ниском нивоу контаминације, недовољном да изазове инфекцију
- Са друге стране, силажа лошег квалитета, неадекватно конзервисана ($\text{pH} > 5,0 - 5,5$), и при том контаминирана, омогућава размножавање *Listeria monocytogenes* до високог броја, и сасвим вероватно представља уобичајени пут инфекције фармских животиња
- Значајно већа преваленција *Listeria monocytogenes* се утврђује у узорцима фецеса музних крава у поређењу са узорцима земљишта, воде (фармско окружење) и сточне хране
- Говеда, као домаћини, амплификују *Listeria monocytogenes* ингестирану кроз контаминирану силажу, и на тај начин представљају критични фактор у одржавању контаминације високог нивоа на фарми
- Расејавањем *Listeria monocytogenes* путем фецеса клинички оболелих животиња и/или асимптоматских клицоноша, долази до контаминације непосредног окружења животиња, и циклус фекално-оралне трансмисије се наставља

Контаминација сировог млека

- Примарна контаминације млека подразумева субклинички маститис, где се као узрочни агенс идентификује *Listeria monocytogenes*
- контаминација млека са *Listeria monocytogenes* углавном резултат секундарне контаминације (контаминација површине вимена фекалним материјалом или из околине), односно резултат стварања биофилма у линији система за мжу

Listeria monocytogenes

- Психротолерантност
 - Ацидотолерантност
 - Халотолерантност
 - Микроаерофилност
-
- **ХРАНА СПРЕМНА ЗА КОНЗУМИРАЊЕ** - храна коју је субјект, односно произвођач или прерађивач наменио за исхрану људи без потребе да се она претходно обради топлотом или неком другом врстом обраде, чији циљ би био да се елиминише или смањи на прихватљив ниво број микроорганизама од значаја;

ХРАНА СПРЕМНА ЗА КОНЗУМИРАЊЕ која не подржава раст ЛМ

- производи са $pH \leq 4.4$ или $a_w \leq 0.92$,
- производи са $pH \leq 5.0$ и $a_w \leq 0.94$,
- производи са роком употребе краћим од пет дана, аутоматски се сврставају у ову категорију,
- замрзнути производи,
- друге категорије производа могу да буду укључене у ову групу, ако за то постоји научна оправданост.

Табела 6.3.1.1 Храна спремна за конзумирање

Критеријум број	Микроорганизам и категорија хране	Примери (листа није затворена)
1.1	<i>L. monocytogenes</i> у храни спремној за конзумирање која подржава раст <i>L. monocytogenes</i>	<p><u>ХЛАДНИ ПРОИЗВОДИ СПРЕМНИ ЗА КОНЗУМИРАЊЕ СА РОКОМ УПОТРЕБЕ ДУЖИМ ОД ПЕТ ДАНА.</u></p> <p>Претходно упаковани нарезани производи од меса, Ферментисане кобасице: кулен, зимска салама, сремска кобасица, његушка кобасица, сузук и чајна кобасица, панонска кобасица, ферментисане кобасице за мазање; сувомесанти производи: сува шунка (пршут), сува шунка без кости, сува плећка, сува плећка без кости, пршута, суви врат, буђола и сува сланина; барене кобасице: хреновка, франкфурте, паризер и бела кобасица, крањска кобасица, тиролска кобасица, роштиљска кобасица, шункарица, месни хлебови, и мортадела; куване кобасице: јетрена кобасица, јетрена паштета, крвавица са језицима, крвавица; кобасице са желеом: језици са желеом, месо са желеом, шваргла, месна паштета, димљена шунка, димљена плећка и димљени каре, димљени производи; припремљена печења, роштиљ месо, језа у желеу, месне салате, и сродни производи; пастеризоване конзерве</p> <p>Хладно димљени упаковани производи; нпр. димљени лосос, димљена пастрмка,</p> <p>Маринирани производи (хладне маринаде у уљу или течности са мајонезом или ремуладом)</p> <p>Мекни сиреви Кајмак;</p>
1.2	<i>L. monocytogenes</i> у храни спремној за конзумирање која не подржава раст <i>L. monocytogenes</i>	<p>Производи са роком употребе краћим од 5 дана (нпр. сендвичи)</p> <p>Сладолед</p> <p>Ферментисани производи од млека</p> <p>Млечни десерти</p> <p>Млечни намази</p> <p>Сирни намази и сирни десерти</p> <p>Полутврди и тврди сир</p> <p>Производи у којима је рН нижи од 4,4: нпр. туршија</p>

ГРАНИЧНЕ ВРЕДНОСТИ

- ХРАНА СПРЕМНА ЗА КОНЗУМИРАЊЕ КОЈА ПОДРЖАВА РАСТ ЛМ
 - 1) 100 CFU/g хране у промету током рока употребе
 - 2) одсуство ЛМ у 25 g испитиване хране – пре него што храна престане да буде под непосредном контролом субјекта у пословању храном

- ХРАНА СПРЕМНА ЗА КОНЗУМИРАЊЕ КОЈА НЕ ПОДРЖАВА РАСТ ЛМ
 - 1) 100 CFU/g хране у промету током рока употребе

ИНТОКСИКАЦИЈЕ ЕНТЕРОТОКСИНИМА СТАФИЛОКОКА

- 25 имунолошки различитих ентеротоксина (Staphylococcal Enterotoxins –SEs) и протеина сличних ентеротоксинима (Staphylococcal Enterotoxin-like, SEI) (SEA–SEIZ)
 - SEA–SEE are considered "classical enterotoxins", while SEG–SEIZ are termed "new enterotoxins". Historically, classical toxins were demonstrated to be emetically active in rhesus monkey feeding assays, while new toxins were either not emetic or had not been tested in monkeys
- 1) Способност да изазову повраћање и ГЕ код примата
 - 2) Суперантигеност – неспецифична активација Т лимфоцита - ослобађање цитокина и системски шок
 - 3) Отпорност на топлоту и дигестију пепсином
 - 4) Структурна сличност
 - 5) Молекулске масе 25-29 kD



SRPS EN ISO 6888-1:2021

Микробиологија ланца хране – Хоризонтална метода за одређивање броја коагулаза-позитивних стафилокока (*Staphylococcus aureus* и друге врсте) – Део 1: Метода употребе агара по Берд-Паркеру

Microbiology of the food chain - Horizontal method for the enumeration of coagulase-positive staphylococci (*Staphylococcus aureus* and other species) - Part 1: Method using Baird-Parker agar medium (ISO 6888-1:2021)

Датум објављивања: 30. 9. 2021.

ИНТОКСИКАЦИЈЕ ЕНТЕРОТОКСИНИМА СТАФИЛОКОКА

- The *Staphylococcus* genus comprises at least 70 species and subspecies associated with an array of host species and habitats
- In addition to *S. aureus* (*S. aureus subsp. aureus*, *S. aureus subsp. anaerobius*) there are eight described coagulase-positive staphylococci (CoPS) including *Staphylococcus argenteus*, *Staphylococcus cornubiensis*, *Staphylococcus delphini*, *Staphylococcus intermedius*, *Staphylococcus lutrae*, *Staphylococcus pseudintermedius*, *Staphylococcus coagulans*, and *Staphylococcus schweitzeri*, with *Staphylococcus agnetis*, *Staphylococcus chromogenes*, and *Staphylococcus hyicus* described as coagulase variable

Article

Enterotoxigenic Potential of Coagulase-Negative Staphylococci from Ready-to-Eat Food

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Abstract: Although coagulase-positive staphylococci are considered to be the main factor responsible for food poisoning, an increasing role for the coagulase-negative staphylococci in the production of enterotoxins has been observed in recent years. This study was conducted to assess the occurrence of genes responsible for the production of staphylococcal enterotoxins (SE), enterotoxin-like toxins (SEI) and toxic shock syndrome toxin-1 (TSST-1) in coagulase-negative staphylococci (CoNS) isolated from ready-to-eat food from bars and restaurants. One hundred and eighteen CoNS strains were tested using polymerase chain reaction (PCR) to five superantigenic toxin genes, including five different types of classical enterotoxins (*sea*, *seb*, *sec*, *sed* and *see*) and the toxic shock syndrome toxin-1 (*tsst-1*) as well as to supertoxin-like genes. PCR-positive isolates were then tested using immunoenzymatic methods (SET-RPLA, Vidas SET 2) for toxin expression. Out of 118 CoNS strains, the presence of staphylococcal enterotoxins was confirmed in 72% of them. The most frequently found enterotoxin-like genotype was *ser*, *selu*. Two of the tested strains had up to ten different enterotoxin genes in the genome at the same time. Although no production of enterotoxins was detected in the CoNS, which means that their possible role in the epidemiology of food-borne diseases is minimal, the data demonstrated that the toxigenic capacity of the CoNS should not be ignored, and that this group of microorganisms should be continuously monitored in food.

Keywords: coagulase-negative staphylococci; ready-to-eat food; staphylococcal enterotoxins

ИНТОКСИКАЦИЈЕ ЕНТЕРОТОКСИНИМА СТАФИЛОКОКА

- The robustness of *S. aureus* under a wide range of environmental conditions should be considered a virulence parameter, making it difficult to predict the general behavior of the pathogen in various food matrices under different environmental conditions.
- The series of events in an SFP outbreak typically include the following: (i) the presence of the pathogen in raw materials or the food handler(s), (ii) contamination of the food, for example, through processing equipment or through the food preparer, (iii) inappropriate storage conditions and/or inadequate temperature control that allow for bacterial growth and enterotoxin production, and (iv) ingestion of contaminated food containing a sufficient amount of SE to trigger symptoms of the disease.
- The majority of well-documented outbreaks indicate that the most common means of contamination in cases of SFP are poor hygiene practices during the processing, cooking, and distribution of food products. Inadequate cooling of food products is the main cause of *S. aureus* growth leading to disease

								Оптички највећи	
2.2.3.	Сиреви произведени од сировог млека	Коагулаза позитивне стафилококе	5	2	10 ⁴ cfu/g	10 ⁵ cfu/g	EN ISO 6888-2		
2.2.4.	Сиреви произведени од млека које је обрађено топлотом на температури нижој од температуре пастеризације ⁽⁷⁾ , сиреви са зрењем произведени или од пастеризованог млека или сурутке, или од млека или сурутке обрађених јачим режимом топлотне обраде ⁽⁷⁾	Коагулаза позитивне стафилококе	5	2	100 cfu/g	1000 cfu/g	EN ISO 6888-1 или EN ISO 6888-2	За време производног процеса, у време када се очекује да ће број стафилокока бити највећи	Побољшање хигијене производње и избора сировина. Ако се утврде вредности >10⁵ cfu/g , та производна партија сира се мора испитати на присуство стафилококних ентеротоксина.
2.2.5.	Меки сиреви без зрења (свежи сиреви) произведени од млека или сурутке који су пастеризовани или обрађени јачим топлотне обраде ⁽⁷⁾	Коагулаза позитивне стафилококе	5	2	10 cfu/g	100 cfu/g	EN ISO 6888-1 или EN ISO 6888-2	Крај производног процеса	Побољшање хигијене производње. Ако се утврде вредности >10⁵ cfu/g , та серија сира се мора испитати на присуство стафилококних ентеротоксина.

1.19.	Непастеризирани сокови од воћа и поврћа (спремни за конзумирање)	<i>Salmonella</i>	5	0	Не сме бити у 25 g		EN ISO 6579	Производ у промету током његовог рока употребе
1.20.	Сиреви, млеко у праху и сурутка у праху како је наведено у критеријуму за коагулаза – позитивне стафилококе у Поглављу 2, одељак 2.2, тачка 2.2.3. овог прилога	<i>Stafilokokni enterotoksini</i>	5	0	Нису доказани у 25 g		Европска скрининг метода за CRL за млеко (13)	Производ у промету током његовог рока употребе
1.21.	Живе шкољке и остали мекушци, живи бодљокошци, плашташташи и пужеви	<i>E. coli</i> (14)	5 (15)	1	230 MPN/ 100 g меса и међуљуштурне течности	700 MPN/ 100 g меса и међуљуштурне течности	EN/ISO 16649-3	Производи у промету током његовог рока употребе

Enterotoxin production and antimicrobial susceptibility in Staphylococci isolated from traditional raw milk cheeses in Serbia

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Radoslava Savic-Radovanovic¹, Jelena Asanin³, Tijana Ledina¹

Affiliations + expand

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Abstract

This study was undertaken to determine the prevalence of coagulase positive staphylococci (CPS) by examining a total of 71 raw milk cheeses. Additionally, enterotoxigenicity, antimicrobial susceptibility and the presence of *mecA* and *mecC* genes in the staphylococcal isolates were investigated. The isolation and enumeration procedure of CPS followed the International Organization for Standardization (ISO) standard. The presumptive staphylococci were identified by matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) using the VITEK MS system. VIDAS® Staph enterotoxin II assay was used for the detection of classical enterotoxins. Antimicrobial susceptibility testing (AST) was accomplished performing the disk diffusion method. All suspected methicillin resistant staphylococci were investigated for the presence of *mecA* and *mecC* genes by PCR assay. A high prevalence (87.32%) of CPS was detected in the cheeses at contamination levels up to 5.58 log CFU g⁻¹. Among 47 staphylococcal isolates screened for enterotoxin production, only one isolate, identified as *S. hyicus*, was confirmed as being enterotoxigenic. Resistance to penicillin (63.70%) was the most common resistance among the tested *Staphylococcus aureus* isolates. The dominant phenotypic resistance patterns in coagulase negative staphylococci (CNS) were resistance to ofloxacin and fusidic acid. All CNS isolates were susceptible to the clinically important antibiotics clindamycin, chloramphenicol, gentamicin, linezolid, rifampicin and trimethoprim-sulfamethoxazole. The *mecA* and *mecC* genes were not detected. To the best of our knowledge, this is the first study concerning evaluation of the presence of methicillin resistant staphylococci (MRS) in dairy products in Serbia.

ЕНТЕРОВИРУЛЕНТНЕ *ESCHERICHIA COLI*

- 7 ИНТЕСТИНАЛНИХ ПАТОВАРОВА
 - 1) ЕНТЕРОПАТОГЕНА (ЕРЕС)
 - 2) ЕНТЕРОТОКСОГЕНА (ЕТЕС)
 - 3) ЕНТЕРОИНВАЗИВНА (ЕІЕС)
 - 4) ЕНТЕРОХЕМОРАГИЧНА (ЕНЕС)
 - 5) ЕНТЕРОАГРЕГАТИВНА (ЕАЕС)
 - 6) ДИФУЗНО АДХЕРЕНТНА (ДАЕС)
 - 7) АДХЕРЕНТНО ИНВАЗИВНА (АІЕС)

Review

Virulence Factors of Enteric Pathogenic *Escherichia coli*: A Review

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Abstract: *Escherichia coli* are remarkably versatile microorganisms and important members of the normal intestinal microbiota of humans and animals. This harmless commensal organism can acquire a mixture of comprehensive mobile genetic elements that contain genes encoding virulence factors, becoming an emerging human pathogen capable of causing a broad spectrum of intestinal and extraintestinal diseases. Nine definite enteric *E. coli* pathotypes have been well characterized, causing

ЕКСТРАИНТЕСТИНАЛНИ: МАММАРИ ПАТХОГЕНИС *E. coli* (МРЕС), UPEC, NMES, SEPEC, APES

Table 1. Virulence factor genes of enteric *E. coli* pathotypes: Colonization, fitness, toxins, and effectors.

Class	Virulence Factor	Activity/Function	Pathotype
Colonization	bfp	adherence,	EPEC
	eae	attaching and effacing of enterocyte,	EPEC, EHEC
	tir	translocated intimin receptor,	EPEC, EHEC
	lifA	initial attachment to the enterocytes,	EPEC
	csgA	curli fimbriae,	EPEC, EHEC
	fimA	type I fimbriae,	EPEC, EHEC, DAEC
	fimH	type I fimbriae,	ETEC, AIEC
	bcgA	cellulose structure,	EPEC
	eha	biofilm formation,	EHEC
	saa	biofilm formation,	EHEC
	sab	biofilm formation,	EHEC
	toxB	biofilm and adhesion establishment,	EHEC
	nleB	biofilm formation,	EHEC
	nleE	biofilm formation,	EHEC
	nleH	biofilm formation,	EHEC
	bleG	biofilm formation,	EHEC
	lfp	long polar fimbriae, initial attachment,	EHEC
	CFA/I	colonization factor,	ETEC
	CFA/II	colonization factor,	ETEC

Table 1. Cont.

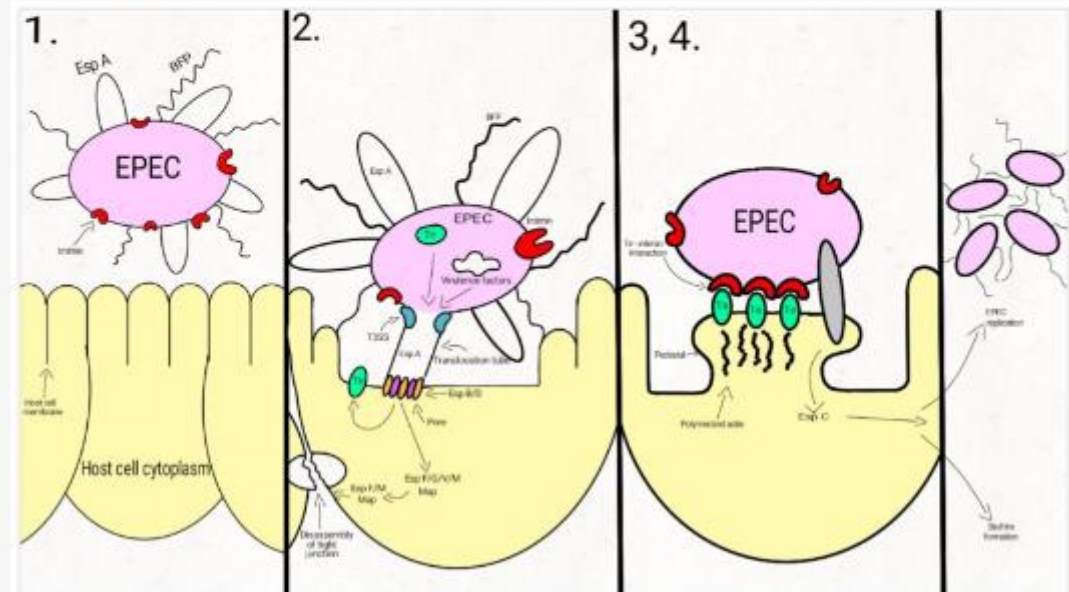
Class	Virulence Factor	Activity/Function	Pathotype
Fitness	sdiA	quorum sensing signaling,	EPEC
	iutA	aerobactin synthesis,	EIEC
	iucB	complex siderophore iron receptor,	EIEC
	yjaA	polypeptide stress response protein,	AIEC
	fyuA	ferric yersiniabactin uptake,	AIEC
	kpsMT II	capsule synthesis,	AIEC
Toxins	stx1	shiga toxin, surface localization of nucleolin and cytotoxic effect,	EHEC
	stx2	shiga toxin, surface localization of nucleolin and cytotoxic effect,	EHEC
	estA	ST I toxin, watery and secretory diarrhea, secretion of chemokines and cytokines,	ETEC
	estB	ST II toxin, watery and secretory diarrhea, secretion of chemokines and cytokines,	ETEC
	LT I	watery diarrhea,	ETEC
	LT II	watery diarrhea,	ETEC
	eatA	SPATE,	ETEC, EIEC
	astA	enteroaggregative heat-stable toxin, secretory diarrhea,	ETEC, EAEC, DAEC
	ShET1	shigella enterotoxin 1, secretory intestinal activity,	ETEC
	ShET2	shigella enterotoxin 2, secretory intestinal activity,	ETEC
	pet	SPATE, plasmid encoded toxin, inducing epithelial cell extrusion, host cell entering,	EAEC, DAEC
	pic	SPATE, ShET1 expression, inducing epithelial cell extrusion, mucolytic activity,	EIEC, EAEC
	sigA	SPATE, cytotoxin, accumulation of intestinal fluid,	EIEC, EAEC, DAEC
	stx	SPATE, secreted autotransporter toxin, impairing tight	EAEC, DAEC

Effectors	hlyE	protease like homologue, alpha hemolysin toxin,	EAEC
	espA	translocator structures of T3SS, E. coli common pili,	EPEC, ETEC
	espB	translocator structures of T3SS, phagocytosis inhibition,	EPEC
	espC	cleavage of T3SS translocator structures,	EPEC
	espD	translocator structures of T3SS,	EPEC
	espF	mitochondrial death, tight junction disruption, immune evasion, host cell death,	EPEC, EHEC
	espH	phagocytosis inhibition,	EPEC
	espJ	phagocytosis inhibition, biofilm formation,	EPEC, EHEC
	espP	cleavage of T3SS translocator structures,	EPEC, DAEC
	espT	host cell death,	EHEC
	MAP	disrupt mitochondrial membrane functionality, host cell death,	EPEC
	nleA	inflammasome activation, tight junction disruption, cytokines secretion inhibition,	EPEC
	etp	Autotransporter protein,	ETEC
	tolC	secretion of ST toxins,	ETEC
	nleF	host cell death, inflammasome activation,	EPEC, EHEC
	cif	cell cycle disruption, delays apoptosis,	EPEC
	ipaA	Type III effector, cytoskeleton reorganization, cell death blockage,	EIEC
ipaB	Type III effector, adhesion, phagosome escape, cell turnover,	EIEC	
ipaC	Type III effector, adhesion, actin polymerization, phagosome escape,	EIEC	
ipaD	Type III effector, adhesion, phagosome escape, cell death blockage,	EIEC	

ЕНТЕРОПАТОГЕНА (ЕРЕС)

- главни узрочник дијареје код новорођенчади старости испод 6 месеци
- „EPEC strains are defined, based on their virulence factors, as diarrheagenic strains of *E. coli* that can produce attaching and effacing (A/E) lesions on the intestinal epithelium, but unable to produce Shiga toxins and heat-labile (LT) or heat-stable (ST) enterotoxins
- A (attaching) /E (effacing) лезије

bacteria to the host cell. Actin and cytoskeletal elements are accumulated near the site of the bacterial adherence. EspC is inserted into the cell through an autotransporter system, T5SS. 4. The cytoskeletal elements, accumulated near the site of the attachment, leads to the formation of the pedestal structure, characteristic for EPEC. In the first step, EPEC cells express the intimate adhesin intimin, Bfp (bundle-forming pili), and EspA (short filaments surface-associated). Environmental factors regulate the expression of these virulence factors, influencing the site of the bacterial colonization (small/large bowel) [43,44,45].



ЕНТЕРОТОКСОГЕНА (ЕТЕС)

- главни узрочник „путничке“ („*travelers*“) дијареје и дијареје деце (највећи морбидитет и морталитет код деце старости до две године) у развијеним земљама
- Патогени код животиња (говеда, живина, прасад)
- Профил вируленције
 1. Колонизација (адхеренција на интестинални епител)
 2. Продукција ентеротоксина –
 - ✓ Heat-stabile toxins (STs)
 - ✓ Heat-labile toxins (LTs)
- СЕКРЕТОРНА ДИЈАРЕЈА

ЕНТЕРОИНВАЗИВНА (EIEC)

- Крвава дијареја, абдоминални грчеви и грозница – типични за бациларну дизентерију/шигелозу – *Shigella* spp. и EIEC (single pathovar)
- Облигатни интрацелуларни паразит, не поседује способност адхеренције нити покретљивости (нема флагеле)

ЕНТЕРОХЕМОРАГИЧНА (ЕНЕС)

- Дијареја, хеморагични колитис (крвава дијареја) и хемолитично уремични синдром (ХУС)
- Главни резервоар – интестинални тракт говеда
- Фекално- орални пут, „*person-to-person*“ трансмисија, контакт са животињама., сирово млеко и производи од сировог или недовољно термички обрађеног млека или меса, унарсна контаминација свежег поврћа
- А/Е ПАТОГЕН
- ГЛАВНИ ФАКТОР ВИРУЛЕНЦИЈЕ – SHIGA – LIKE TOXIN (SLT) (VEROTOXIN/VEROCYTOTOXIN) – кодиран *stx* генима (субгрупе *stx1*, *stx2*; субтипови *stx2a*, *stx2c*, *stx2d* – посебно имплициран у случајевима *HC* и *HUS-a*
- O157:H7
- „Also, whenever reports of generic *E. coli* infections or outbreaks are in the news, *E. coli* O157 is usually the implicated strain. However, many other serogroups of STEC can cause disease and are sometimes referred to as “non-O157 STEC” (e.g., serogroups O26, O111 and O103 are the non-O157 STEC that most often cause human illness in the United States).“



1



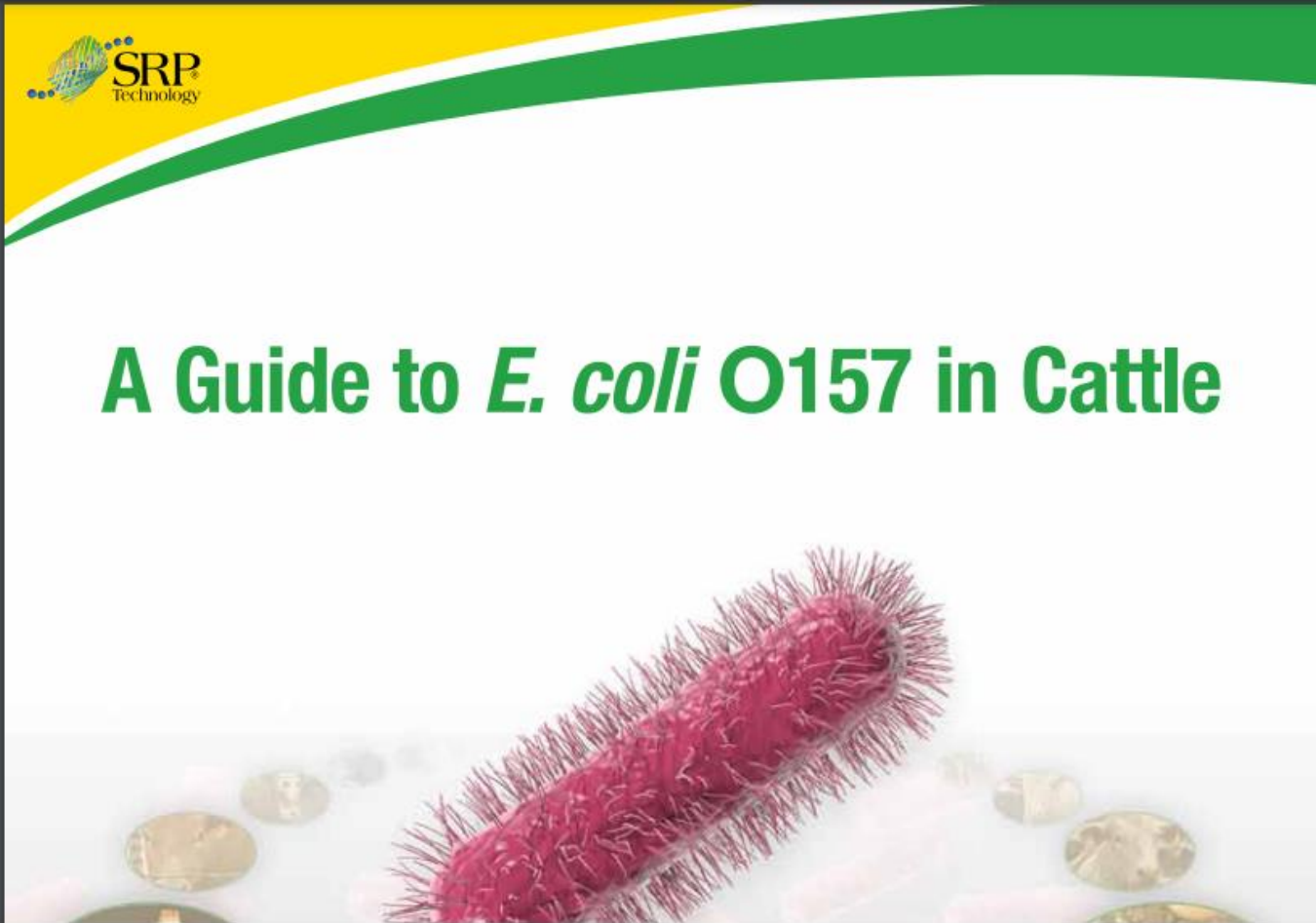
2



3



A Guide to *E. coli* O157 in Cattle



SRP - [®] (siderophore receptors and porins) technology

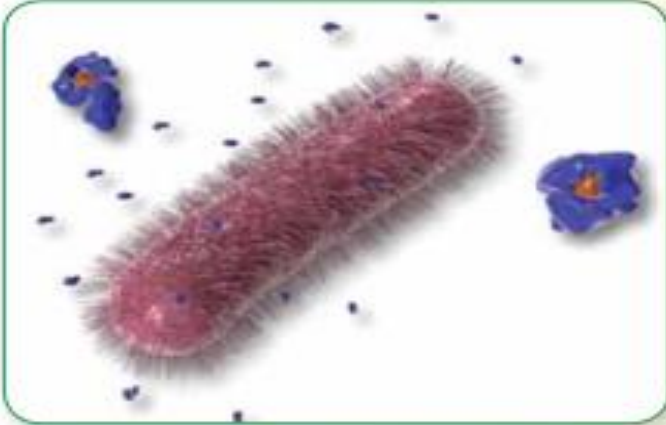


Figure 5: Siderophore proteins (blue) bind to iron, forming siderophore/iron complexes.

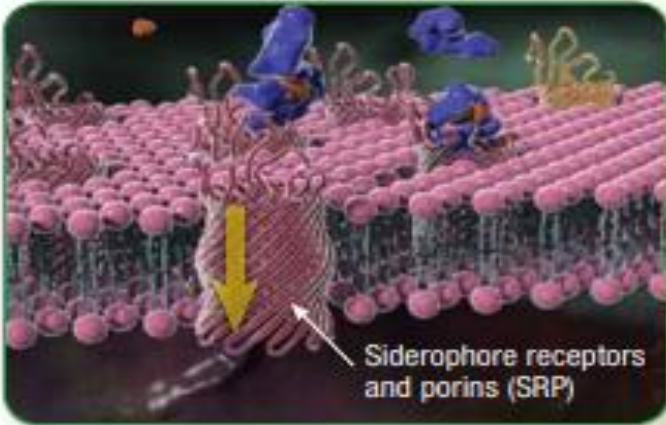


Figure 6: SRP transport siderophore/iron complexes through the cell wall of *E. coli* O157.

Preharvest Control



Figure 8: SRP antibodies that cattle generate after vaccination bind to SRP of *E. coli* O157.

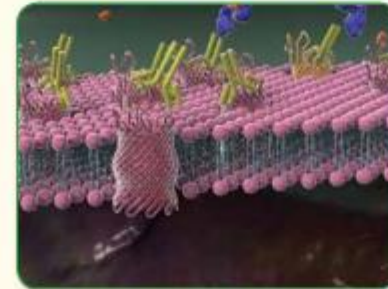
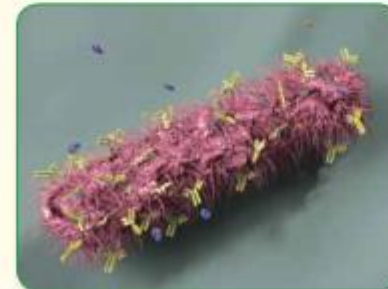


Figure 9: Antibodies blocking SRP help prevent transport of siderophore/iron complexes into cell.



With the SRP technology work by stimulating production of antibodies in cattle, as part of their normal immune response, that help disable the *E. coli* O157 cell wall SRP system required for acquisition of elemental iron (Figure 8). These antibodies help prevent siderophore/iron complexes from passing through the SRP, so bacteria are deprived of iron and die (Figures 9, 10).

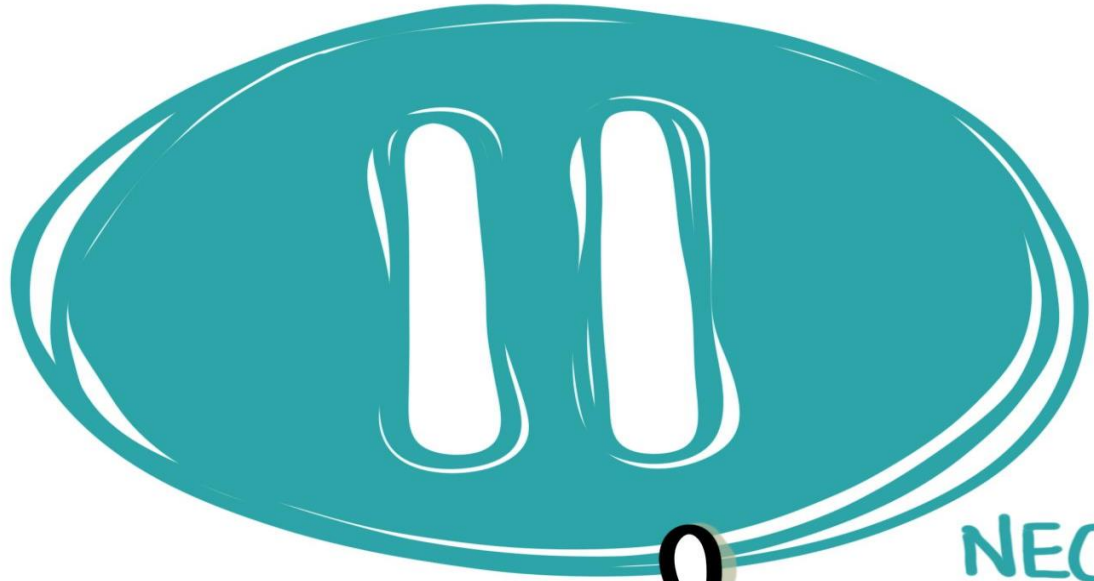
SRP[®] technology targets *E. coli* O157 serotypes because they all use siderophore receptor and porin proteins to capture iron. As a result, SRP helps provide protection against *E. coli* O157 pathogens.

SR
Techno

ЕНТЕРОАГРЕГАТИВНА (ЕАЕС)

- други по реду (након ЕТЕС) узрочник путничке дијареје, и један од главних узрока ентеричних инфекција код HIV/AIDS пацијената
- ПАТОГЕНЕЗА:
 - 1) Адхеренција на интестинални епител путем агрегативних фимбрија
 - 2) Формација биофилма
 - 3) Секреција токсина
 - 4) Мукозна инфламација
 - 5) Цитотоксично оштећење

-
- ДИФУЗНО АДХЕРЕНТНА (DAEC) - дифузна адхеренција на култури Her-2 и HeLa ћелија
 - Дијареја код деце старости 1,5 -5 година, UTI, компликације у трудноћи, али и део комензалне микробиоте
 - АДХЕРЕНТНО ИНВАЗИВНА (AIEC) – најзначајнији узрочни агенс идиопатских инфламаторних обољења (IBD - CD и UC)



NECESITO UNA
(PAUSA)



by @muxotepotolobat