
Yersinia enterocolitica



**Genes
involved in
Cold-Adaptation**

Yersinia enterocolitica



Genes involved in Cold-Adaptation

Yersinia enterocolitica



genen betrokken bij aanpassing aan lage temperatuur

(met een samenvatting in het Nederlands)

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ROSALINA LUCIA JACOBA GOVERDE
geboren op 20 september 1953, te Rotterdam

Promotor: Prof. dr. J. H. J. Huis in 't Veld,
Hoofdafdeling Voedingsmiddelen van Dierlijke Oorsprong,
Faculteit Diergeneeskunde, Universiteit Utrecht

Co-promotor: Dr. F. R. Mooi,
Laboratorium voor Infectieziekten Onderzoek,
Rijksinstituut voor Volksgezondheid en Milieu, Bilthoven

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*The Road goes ever on and on
down from the door where it began.
Now far ahead the Road has gone
and I must follow, if I can.
Pursuing it with weary feet
untill it joins some larger way,
where many paths and errands meet.
And whither then? I cannot say...*

(Bilbo and Frodo Balings, hobbits,
in: 'The Lord of the Rings',
J.R.R. Tolkien)

Opgedragen aan
mijn vader
(† 07-09-1992)

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PREFACE

Scope of the thesis

This thesis concerns the bacterium *Yersinia enterocolitica*, with special attention given to the molecular regulation of its ability to grow and multiply at temperatures around 0°C.

Y. enterocolitica is an important human entero-invasive pathogen with a global distribution [Bottone 1977, 1997; Ostroff 1995]. In contrast to other common bacterial enteropathogens, such as *Salmonella*, *Campylobacter* and *Shigella* species, which cease to grow below circa 8°C, *Y. enterocolitica* is able to grow near 0°C [Stern & Pierson 1979] and even at sub-zero temperatures [Bergann *et al.* 1995]. On account of this cold-tolerance, it has been frequently suggested that the ever increasing application of refrigeration in food storage plays a central role in the continuing expansion of *Y. enterocolitica* as a human pathogen [Christensen 1987; Mollaret 1995]. It could plausibly be argued that this cold-tolerant organism has taken advantage of the forthcoming of a new niche, mindful of Baas Becking's conclusion that "... *life is everywhere, but the environment determines its manifestation.*" [Baas Becking 1927]. Obviously, on the other hand, a causal connection is difficult to prove. Nevertheless, the fact that this hypothesis has never been scientifically documented makes it hard to rate the significance of bacterial cold-tolerance as an indirect threat to human health at its true value. Gaining insight into the suggested relationship requires a closer look at both the history of this bacterium and the milestones in the development of the 'Cold Chain' of food preservation.

Assuming that the ability of *Y. enterocolitica* to proliferate at 5°C or less, either in foods, water or other products, such as blood, truly constitutes a specific hazard for human health, the questions arise whether and how its growth at low temperature could possibly be suppressed. Answering this question, however, requires fundamental knowledge about the specific metabolic factors which enable this organism to multiply at refrigeration temperatures. Unfortunately, although the behaviour and physiology of *Y. enterocolitica* at low temperatures have been investigated extensively, only very few studies addressed the underlying mechanisms. In the present study an attempt is made to determine the vital link(s) in the metabolism at low temperatures, as a first step in elucidating how *Y. enterocolitica* copes with cold.

Outline of the thesis

Chapter 1 is devoted to *Y. enterocolitica* and describes its history and characteristics, as well as its importance as a human pathogen. In Chapter 2, the evolution of chilling into an indispensable factor of modern food preservation is delineated, including the rise of cold-loving ('psychrophilic') and cold-tolerant ('psychrotrophic') organisms in food spoilage and human disease. In Chapter 3, the present knowledge about the molecular aspects of bacterial adaptation to low temperature is reviewed. After these literature-based introductions to the bacterium under study, the development of the Cold Chain, and the phenomenon of microbial cold-adaptation, the Chapters 4 to 7 are based on experimental work with *Y. enterocolitica* and related species. In order to contribute to improved estimations of the prevalence and significance of *Y. enterocolitica*, a rapid and reliable detection method has been developed, which is described in Chapter 4. The central theme in the Chapters 5 and 6 is the identification of factors involved in cold-tolerance, as accomplished by mapping of specific phenotypic adaptations and by analysis of mutations that lead to disruption of the psychrotrophic phenotype. By the latter approach, it was deduced that expression of the *pnp*-gene, encoding polynucleotide phosphorylase (PNPase), is necessary for the ability of *Y. enterocolitica* to grow at low temperatures. Chapter 7 addresses the regulation of *pnp*-expression in *Y. enterocolitica* and other *Yersinia* species. Finally, an evaluation of the results described in the preceding chapters, and a discussion of the possible role of PNPase in the mechanisms that might enable growth at low temperature is the topic of Chapter 8.

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1

Yersinia enterocolitica

**a versatile
human enteric
pathogen**

ABSTRACT

Y. enterocolitica is a Gram-negative bacterium which belongs to the family of the Enterobacteriaceae. Within this species, several bio-/serotypes are distinguished which are pathogenic to humans. Infection with virulent *Y. enterocolitica* mainly causes an acute gastroenteritis, called 'yersiniosis', which in many cases is due to consumption of contaminated foods. The pathogenesis of the bacterium is strongly associated with its enormous capacity to adapt to varying environmental conditions. This versatility enables the organism to multiply at temperatures near zero (e.g. in refrigerated foods), but also to switch over to a life at 37°C (e.g. in a warm-blooded host). This switch includes the expression of 'invasion factors' (to enable entrance of the host's tissues), and the production of serum resistance- and anti-phagocytosis factors (to restrain the host's immune response). In so doing, the bacterium can avoid the host's defense mechanisms, and may easily spread from the intestinal tract to other organs, which leads to a wide spectrum of serious post-infective extra-intestinal diseases and long-term sequela.

Y. enterocolitica, although first isolated in North America in the 1930s, emerged as an important enteric pathogen in much of the industrialized world in the 1970s and 1980s. There is a considerable geographic variation in the incidence of yersiniosis, ranging from < 0.0001% in low-incidence countries to ≥ 0.01% in high-incidence regions (<1 to ≥100 cases/year/ 1 million inhabitants).

The gastrointestinal tract of swine is the main natural habitat of virulent strains. The improvement of slaughtering procedures (i.e. to prevent the contamination of carcasses), and the amelioration of household hygiene (i.e. to repel the consumption of raw pork and the risk of cross-contaminations in the kitchen) have lead to a decline of yersiniosis, especially in the high-incidence countries, in the 1990s.

In addition to contracting yersiniosis via the oral route, infection with the bacterium may also occur after transfusion with contaminated blood products, which leads in most cases to a life-threatening septicaemia. Transfusion-associated infections are not seldomly caused by blood products which had been obtained from asymptotically infected donors, and which had been stored at 4°C for several weeks prior to the transfusion. Features like its psychrotrophic character, its ability to invade eukaryotic cells, its resistance to intracellular killing at low temperatures, and its capacity to benefit from iron enrichment due to aging erythrocytes, all contribute to proliferation of the bacterium under these conditions.

In conclusion, reduction of the contamination level of raw materials and subsequent chilling is not enough to restrain the cold-adapting pathogen *Y. enterocolitica*, neither in foods nor in blood products. Hence, additional methods are required to prevent the organism from unfolding its psychrotrophic character during storage at low temperature.

Yersiniosis: a foodborne disease

In september 1976, more than two hundred children at five schools in a restricted area of the USA fell ill with symptoms of abdominal pain, fever and diarrhoea, whereupon dozens of them were hospitalized and appendicetomized upon suspicion of acute appendicitis. In the same year, two outbreaks of gastric infection with identical symptoms, involving ca. 150 schoolchildren, were reported in Canada. In 1981, over two hundred members of a summer camp population in the USA fell victim to the gastrointestinal symptoms described above, and the next year two outbreaks of the same kind affected more than a thousand people, spread over several states in the USA. Between 1972 and 1984, ten explosive outbreaks of a similar illness, each affecting several hundreds up to over a thousand children of rural primary schools and junior-highschools, occurred in Japan. Outbreaks of the same kind had previously been reported from nursery schools in Czechoslovakia and, at a smaller scale, in families in Hungary and the USA, and in hospitals in Finland. All of these cases of human gastric infection had in common the fact that the causative agent identified was not one of the thus far commonly found enteropathogenic bacteria, but another species, called *Yersinia enterocolitica*. The disease was therefore called yersiniosis. An important resemblance in these outbreaks of yersiniosis was the presumed or proven implication of contaminated food as the source of infection.

1.1 HISTORY

1930s: First appearance

The organism presently known as *Yersinia enterocolitica* can be labelled as a 'recent' organism: its written history dates back only to 1934. In that year, a bacterium isolated from the facial ulcers of an American farm dweller was described that could not be identified as any

Chapter 1

species known at that time, although its morphology and certain biochemical characteristics indicated "... a similarity to the *Pasteurella* genus." [McIver & Pike 1934]. The isolate fell into oblivion for a couple of years, but attracted renewed interest in 1939, when at the New York State Department of Health three look-alike bacterial cultures were received that had been isolated from patients with life-threatening intestinal infections [Schleifstein & Coleman 1939]. The New York investigators thought these organisms, including a fifth identical culture from the NYSDH-collection (that had been isolated as early as 1923 from a chronic skin lesion in a carpet worker), particularly resembled *Pasteurella pseudotuberculosis*, a microbial species that had been known since the end of the last century to cause serious disease in animals. In the following years, annual reports of the New York State Health Department contained sporadic notes of the isolation of bacteria similar to those described in 1939 [Gilbert 1940]. Since these isolates mostly originated from children suffering from enteritis, the yet unclassified organism was temporarily called *Bacterium enterocoliticum* [Schleifstein & Coleman 1943].

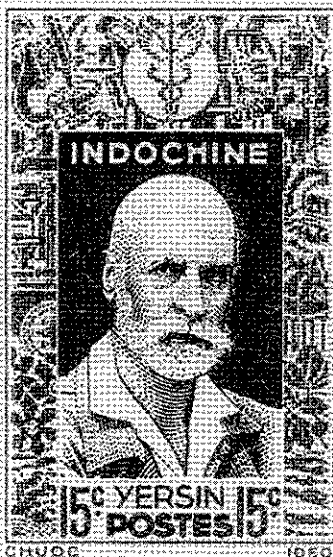
1940s - 1960s: Secluded existence

Little was heard about *B. enterocoliticum* for about twenty years, and from 1957 to 1968 complete silence surrounded the organism in the USA, when no cases of human infection due to it were reported. In the meantime, however, bacteria 'resembling *P. pseudotuberculosis*' were also recognized to be involved in human illness in Europe. The isolation of two such strains from patients who had died of septicemia was reported in Switzerland in 1949, whereupon the species was temporarily designated *P. pseudotuberculosis* ssp. *rodentium* [von Hüssig *et al.* 1949].

1960s: Coming out again

In the early 1960's, the bacterium was recognized as an animal pathogen, when *P. pseudotuberculosis*-like bacteria were reported to be causative agents in enzootics among various wild and captive animals, including chinchillas in Europe and North- and Central America, hare in Europe, and pigs in North Africa [Akkermans & Terpstra 1963; Daniëls & Goudzwaard 1963; Mollaret 1964; reviewed by Hurvell in 1981]. At approximately the same time, the organism, then referred to as *Germe X* or *P. pseudotuberculosis X* or *type B*, was again shown to be involved in human infections, but now in Sweden, France, and Belgium [Carlsson *et al.* 1964; Mollaret & Destombes 1964; Winblad *et al.* 1966; Vandepitte *et al.* 1973]. In addition, various animal hosts, such as deer and pigs, frequently appeared to be healthy carriers of the bacterium [Dickinson & Mocquot 1961; Wetzler & Hubbert 1968].

From then onwards, this intriguing organism became the focal point of intensive investigations. In 1963/64, the similarity was established between the American and European strains of both animal and human origin bearing the aforementioned epithets [Knapp & Thal 1963], and it was then proposed to define this organism as a new species in the genus *Yersinia*, which in 1944 had been split off from *Pasteurella* [Frederiksen 1964]. The name *Yersinia* for this new genus had



previously been chosen to honour the French bacteriologist Dr. Alexandre Jean Emile Yersin who, in 1894, first isolated the infamous plague bacillus, which is now known as *Yersinia pestis* [Butler 1983; Solomon 1995]. The suffix *enterocolitica* refers to the organism's most frequent habitat in cases of human disease: the intestine and the colon.

Alexandre Yersin (1863-1943), shown on a stamp, issued in 1944 in Indochine. Even today, Yersin is a legendary figure in this region, the present Vietnam. He is still greatly honoured, not only for his work in beating the plague but also for his many other contributions to improve the welfare of the Vietnamese people, including the introduction of the rubber tree (*Hevea brasiliensis*) and the quinine tree (*Cinchona leidgeriana*) in this part of the world.

1970s - 1990s: Expansion and establishment

Whereas by 1965 less than 30 cases had been reported world-wide [Weir 1985], over 600 reports appeared on the association of *Y. enterocolitica* with human disease during the second half of the 1960s [Morris & Feeley 1976]. Simultaneously, a rapid expansion of the geographical distribution of the bacterium was seen: it was rediscovered in the USA in 1968 [Sonnenwirth 1968], and at approximately the same time reported from the Netherlands [Wulf *et al.* 1969], Canada [Albert & Lafleur 1971], South Africa [Rabson & Koornhof 1973] and Japan [Zen-Yoji & Maruyama 1972]. Within a decade, the collection of the International Reference Centre at the Pasteur Institute in Paris comprised more than 6,600 strains covering 35 countries on six continents [Mollaret *et al.* 1979]. In the 1970s and 1980s, yersiniosis evolved into a serious threat to human health, when it was implicated in recurrent outbreaks of foodborne disease in Japan [Zen-Yoji 1981] and North America [Shayegani & Parsons 1987], and gained endemic character in north western Europe and some Asian regions [WHO 1981; Markov *et al.* 1989; Dmitrovsky *et al.* 1998]. To some extent, the steady increase in reported isolates of *Y. enterocolitica* obviously reflects the growing interest of microbiologists in this species. However, worldwide surveillance data show an explosion in the number of reported non-outbreak isolates and cases of yersiniosis in the last two decades. Obviously, the increased investigative activity can only marginally account for it, and this notice inclined several authors to refer to *Y. enterocolitica* as a worldwide emerging enteric human pathogen [Cover & Aber 1989; McCarthy & Fenwick 1990; Lee *et al.* 1991; Ostroff 1995; Tauxe 1997].

1.2 CLASSIFICATION

1.2.1 Characteristics

Yersinia enterocolitica is a Gram-negative, non-sporeforming, facultatively anaerobic rod of 1.3-3.5 x 0.5-1.0 μm in size. Based on morphological and overall biochemical characteristics, this bacterium belongs to the family *Enterobacteriaceae* [Bercovier & Mollaret 1984]. The optimum growth temperature of *Y. enterocolitica* is about 28°C, but the organism is able to multiply at 40°C, as well as at temperatures around zero [García de Fernando *et al.* 1995; Greer *et al.* 1995; Bergann *et al.* 1995; Miller *et al.* 1997]. The ability to grow at refrigerator temperatures is a feature shared with all the other members of the genus, including *Y. pseudotuberculosis* and the ill famed *Y. pestis* [Bercovier & Mollaret 1984; Gray 1995]. *Y. enterocolitica* is motile by means of several flagellae when grown in cultures at 30°C or less, but non-motile when grown at 35-37°C (Figure 1.1). Many other phenotypic characteristics, such as lipopolysaccharide (LPS) composition and virulence determinants like enterotoxin production and synthesis of secreted proteins (the so-called Yops), are temperature-dependent [Straley & Perry 1995].

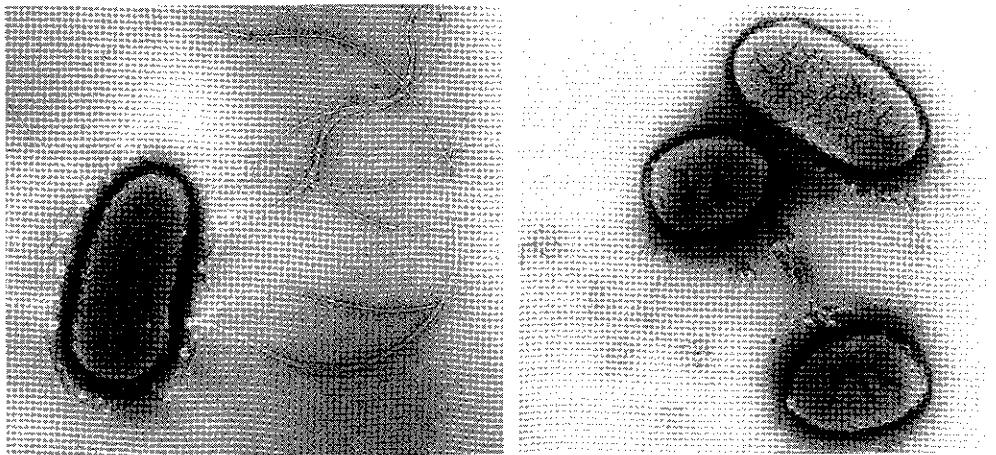


Figure 1.1 *Yersinia enterocolitica*. On the leftside: cells grown at 5°C; rightside: cells grown at 37°C

1.2.2 Related Species

Because the biochemical criteria initially proposed for the species *Y. enterocolitica* incorporated a rather heterogeneous group of bacteria of human and animal origin, several bio- and serotyping schemes have been developed to sub-group these isolates [Winblad 1967; Niléhn 1969; Wauters 1970; Knapp & Thal 1973]. Classification by these methods soon revealed certain

relationships between biotypes, ecological distribution and virulence [Alonso *et al.* 1976; Mollaret 1976; Mollaret *et al.* 1979]. Moreover, taxonomic studies applying DNA hybridization techniques elucidated differences in DNA-relatedness between typical *Y. enterocolitica* strains and those which were aberrant in phenotypic characteristics to such an extent that they had been referred to as '*Y. enterocolitica*-like' [Bercovier *et al.* 1980a; Brenner 1979; Brenner *et al.* 1976 1980a]. Hence, several groups of strains were reclassified as separate species and renamed *Y. intermedia* [Brenner *et al.* 1980b, *Y. kristensenii* [Bercovier *et al.* 1980], or *Y. frederiksenii* [Ursing *et al.* 1980]. The latter names were chosen in honour of the Danish microbiologists Kristensen and Frederiksen, who played important roles in the unraveling of the relationships of *Yersinia*-like organisms. In 1935, Dr. Martin Kristensen published a large study on so-called 'Paracolibacilli', originating from human faeces or urine [Kristensen *et al.* 1935], and in the 1960s one of these isolates was recognized as a *Yersinia* by Dr. Wilhelm Frederiksen. This strain was later chosen as the type strain for the newly defined species *Y. frederiksenii*.

When the relationships between the various strains became further unravelled, several other species were newly defined and - with reference to some other famous players in the continuing story of *Yersinia* - designated *Y. aldovae* [Bercovier *et al.* 1984], *Y. rohdei* [Aleksić *et al.* 1987], *Y. mollaretii* or *Y. bercovierii* [Wauters *et al.* 1988a]. Initially, these close relatives of *Y. enterocolitica* were very rarely associated with yersiniosis. However, their innocence is questionable, since several atypical cases of yersiniosis due to these strains have been described, more recently [Lewis & Chattopadhyay 1986; Cafferkey *et al.* 1993; Necrasova *et al.* 1998b].

1.2.3 Bio- and Serotypes

Despite the split off of the aforementioned related species, the bacteria currently classified as *Y. enterocolitica* by no means constitute a homogeneous group: yet several biotypes, based on their biochemical profiles, and a still increasing number of over 60 different serotypes, based on their somatic (O) and flagellar (H) antigens, can be distinguished [Wauters 1981; Wauters *et al.* 1991; Fenwick *et al.* 1996]. The situation is further complicated by the fact the H-antigens are species-specific, while the O-antigens are not [Aleksić 1995].

Although *Y. enterocolitica* was first recognized in relation to human illness, it soon appeared to be ubiquitous in nature: the bacterium has now been isolated from many vertebrate wild and domestic animals, from a variety of terrestrial and freshwater ecosystems, from drinking water and from raw and prepared food products [Mollaret *et al.* 1979]. As the number of isolates increased, a striking dichotomy was seen, with on the one side acknowledged pathogens and on the other side a range of so-called environmental strains. A fair correlation appeared to exist between biogroups, antigenic patterns and ecologic behaviour. Virulence was associated with only a dozen bio/-serotypes, whereas the vast majority of strains recovered from environmental sources were either non-typeable or serotypes which have never been implicated in human infections (Table 1.1, adapted from [Aleksić & Bockemühl 1990]).

Table 1.1 *Yersinia enterocolitica* bio- and serotypes which are regularly involved in human disease: ecological & geographical distribution and recognized transmission vehicles.

STRAIN TYPE		DISTRIBUTION		TRANSMISSION	
Bio type	Sero-type	Ecological spread (main hosts)	Geographical spread (main areas)	Source / Vehicle in outbreaks or trans-fusion-acquired cases of yersiniosis	References
1B	O:4	environment	USA/Canada, India	well-water? humans	142 417
	O:8	pigs, dogs, rodents	worldwide (before 1980 only in the USA)	milk (-products) pre-cooked meat pork processing-water surface-water humans, pets	77, 369, 376 369 220 11, 59 241 191
	O:13a,b	monkeys, environment	USA Europe	milk? well-water	396 261
	O:18	environment	USA	well-water? milk?	142 396
	O:20	dogs, rats	USA	pets blood	435 404
	O:21	environment	USA/Canada	surface-water? milk? humans?	276
2	O:9	pigs, dogs, cats, rodents	Europe, Japan, Australia	pork humans, pets blood citrus-fruit	342 33, 417 12, 404 273
	O:5,27	pigs	worldwide	pork, milk blood	240 404
3	O:5,27	pigs	Europe, Asia	citrus-fruit	273
	O:1,2,3	chinchilla, pigs,	worldwide	humans? blood	198,349 404
4	O:3	pigs, dogs, cats, rodents	worldwide (not in the USA before 1980)	pork, milk? processing-water well-water pets blood	45, 262,263,401 26 124 33 12, 288,253,402

In addition to the specific ecological spread of the distinct bio/serotypes, a certain geographical distribution was initially also manifest. One group of strains, i.e. the biotype 1B strains, comprising the serotypes O:4, O:8, O:13a/b, O:18, O:20 and O:21, were mainly isolated in the USA [Wilson *et al.* 1976; Eden *et al.* 1977; Martin *et al.* 1982; Black *et al.* 1978; Shayegani *et al.* 1983; Tacket *et al.* 1984, 1985] and these were therefore referred to as 'American strains'.

On the other hand, the strains that were the most common causes of yersiniosis in Europe and Japan, i.e. serotypes O:3 and O:9, were virtually unknown from America. Only one pathogenic serotype, i.e. O:5,27, seemed to have a global spread from the very beginning. Since the early 1980s, however, the distinction between 'American' and 'non-American' strains no longer applies as a result of worldwide serogroup shifts, involving an increase in the proportion of formerly rare serotypes and a concomitant decline of others [WHO 1981; Bottone 1983; Neogi *et al.* 1985; Hoogkamp-Korstanje *et al.* 1986; Bottone *et al.* 1987; Lee *et al.* 1990]; and [Chiesa *et al.* 1991; Ichinohe *et al.* 1991; Prentice *et al.* 1991; Kontiainen *et al.* 1994; Stolk-Engelaar & Hoogkamp-Korstanje 1996]¹.

Furthermore, evidence has been growing in the last decades that classification by bio- or serotyping may not always predict pathogenicity: whereas formerly only biotypes 1B, 2, 3, 4 and 5 were thought to be indicative for virulence, several sub-groups of biotype 1A have by now also been shown to be involved in human disease [Noble *et al.* 1987; Bissett *et al.* 1990; Greenwood & Hooper 1990; Burnens *et al.* 1996], especially among young children [Glenn Morris *et al.* 1991] and immuno-compromised persons [Sulakvelidze *et al.* 1998].

¹ In the first decades of *Y. enterocolitica* research, the strains which were pathogenic for humans could be divided in 'American' and 'non-American' strains, based on their restricted geographical distribution. Since the onset of the 1980s, however, the formerly uneven spread of certain serotypes has gradually flattened out. Serotype O:3, for example, which was rarely isolated in America until 1983, has since then increasingly been recovered from sporadic cases of yersiniosis in the USA. In 1990, this serotype was for the first time reported to be involved in an outbreak, and nowadays O:3 predominates in North America, whereas most of the serotypes implicated in early outbreaks are rarely seen. The reverse movement was seen with the 'American' serotype O:8. Such strains were initially unknown outside North America, but around 1985, isolations from human patients started to be reported from Asia and Europe. In fact, the first recorded case of yersiniosis in Bangladesh, which occurred in 1984, was due to infection with an O:8 strain. Although serotype O:8 is still very rare in Belgium and Scandinavia, it now forms approximately 4% of the recorded *Y. enterocolitica* isolations in the Netherlands and the United Kingdom. In addition to the arrival of the formerly absent serotype O:8, the initially uneven distribution of serotype O:9 over Europe gradually flattened out. In the British Isles, for example, serovar O:9 was unknown until 1980, but today, over 50% of the pathogenic strains isolated from human faeces belong to this serotype. Inversely, the proportion O:9 in Finland changed from 41% in 1974 to 1% in 1994, and this serotype is still extremely rare in Denmark.

1.3 CLINICAL MANIFESTATION

1.3.1 Gastrointestinal Syndromes

The clinical spectrum of *Y. enterocolitica* infections varies with age and underlying conditions [Bottone 1997]. The most common presentation of an orally acquired infection is a diarrhoeal disease, associated with low grade fever and abdominal pain, lasting for a few days to several weeks. This type of - usually mild - gastroenteritis is particularly found in infants and young children and is normally self-limiting. The symptoms can even be so faint and short-lived that yersiniosis is not diagnosed, despite faecal carriage [Ossel 1990]. Sometimes, however, the clinical course of the infection is much more serious and destructive. Syndromes like extensive ulceration of the intestine and subsequent peritonitis or an acute abdomen, due to invagination of the infected section of the intestine into a neighbouring part ('intussusception'), are not uncommon in young children, and several fatalities have been reported [Gutman *et al.* 1973; Martin *et al.* 1982; Staatz *et al.* 1998]. In older children and adults, clinical syndromes known as 'terminal ileitis' and 'mesenteric lymphadenitis' are more common, which refer to strong inflammatory reactions in the distal small intestine and to swelling of regional lymph nodes [Bottone 1977]. Unlike infections with other common foodborne pathogens, yersiniosis frequently manifests itself with symptoms that mimic appendicitis, leading to sometimes unnecessary appendix operations [Shorter *et al.* 1998]. The upper part of the gastrointestinal tract may also be affected, leading to symptoms of pharyngitis [Gutman *et al.* 1973; Tacket *et al.* 1984]. In elderly people, or persons whose normal host-defense mechanisms have been compromised, the bacterium may persist in intestinal tissue, causing chronic inflammatory bowel diseases [Kallinowski *et al.* 1998].

1.3.2 Complications and Sequela

Due to subsequent spread of the bacterium via the blood stream, other body parts may become infected and a generalized, extraintestinal infection ('septicemia') may occur. Although this complication is especially found among people with an iron-overload [Piroth *et al.*, 1997; Adamkiewicz *et al.* 1998] or suffering underlying diseases [Jensen *et al.* 1995], septicemia may also occur in otherwise healthy persons [Hosaka *et al.* 1997]. Its manifestation includes not only relatively harmless skin inflammations [Gauthier & So 1997], but also abscess formation in liver and spleen [Schiemann 1989], as well as life-threatening infections of brain ('meningitis'), lung ('pneumonia'), heart ('endocarditis') and blood vessels ('aneurysm') [Challa & Marx 1980; Giamarellou *et al.* 1995; Donald *et al.* 1996; Mercié *et al.* 1996], and [Bin-Sagheer *et al.* 1997; Bottone 1997; La Scola *et al.* 1997; Tame *et al.* 1998].

As a result of the host's immune response, *Y. enterocolitica* may also induce secondary, post-infectious auto-immune diseases such as cutaneous granuloma on the extremities ('erythema nodosum') [Niemie *et al.* 1976; Schiemann 1989], and acute and chronic arthritis [Petrus *et al.* 1997;

Heyden *et al.* 1997], especially in adolescents and older adults possessing the tissue type HLA-B27 [Ahvonen & Rossi 1970; Larsen 1980; Falcão *et al.* 1995]. There is also substantial evidence that subclinical persistent infections with *Y. enterocolitica* may induce auto-immune thyroid diseases [Wenzel *et al.* 1996].

1.4 PATHOGENESIS

1.4.1 Entrance, Colonization and Spread

Historically, *Y. enterocolitica* is primarily a gastro-intestinal tract pathogen, although it has also emerged as a significant cause of blood transfusion-associated bacteraemia in the last two decades (see section 1.6.5). The sequence of events following ingestion of virulent *Y. enterocolitica* cells can be summarized by five steps: (i) invasion of intestinal epithelial cells, (ii) penetration of the lamina propria, (iii) multiplication in underlying tissues, (iv) drainage to mesenteric lymph nodes, and (v) entrance into the bloodstream eventually leading to systemic infection [Cornelis *et al.* 1987; Bottone 1997] (Figure 1.2).

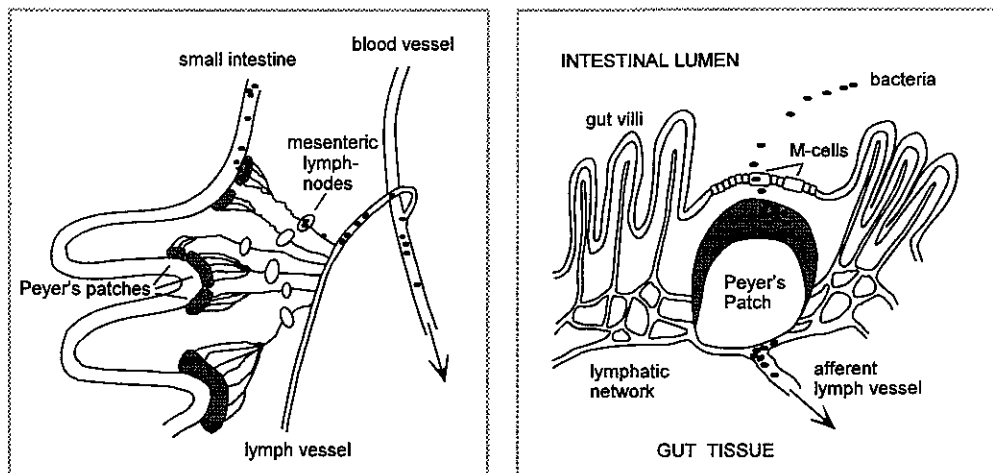


Figure 1.2 Entrance and spread of *Yersinia enterocolitica* in the human host

The first step, entry of the intestinal epithelium, is also seen in other entero-invasive bacteria, like *Shigella* and *Escherichia coli*, but while these enteropathogens usually invade the colonic epithelial layer, *Y. enterocolitica* preferentially localizes, like *Salmonella* species, to the distal

small intestine, the ileum. Secondly, *Y. enterocolitica* has, in contrast to other enteropathogens which usually remain and multiply locally in the epithelial cells, a strong propensity to penetrate the underlying lamina propria and to invade the gut associated lymphoid tissue, especially the organized lymphoid follicles known as Peyer's patches [Hanski *et al.* 1989]. Virulent strains of *Y. enterocolitica* can survive at this site, and multiply as extracellular microcolonies because they are able to resist phagocytosis by macrophages and polymorphonuclear leucocytes.

On the other hand, the organism can withstand intracellular killing by non-professional phagocytes. Hence, the bacterium can use leucocytes to translocate through endothelial monolayers [Rüssmann *et al.* 1996], thus allowing them to drain from the Peyer's patches into lymphatic vessels and to colonize the regional lymph nodes, the liver, and the spleen. Eventually, entrance into the bloodstream may lead to further spread of the infection, inducing various systemic diseases and immunologically mediated sequelae.

Based on their role in the various steps of pathogenesis, several types of virulence factors can be distinguished in *Y. enterocolitica*.

1.4.2 Virulence Factors

Invasion factors (Figure 1.3)

The first steps of infection - adherence to and invasion of the epithelial layers of the host gut - require at least two chromosomal factors, called *ail* (for Adhesion Invasion Locus) and *inv* (for invasion) [Miller & Falkow 1988].

The *inv* gene is present in virulent as well as in non-virulent strains, whereas the *ail* gene is only found in pathogenic serotypes of *Y. enterocolitica* and in *Y. pestis* and *Y. pseudotuberculosis*, [Miller *et al.* 1989]. The *inv* product of *Y. enterocolitica*, invasins, is a ca. 90 kDa outer membrane protein that mediates cellular entry by binding to integrin receptors on the surface of certain epithelial cells, the so-called M-cells [Pierson 1994]. These cells, which cover the Peyer's patches, are specialized in delivering internalized particles to the underlying macrophages, and the bacterium thus exploits this host cell function to pass through the cellular barrier of the intestinal epithelium and invade the underlying tissue [Finlay & Cossart 1997]. The mode of action of the 17 kDa *ail* product, Ail, which is also an outer membrane protein, has not been elucidated so far.

In addition to the chromosomal factors, at least one extrachromosomally encoded factor directly contributes to invasion. This factor, formerly known as POMPI, P1 or YopA (for Yersinia Quter Protein A) [Cornelis *et al.* 1987 1989] but now generally referred to as YadA (for Yersinia adhesin), is the product of the *yadA* (or *yopA*) gene, which is one of the genes present on pYV, the Yersinia virulence plasmid (see below). YadA consists of subunits of about 50 kDa and forms a fibrillar structure on the surface of the bacterium, which, among other functions, mediates clumping and adherence to intestinal mucin [Straley & Perry 1995].

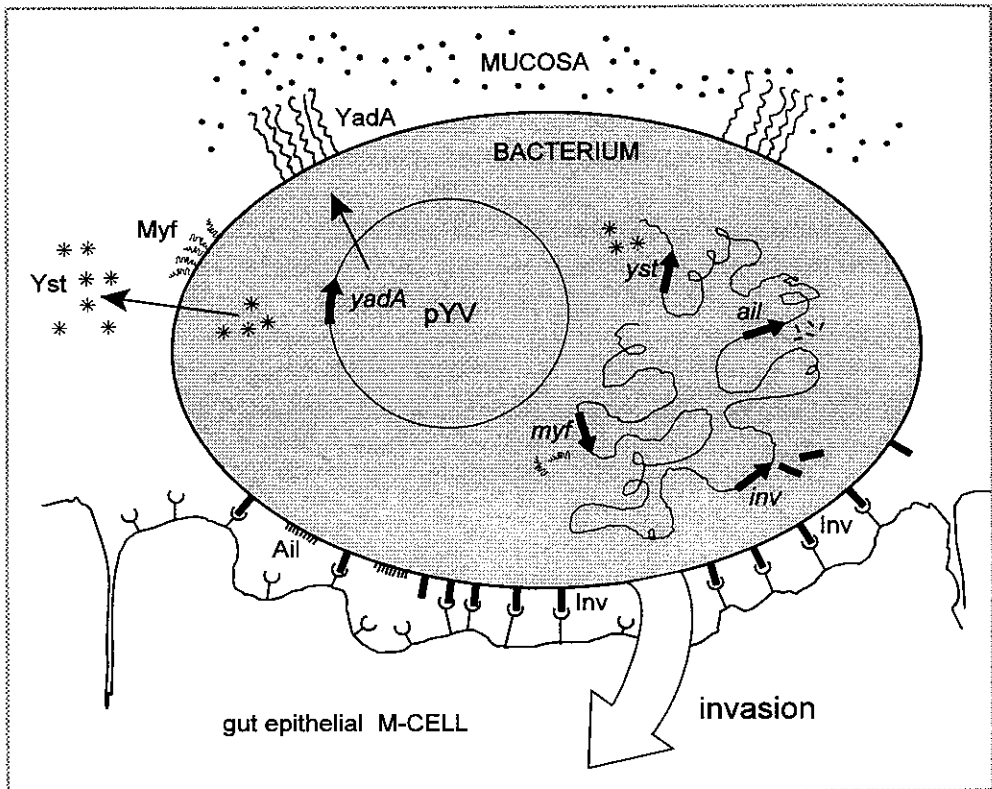


Figure 1.3 *Yersinia enterocolitica* in the intestine:
genes and gene-products which are involved in the invasion of the host epithelial tissues

Anti-phagocytosis factors

After invasion of the intestinal mucosa, the bacterium has to defend itself to the non-specific immune response of the host, especially to phagocytosis by polymorphonuclear leucocytes. The anti-phagocytosis strategy relies mainly on a dozen secreted proteins, called Yops (for *Yersinia* *outer* protein's), their individual cytosolic chaperones, called Syc proteins (for *S*pecific *Y*op *c*haperone), a dedicated secretion apparatus which is made up of a twenty Ysc (for *Y*op *s*ecretion) proteins, and several regulatory proteins [Cornelis 1994; Boland *et al.* 1996].

Both the *yop*, *syc* and *ysc* genes, as well as the *vir* genes that regulate their expression, are found on a high molecular weight (70-75 kb) plasmid called pYV (for *Yersinia* *V*irulence) [Cornelis *et al.* 1987 1989; Bliska 1994; Iriarte & Cornelis 1998]. This plasmid is highly conserved among all virulent *Yersinia* species and serotypes, and pathogenicity is lost upon loss of pYV [Gemski

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et al. 1980; Schiemann & Devenish 1982; Heesemann *et al.* 1983; Portnoy & Martinez 1985]. Cells which harbour pYV require Ca^{++} for growth at 37°C . In the absence of calcium ions, virulent *Yersiniae* restrict their growth at 37°C and synthesize, instead, large amounts of Yops. This phenomenon reflects a phase transition that allows the bacterium (i) to adapt to its environment - the infected host - and (ii) to proceed with the successive steps in infection.

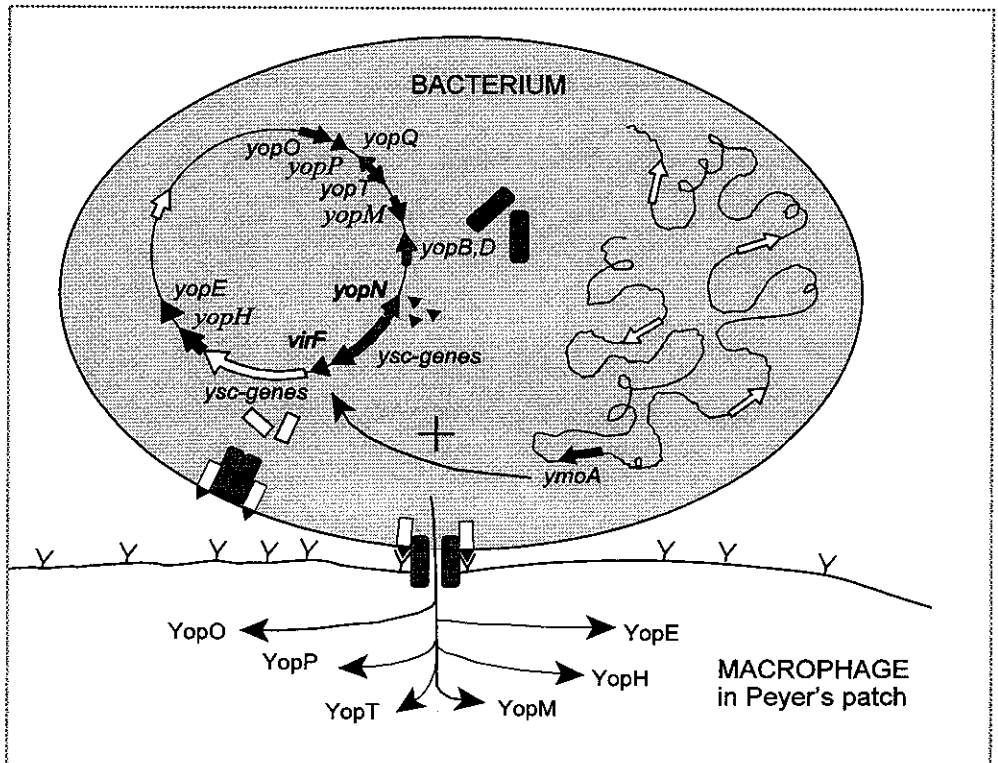


Figure 1.4 *Yersinia enterocolitica* in the Peyer's patch: genes and gene-products involved in the process of anti-phagocytosis.

The mode of action of several Yops has now largely been elucidated and a model has been proposed to explain the interaction between *Y. enterocolitica* and the target cell [Cornelis & Wolf-watz 1997] (Figure 1.4). Upon contact of bacteria with the host cell surface, the membrane associated proteins YopB and D act, in co-operation with the membrane-bound Ysc secretion system, as a translocation apparatus to inject YopE, H, M, O, P and T into the phagocytic cells [Rosqvist *et al.* 1994; Persson *et al.* 1995; Boland *et al.* 1996; Mills *et al.* 1997; Iriarte & Cornelis 1998]. YopN

exerts, probably as the sensor of Ca^{++} and/or by binding to a specific receptor on the eukaryotic cell, a control function on assembly of the delivery apparatus [Cornelis 1994; Cornelis & Wolf-Watz 1997]. After internalization, YopH, M and O interfere with signal transduction pathways, thus inhibiting the functioning of the host cell, while YopE and YopT damage the infected cell by paralysing its actin cytoskeleton, and YopP induces programmed cell death (apoptosis) [Mills *et al.* 1997].

Serum resistance factors

In addition to favouring invasion and/or extracellular survival of the bacterium, some of the above proteins also interfere with other, blood-related, non-specific host defence mechanisms. Yop M, for example, acts as a serum resistance factor by binding to thrombin, thus inhibiting thrombin-induced platelet aggregation [Bliska 1994]. Similarly, YadA prevents the formation of the membrane attack complex of complement by binding of the complement factor H [Cornelis 1994]. There is some evidence that Ail also contributes to serum resistance, but its mode of action is still unknown [Bliska & Falkow 1992].

Serum resistance is also thought to play a role in transfusion acquired *Yersinia* infections. While serogroup O:8 strains present in leucocyte-filtered human blood are rapidly killed by the serum bactericidal activity at 25°C or during storage at 4°C, serotype O:3, O:5 and O:9 strains survive 25°C holding temperatures and ultimately multiply during storage at 4°C [Bottone 1997].

Auto-immune response inducing factors

The mechanisms promoting auto-immunity and chronicity in arthropathies are far less understood than those of the acute illness. Most patients manifesting post-*Yersinial* reactive arthritis are HLA-B27 positive, but the reasons underscoring this predisposition are still obscure [Märker-Hermann & Höhler 1998]. Nevertheless, several positively charged *Yersinia* proteins, such as O-polysaccharide antigens and the small β -subunit of urease, are suspected of playing a role in *Yersinia*-triggered reactive arthritis [Bottone 1997]. Such cationic proteins might easily bind to the negatively charged structures of the joint cartilage or synovial lining. Indeed, O-polysaccharide antigens have been detected in synovial fluid cells from arthritic patients [Granfors *et al.* 1989; Viitanen *et al.* 1991], and the urease-subunit was shown to be an immunodominant target antigen for synovial T-lymphocytes [Mertz *et al.* 1994].

Enterotoxins

Y. enterocolitica and related species produce a heat-stable, chromosomally encoded enterotoxin (Yst, or YEST) when the bacteria are cultured in typical bacteriological media at 20-30°C [Pai *et al.* 1978]. It has long been doubted whether the enterotoxin is an element of virulence because absence of its *in vitro* production at temperatures above 30°C suggested that this toxin is not produced in the host intestinal lumen. More recently, however, it was shown that high osmolarity and weakly alkaline pH, conditions that are present in the normal ileum

lumen, allow significant transcription of *ystA*, the major Yst gene, at 37°C [Mikulskis *et al.* 1994], and this might also occur with two newly detected enterotoxin genes, *ystB* and *ystC* [Huang *et al.* 1997]. Furthermore, after *ystA* was cloned and sequenced [Delor *et al.* 1990], the implication of Yst in the onset of diarrhoea in infected rabbits could be demonstrated [Delor & Cornelis 1992]. In addition, a surface antigen called Myf (for Mucoid yersinia factor; see Figure 1.3) might be a colonization factor acting in conjunction with Yst to cause diarrhoea, because it closely resembles enterotoxin-associated fimbriae described in other bacteria, and presence of the *myf* genes (like that of *yst*) is restricted to pathogenic serotypes [Iriarte *et al.* 1993]. Furthermore, both Yst and Myf are produced only when bacteria enter the stationary growth phase [Iriarte *et al.* 1995].

In addition to putative enterotoxin production in the infected host, intoxication by means of preformed enterotoxin can not be excluded: YEST is also produced at 4°C, in foods and drinks [Boyce *et al.* 1979; Kapperud & Langeland 1981; Olsvik & Kapperud, 1982] as well as in blood products [Bradley *et al.* 1997] and its activity is not destroyed by heating or chilling during foodprocessing [Francis *et al.* 1980], nor by the influence of gastric acidity [Boyce *et al.* 1979].

Iron-scavenging factors

Since iron is an essential nutrient for almost all microorganisms, *Y. enterocolitica*, like other pathogenic bacteria, must obtain iron from the host to establish an infection. In the mammalian tissues and intestinal environment however, the abundantly present iron is not readily available for bacteria since it is tightly bound to eukaryotic proteins such as haemoglobin, ferritin, transferrin and lactoferrin. Therefore, the ability to capture iron *in vivo* is one of the critical factors that differentiate high- and low- pathogenicity *Y. enterocolitica* strains.

In response to iron limitation, the highly pathogenic 'American' biotype 1B strains O:4, O:8, O:21 and O:40 synthesize both an iron-chelating molecule, designated Yersiniabactin, and a specific outer membrane receptor for Yersiniabactin, i.e. FyuA (for ferric yersiniabactin uptake) [Heesemann 1990; Chambers & Sokol 1994]. The production of Yersiniabactin, is regulated by HMWP2, a high molecular weight protein encoded by *irp2*, which is also synthesized only by high-pathogenicity strains, under iron-stress conditions [Carniel *et al.* 1992; Guilvout *et al.* 1993]. All other *Y. enterocolitica* strains, including the serotypes O:3, O:5, 27 and O:9, do not produce Yersiniabactin, nor any other 'siderophore'. Nevertheless, these strains can, to a certain level, also fill their iron need, since they do express in their membrane various receptors for siderophores produced by the host or by other intestinal bacteria (like YfuA for polyphosphate-bound ferric iron, FoxA for ferrioxamines, FcuA for ferrichrome, and Hem R for haemin) [Straley & Perry 1995; Heesemann *et al.* 1997]. The fact that several of these siderophores (i.e. ferrioxamine B) are used to treat patients with an iron overload might explain why systemic *Y. enterocolitica* infections, which are commonly encountered in such patients, are mostly due to O:3, O:5 or O:9 strains [Robins-Browne *et al.* 1987; Carniel 1995; Piroth *et al.* 1997].

1.4.3 Temperature-dependent Gene Regulation

During its pathogenic life cycle, *Y. enterocolitica* transits from environmental niches into the tissues of the host. To avoid inappropriate virulence gene expression, the bacterium has developed a sophisticated regulation of its pathogenicity determinants in response to temperature stimuli. *Inv* and *yst* are expressed well at 30°C and at lower temperatures, but their expression and/or activity drops at the mammalian host temperature of 37°C, under the influence of a common factor, the chromosomal *ymoA* (for 'Yersinia modulator') gene [Pierson 1994; Cornelis 1994; Straley & Perry 1995]. In contrast to this downregulation, the expression of many other virulence genes, including *ail*, *yadA*, and the *yop*, *vir* and *ysc* genes, is largely enhanced at 37°C, under direct or indirect control of *ymoA*. Actually, *VirF* functions as transcriptional activator of the *yop* genes, after its own induction by the histon-like protein YmoA.

1.5 EPIDEMIOLOGY

Y. enterocolitica has emerged as an important enteric pathogen, associated with a wide spectrum of clinical and immunologic manifestations, in much of the industrialized world. Nevertheless, the true incidence and prevalence of *Y. enterocolitica* infections are not known. In general, the incidence rate, that is the total occurrence of new cases among a certain population during a certain period of time, is estimated from the reported number of cases. In addition, estimates of prevalence, that is the proportion of the population having the disease at a certain time point, are derived from the faecal carriage of the bacterium among patients with gastro-enteritis, or from the prevalence of specific antibodies in the population.

1.5.1 Incidence

Since yersiniosis is a notifiable disease in only a few countries, our knowledge about its global incidence is far from complete. Nevertheless, the scattered data (Table 1.2) show that there are a few high-incidence regions in the temperate zones and many countries with a low to medium incidence.

Europe

In several West-European countries, especially in Scandinavia and Belgium, yersiniosis shows endemic character. At the end of the 1970s, it was the most frequent enteric infection in **Denmark**, and today, at the end of the 1990s, *Y. enterocolitica* is the third most common enteropathogen, after *Salmonella* and *Campylobacter* [Nielsen & Wegener 1997], a situation that is also seen in **Belgium** and **Sweden** [Verhaegen *et al.* 1991; Borch *et al.* 1996]. In medium-incidence countries, like **Norway**, **the Netherlands** and **the United Kingdom**, the bacterium now ranks

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as number four after *Salmonella*, *Campylobacter* and *Shigella* [Nesbakken & Skjerve 1996; Esveld *et al.* 1996; Adams & Moss 1995]. In most of these countries, the incidence of yersiniosis peaked in the mid-eighties, after which it declined progressively (Figure 1.5), probably due to improved food hygiene at the industrial as well as at the household level [Nesbakken & Skjerve 1996; Verhaegen *et al.* 1998].

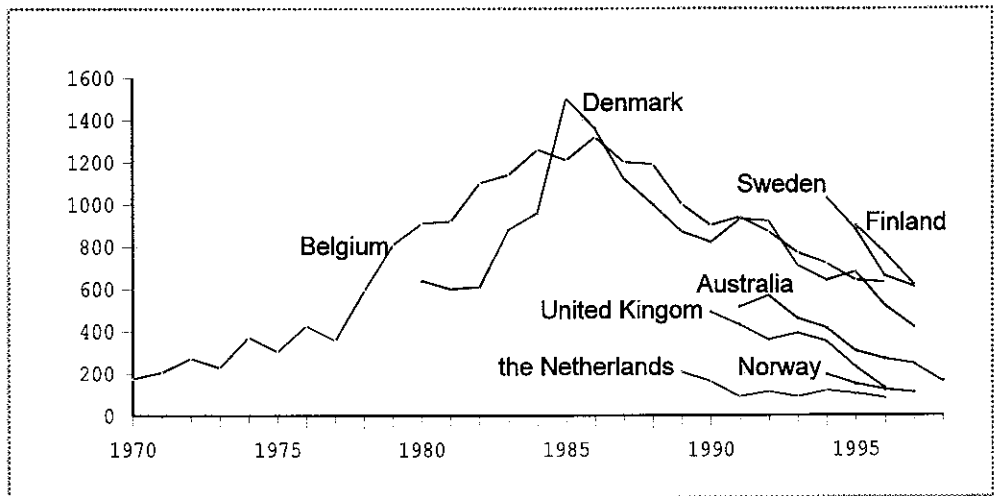


Figure 1.5 Trends in the incidence of yersiniosis: amounts of annually reported cases in various countries

In the UK, the epidemiology seems to be somewhat different from that on the continent: whereas in the Scandinavian countries and Benelux nearly all yersiniosis concern sporadic cases, small outbreaks are much more regularly reported to occur in Great Britain [Cheasty *et al.* 1998]. Published data concerning yersiniosis in other European countries are scarce and/or out-of-date. Nevertheless, the disease seems to be less common in Central and Southern Europe, although strong geographic differences are seen, even between neighbouring countries (confer **France** versus **Spain**, or **Germany** versus **Switzerland**). Medium to high incidences have been reported in the 1970s and 1980s from several East-European countries, such as **Hungary** and the former **Czechoslovakia**, but recent data are not available. Absence of such data does not necessarily mean that yersiniosis has become less important in these regions, as is evident from the fact that several large epidemics have been reported to occur in **Romania** in the past decades, although incidence data have not been published [Constantiniu *et al.* 1998].

North America

Y. enterocolitica infections are also frequently reported from North America.

In the 1970s and 1980s, the epidemiology of yersiniosis in the USA and Canada was characterized by recurrent foodborne outbreaks, each affecting hundreds to thousands of people, mostly children [Schiemann 1989]. In the 1990s, outbreaks are still reported from these countries, but the number of patients is generally restricted to a few dozens [DeBuono 1995; Shorter *et al.* 1998]. This does not automatically imply that the disease is over the hill in this part of the world, for sporadic cases of foodborne disease - although less likely to be reported - are far more common than are cases that are part of recognized outbreaks [Bean & Griffin 1990]. Furthermore, under-reporting is very likely, since surveillance of foodborne disease is largely a voluntary system. Consequently, very low annual incidence rates (i.e. 0.2-0.4 cases per 1 million inhabitants) have been calculated from the amount of nationwide reported cases in the USA., [Bean & Griffin 1990], whereas much higher incidence rates are found in regions with a reporting obligation, such as California and New York State, i.e. 2-5 cases per 1 million inhabitants [Bissett *et al.* 1990; Shayegani *et al.* 1995]. In the period 1973-1987, the bacterium ranked number ten after *Salmonella*, *Shigella*, *Staphylococcus aureus*, *Clostridium perfringens*, *Campylobacter jejuni*, *Streptococcus*, *E. coli*, *Bacillus cereus* and *Vibrio cholera* as causative agent in sporadic cases of foodborne disease of known etiology in the USA [Bean & Griffin 1990]. However, despite its relatively low ranking, *Y. enterocolitica* is considered to be a serious and still increasing problem in North America. Whereas the American Centers for Disease Control (CDC) estimated in 1985 that 5000 cases of yersiniosis would occur annually in the USA [Bennett *et al.* 1987], this estimate was increased to 17,000 in 1991 [CDC 1998a]. Since 1996, *Y. enterocolitica* is one out of seven bacterial agents for which CDC developed an active surveillance network (FoodNet), in order to better understand and respond to foodborne illnesses in the USA [CDC 1998b]. This surveillance, which now covers approximately 30 million persons (more than 10% of the US-population), has shown that the incidence of yersiniosis changed little from 1996 to 1998 [CDC 1998b].

In **Canada**, *Y. enterocolitica* has rivaled *Salmonella* and *Campylobacter* as a cause of acute gastroenteritis since the end of the 1980s, being reported from both isolated cases and small-scale outbreaks [Cover & Aber 1989; Harnett *et al.* 1998].

South America

No pronounced history of yersiniosis is known from South America, but data which were produced from studies among childhood populations in **Chile** suggest that yersiniosis is also much more common on this continent than might be assumed from the virtual absence of reported cases [Glenn Morris *et al.* 1991].

Table 1.2 The occurrence of human yersiniosis in various countries:
average annual incidences (cases per 1 million inhabitants)

COUNTRY	untill 1970	1970- 1979	1980- 1989	1990- 1994	1995- 1999	REFERENCES
Belgium	4	38	123	90	70	413, 420, 421
Czech-Slov.	47	.	40	.	.	36, 348
Crete	.	.	.	65	.	361
Denmark	.	40,000*	200	153	96	47, 125, 257, 305
France	<1	<1	.	.	>10	44
Finland	.	39	.	166	117	1, 32, 169
Germany	.	.	.	2	.	41
Hungary	3	36	.	.	.	394, 434
Italy	.	<1	2	.	.	122
Lithuania	10*	256
Netherlands	.	53*	34* - 80*	13	9	148, 149, 206, 207, 210
Norway	.	.	57	46	25	230, 317, 318, 331
Spain	.	.	25	.	.	182
Sweden	13	.	80*	113	80	86, 377, 437
Switzerland	.	.	.	14	8	60, 61, 104
UK	.	<1	6	10	3	28, 121, 344, 429
Canada	.	3	.	17	17	198, 406
USA	.	<1	1* - 20*	5	10 - 65*	64, 66, 75, 115, 116, 248, 368
Chile	.	7	13	.	.	181
South Africa	.	7*	16* - 30*	.	.	212, 228, 352
Israel	.	35*	.	.	.	375
Georgia	.	.	6	.	.	391
Australia	.	.	.	28	14	118
Nw Zealand	.	.	157*	93 - 150	153	155, 156
Yakutia	.	73	73	73	.	143
Kazakhstan	27*	283
Japan	.	5*	.	.	.	233
Bangladesh	.	.	<1	.	.	105

In general, the incidence-data are calculated from the amount of culture-proven cases, as reported to National Reference Centers, or published in occasional reports. Data marked with an asterisk (*) are either estimated by a National Health Office or based on studies in restricted areas. Dots in the list mean that no data were available.

Africa and Middle-East

Very few documented cases are known from developing countries in Africa. This could be due to lack of compulsory reporting, or yersiniosis is probably not a significant cause of enteric infection in these countries. Reports from **South-Africa** [Househam *et al.* 1988] and **Israel**, [Shmilovitz & Kretzer 1978] on the other hand, indicate that *Y. enterocolitica* infections are not uncommon in the more industrialized regions.

Oceania

Y. enterocolitica is nowadays one of the more commonly isolated bacterial enteric pathogens in **New Zealand**. Until 1988, yersiniosis was rare in this country but in the 1990s, the number of isolates was reported to be rising, and in some areas *Yersinia* now ranks second or third after *Campylobacter* and/or *Salmonella* [Fenwick & McCarthy 1995]. In **Australia**, on the other hand, a gradual decrease in the incidence of yersiniosis has been observed since it became a notifiable disease in 1991 [CDN Australia/New Zealand 1998].

Asia

Although incidence data are largely absent from Asian countries, yersiniosis is far from uncommon in certain areas. Large, most likely foodborne, outbreaks were reported to occur in Japan between 1972 and 1984 [Zen-Yoji 1981]. More recently, a lingering epidemic, with over 1000 cases (1% of the population!) each year, was reported to infest a certain region of **East-Kazakhstan** from the early 1990s onwards [Dmitrovsky *et al.* 1998]. In addition, small outbreaks have been reported from several other Asian countries such as **Mongolia** [Markov *et al.* 1989], **China** [Anonymus 1987] and **India** [Abraham *et al.* 1997].

1.5.2 Faecal Carriage in Humans

A second source of information that is used to estimate the actual amount of foodborne disease caused by a certain species is the number of isolates from clinical specimens obtained from patients under medical care for gastro-intestinal disorders. Data concerning faecal carriage of pathogenic strains of *Y. enterocolitica* are shown in Table 1.3.

Europe

The most complete picture is from **Belgium**, based on the number of isolations from hospital stools between 1970 and 1992. Until 1980, a steady increase is seen in the percentage of coprocultures positive for pathogenic *Y. enterocolitica*, which is thought to be due to improved isolation techniques and higher awareness of the pathogen [Verhaegen *et al.* 1998]. After peaking at 3.5% around 1980, a progressive decline in faecal carriage rate is seen from 1984 onwards [Van Noyen *et al.* 1987a, 1987b, 1995]. A similar pattern of rise and fall in the percentage of *Y. enterocolitica* in coprocultures is seen in **the Netherlands** and in **Italy**. But general trends are difficult to deduce since (i) published data are scarce and (ii) investigators have not always

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distinguished between pathogenic and non-pathogenic strains. Evaluation of the data is further complicated by the bias that might be introduced by the selection criteria used to define patients and for taking samples in culture [Hoogkamp-Korstanje *et al.* 1986; Esveld *et al.* 1996]. In a Dutch study, for example, a higher faecal carriage rate (2.9%) was observed when every diarrhoeal stool sample sent to a Public Health Laboratory was cultured for *Y. enterocolitica* instead of only those which were suspected upon diagnosis by a general physician versus (1.6%) [Hoogkamp-Korstanje *et al.* 1986]. Furthermore, surveys in both **Italy** and **Sweden** showed that rather different levels of faecal carriage were observed between childhood out-patients and patients hospitalized for gastroenteritis, i.e. 0.6% versus 3.7% and 1.5% versus 5.6% [Figura & Rossolini 1985; Uhnou *et al.* 1986]. Such bias factors might also play a role in the aberrantly high faecal carriage rate that has been reported from certain areas in the **United Kingdom**.

America

In the American countries with a pronounced history of yersiniosis, i.e. the **USA** and **Canada**, the faecal carriage rate has also declined since the mid-1980s. Surprisingly, pathogenic strains are also regularly isolated from diarrhoeal stools in regions where *Y. enterocolitica* is less prominent as a cause of enteric infection, such as **Chile** [Glenn Morris *et al.* 1991].

Africa and Middle-East

Very low isolation rates are found in **Israel** [Shmilovitz & Kretzer 1974], in Moslem countries such as **Iran** and **Nigeria** [Haghighi 1979; Anyanwu 1995], and in tropical African countries such as **Senegal** and **Kenya** [Franzin *et al.* 1987; Turkson *et al.* 1988]. In **South-Africa**, on the other hand, the bacterium is less rare. However, large differences can be found between different age groups. In one study, for example, the overall isolation rate of the bacterium in cases of acute gastroenteritis was found to be 0.1% [Baxter *et al.* 1994], but a ten-fold higher faecal carriage was observed among a sub-population of diarrhoeic children [Jennings *et al.* 1987; Househam *et al.* 1988].

Asia

High isolation rates have been reported from **Japan** in the 1970s and 1980s, but today the faecal carriage seems to be much less. In **India**, where *Y. enterocolitica* is surpassed by many other, more virulent pathogens, the bacterium has been isolated from up to 3% of loose stools [Ram *et al.* 1987]. Much lower isolation rates are reported from other Asian countries, like **China** [Zheng & Xie 1996] and **Bangladesh** [Samadi *et al.* 1982; Butler *et al.* 1987].

1.5.3 Prevalence of Antibodies in the Population

A third criterion used to estimate the frequency of a certain bacterial infection (including subclinical cases) in a population, is the prevalence of specific antibodies. This is, however, a subject full of pitfalls, since the diagnostic value of a single titre not only depends on multiple host variables, such as age, underlying disorders, or the administration of immunosuppressive

Table 1.3 Human carriage of pathogenic *Yersinia enterocolitica*::
% of culture proven infections in diarrhoeal stools

COUNTRY	1970-1980	1980-1984	1985-1989	1990-1999	REFERENCES
Belgium	1.0	1.2 - 3.5	2.1	0.2	414,415,416,421
Czech/Slov.	0.1	.	.	.	337
Crete	.	.	.	0.7	361
France	(< 0.1)*	.	.	.	301
Finland	2.0	.	.	1.1	32, 247
Germany	0.1 - 1.5	.	.	.	62, 80
Italy	.	(0.3) - 1.4 (3.1)	0.6 - (3.2)	0.4	100, 109, 158, 159, 295
Netherlands	1.0	1.6 - 2.9	2.1 - (2.4)	0.2 - 0.7	148, 149, 210, 389, 439
Romania	10	(1.8)	(1.8)	(1.8)	126, 357
Spain	.	0.8	1.0	.	182, 190
Sweden	.	1.5 - (3.1) 5.6	.	.	393, 410
Switzerland	.	.	.	0.4	104
UK	.	.	0.3 - (3.5)	7.2	185, 186, 265
Canada	(0.2) - 2.6	1.8 - (5.3)	.	.	274, 301, 324,
USA	2.1	3.3	0.8 - (1.6)	.	248,263,370,430
Chile	.	.	0.9 - (1.4)	.	181
South Africa	0.1	(0.9) - 1.0	.	(0.1)	63, 212, 228,352
Nigeria	.	.	.	0.0	51
Senegal	.	.	0.0	.	165
Kenya	.	.	0.0	.	409
Malaysia	.	0.0	.	.	227
Zaire	0.4	.	.	.	271
Iran	< 0.1	.	.	(2.0)	192, 382
Israel	< 0.1	.	.	.	375
Georgia	.	.	(1.0)	.	391
Australia	< 0.1	0.9	0.9	.	275
Nw Zealand	.	.	.	0.4 - (0.7)	156, 402
Japan	1.6 - 4.0	0.8 - 1.8	.	0.4	171, 233, 234, 277, 443, 444
India	.	(0.2) 0.6 - 3.0	.	.	349, 379, 417
Bangladesh	.	< 0.1	0.1	.	105, 311, 359
China	.	.	.	0.4	445

* Figures in brackets refer to studies in which the isolates were not bio-/ or serotyped; these may also include strains that are commonly not associated with disease.

agents [Bottone & Sheehan 1983], but also on the type of test used and the antibody background in the healthy population, for antibodies - especially those of the IgA type - may persist for months or even years after infection [Larsen *et al.* 1985; Paerregaard *et al.* 1991].

Diagnostic value of various agglutinin titres

The reference standard for measurement of *Yersinia* antibodies is a tube-agglutination test, but enzyme-linked immunosorbent assays (ELISA) are also used [Benoit *et al.* 1996]. In general, agglutinins titres of dilutions $\geq 1:128$ are supposed to be diagnostic in a previously normal, healthy subject, whereas medium (1:80 up to 1:128) and low ($\leq 1:40$) level titres are presumably indicative of, respectively, recent and less recent back contacts with the antigen.

Background in the population

A few studies have been done to investigate the antibody background in a normal population, with varying results. In Italy, *Y. enterocolitica* antibody medium titres were found in 0.2% (anti O:3) or 1.3% (anti O:9) of general blood donors [Tamburrino *et al.* 1993; Franzin & Curti 1993]. Similar figures were obtained in the USA, i.e. 1.4% with low titres against O:3, O:5,27 and/or O:8 [Bottone & Sheehan 1983], and in France, i.e. 0.8% with low titres against O:3, and 2% with high titres against O:9 [Mollaret 1983]. However, the prevalence of antibodies may vary between sub-populations, as appears from two Irish studies in which it was shown that 2% of a control population of non-yersiniosis hospital patients had high titres, whereas 0% of general blood-donors had titres above 1:40 [Attwood *et al.* 1987; Cafferkey & Buckley 1987]. From a Finnish study, by contrast, it was concluded that a high frequency of *Yersinia* antibodies can be found in healthy populations: in the sera of 19% of Finnish and 33% of German blood donors, enhanced levels of O:9/O:3 specific antibodies were found [Mäki-Ikkoia *et al.* 1997].

High titres in sub-populations

Elevated serum antibody concentrations have been found among people involved in swine breeding or pork production. In Finland, for example, slaughterhouse workers and pig farmers were observed to have elevated antibody levels to *Y. enterocolitica* O:3 twice as frequently as grain- or berry farmers or randomly selected blood donors [Merilahti-Palo *et al.* 1991; Seuri & Granfors 1992]. Significant differences for antibody titres against pathogenic serotypes were also observed between abattoir personnel and general blood donors in Italy, i.e. titres of $\geq 1:40$ in 19% versus 8% of persons, respectively [Franzin & Curti 1993; Franzin *et al.* 1998]. Likewise, similar differences were observed between office personnel and people practically involved in swine slaughtering in Norway [Nesbakken *et al.* 1991].

Practical use

Despite the above drawbacks, serology was shown to be a useful diagnostic tool in acute intestinal disorders: while, in a Swedish case-control study, a significant increase in *Ye* O:3-specific IgM antibodies was found in 85% of children with gastro-enteritis, only 2.9% of them (and none of the controls) shed *Y. enterocolitica* in their stools [Uhnoo *et al.* 1986]. Serology also

appeared to be a useful tool for diagnosis of sub-acute post-infectious complications, such as *Yersinia*-triggered reactive arthritis. In Italy, 33% of children suffering reactive arthritis were found to have medium or high ($\geq 1:80$ to 1:1280) anti-O:3/0:9 IgM titres [Taccetti *et al.* 1994]. Likewise, antibody titres 1:80 to 1:320 against *Ye* O:3, O:8, O:5 or O:6 were found in 19% of adolescent or adult patients with inflammatory joint diseases in Italy [Tamburrino *et al.* 1993].

1.6 TRANSMISSION ROUTES

Human yersiniosis is in many cases due to consumption of contaminated foods, quite often after previous storage of the vehicle at refrigeration temperatures. In addition, contaminated drinking water, contacts with human patients or infected animals, as well as blood-transfusions, have been recognized as modes to acquire a *Y. enterocolitica* infection (Figure 1.6). The minimum infective dose has not been determined, although a dose of 10^9 organisms which was orally taken by a human volunteer caused an acute enteritis within 24 hours, with symptoms lasting for four weeks [Szita *et al.* 1973].

1.6.1 Foods

Diverse food stuffs

Diverse food stuffs have been associated with yersiniosis. In the recurrent American outbreaks between 1976 and 1983, pasteurized chocolate milk [Black *et al.* 1978], reconstituted powdered milk and turkey chow mein [Shayegani *et al.* 1983], bean sprouts [Cover & Aber 1989], tofu [Aulisio *et al.* 1983] and pasteurized milk [Tacket *et al.* 1984] have been traced as vehicles of the bacterium (see the frame at the beginning of this chapter). In addition, there were links between infection and the consumption of bottled milk in outbreaks of yersiniosis in Japan [Maruyama 1987], the United Kingdom [Greenwood & Hooper 1990], Sweden [Alsterlund *et al.* 1995] and, more recently, in the USA [Shorter *et al.* 1998]. However, although raw and pasteurized milk are frequently reported to contain *Y. enterocolitica*, the isolation rates vary largely (0 to 80%) [Swaminathan *et al.* 1982; Davidson & Sprung 1989; Larkin *et al.* 1991; Rea *et al.* 1992; Desmaures *et al.* 1997] and pathogenic strains are only sporadically isolated [Adesiyun *et al.* 1996; Özbaz & Aytaç 1993]. Only in one case, an exceptionally high prevalence (15%) of pathogenic strains in raw milk has been found, i.e. in an area in the USA, but this was blamed on cross-contamination between swine and dairy animals on the farms [Rohrbach *et al.* 1992]. In contrast to their implication in various outbreaks, milk and bean products have never been associated with sporadic disease in the USA, nor in the high incidence countries in Europe [Ostroff 1995]. Worldwide, most of the isolated cases of yersiniosis are related to pork or porcine intestines [Lee *et al.* 1991; AlMohsen *et al.* 1997; Bien 1998; Tauxe *et al.* 1987; Ichinohe *et al.* 1991], like most of the recent outbreaks in the USA [Lee *et al.* 1990; DeBuono 1995].

Pork and pork products

Strong indirect evidence exist that swine (*Sus scrofa*) constitute the main reservoir for *Y. enterocolitica* strains pathogenic to humans, and that the major mode of transmission is pork. **First**, swine are frequently healthy carriers of human pathogenic strains, which live in their oral cavity or as faecal commensals. In Belgium and Norway, for example, serotypes O:3 and/or O:9 have been isolated from 50-100% of porcine tongues and/or tonsils [Wauters *et al.* 1988b; Nesbakken 1988]. Medium to high isolation rates (15-60%) of pathogenic serotypes from pig's throat and/or faeces have been reported from many other European countries [Asplund *et al.* 1990; Andersen *et al.* 1991; de Boer *et al.* 1991 1998; Bülte *et al.* 1992], and [Mousing *et al.* 1997; Atanassova & Ring 1998; Stefanov 1998], as well as from Japan [Shiozawa *et al.* 1991], and North- [Doyle *et al.* 1981; Kotula & Sharar 1993; Funk *et al.* 1998], South- [Escudero *et al.* 1996; Borie *et al.* 1997] and Central America [Adesiyun & Krishnan 1995]. In India, 2% of pigs were found to be infected with *Y. enterocolitica* O:9 [Singh *et al.* 1983]. The genetically close relationship between clinical and porcine isolates has been confirmed by means of various techniques, including total restriction endonuclease analysis, either in chromosomal DNA (REAC) [Kapperud *et al.* 1990] or in virulence plasmids (REAP) [Nesbakken *et al.* 1987; Fukushima *et al.* 1997]; analysis of restriction fragment length polymorphism in rRNA genes (RFLP-'ribotyping') [Andersen & Saunders 1990; Blumberg *et al.* 1991]; and multilocus enzyme electrophoresis (MLEE) [Caugant *et al.* 1989; Dolina & Peduzzi 1993].

Second, the naturally present bacteria may easily contaminate a carcass during the slaughtering process and increase to considerable amounts during prolonged cold storage of the raw product, a practice which is not uncommon in the meat industry [Nesbakken 1992]. Pathogenic *Y. enterocolitica* strains are indeed frequently encountered as surface contaminants in abattoirs [Andersen 1988; Nesbakken 1988], and *Y. enterocolitica* serotypes O:3 and O:9 have been found in the sludge of seven out of thirteen Dutch slaughterhouses [Fransen *et al.* 1996]. The rate of surface contamination of the raw meat could be reduced markedly by improved slaughtering techniques [Andersen 1988; Andersen *et al.* 1991; Nesbakken *et al.* 1994], but residual low levels are still found [Andersen 1998]. Furthermore, abattoirs furnish favourable conditions for psychrotrophic organisms to develop [Sammarco *et al.* 1997], as also appeared from an American study, in which pathogenic *Yersinia* could be isolated from only 0.4% of loins on the slaughter floor, but from 4.4% of vacuum-packed loins stored for 36 days at 2 °C [Saide-Albornoz *et al.* 1995].

Third, *Y. enterocolitica* serotypes O:3 and O:9 are frequently present in pork products at the retail level. In the Netherlands, for example, *Y. enterocolitica* and related species were isolated from a great variety of foods, but minced pork and porcine tonsils were found to be the only source of virulent strains [de Boer *et al.* 1986, 1991; de Boer 1995].

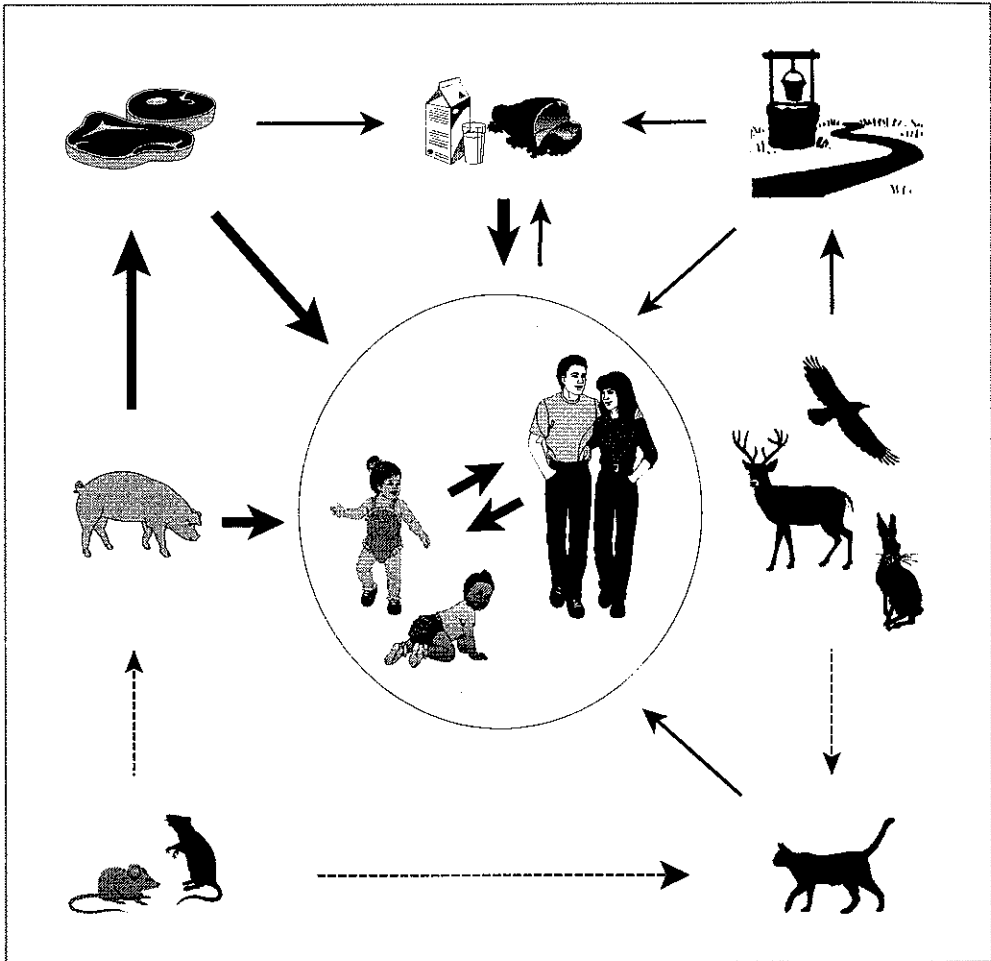


Figure 1.6 Transmission routes and recognized vehicles of *Y. enterocolitica*. The orientation and the heaviness of the arrows correspond with, respectively, the direction of the transmission and the level of documentation (heavy lines: well-documented; thin lines: rare; dotted lines: reasonable, but little or no documentation). Adapted from [Schiemann 1989].

Similarly, not inconsiderable isolation rates of pathogenic serotypes from raw pork have been obtained in many countries, including Belgium (24%) [Wauters *et al.* 1988], Japan (36%) [Shiozawa *et al.* 1987], Denmark (30%) [Andersen *et al.* 1991], Ireland (40%) [Logue *et al.* 1996], Canada (14%) [Durisin *et al.* 1997] and Spain (9%) [Garcia-Jalon *et al.* 1998]. Pathogenic strains have also been isolated from other raw meat products, such as chicken and lamb, but the prevalence

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is usually much lower [Norberg 1981; Logue *et al.* 1996] and might result from cross-contamination, since meat chopping boards in butcher shops are sometimes highly contaminated with these organisms [Asakawa *et al.* 1979; Christensen 1987a].

Fourth, there is a striking relationship between the incidence of human yersiniosis and pork consumption. As early as 1973, a positive relationship was observed between the domestic slaughter of pigs, traditionally in the period December to March, and the yearly increased frequency of yersiniosis in Czechoslovakia [Rakovský *et al.* 1973]. Similarly, the first recorded case - and familial outbreak - of yersiniosis in India was directly linked to consumption of meat from a freshly slaughtered Ye O:9 infected pig [Pramanik *et al.* 1980]. Likewise, raw sausages and minced meats containing pork were identified as transmission vectors of human yersiniosis in Spain [Mendoza *et al.* 1996], and an epidemic in East-Kazakhstan was reported to result from consumption of meat from sick animals after an outbreak of yersiniosis in a pig-breeding farm [Dmitrovsky *et al.* 1998]. Furthermore, the high incidence of yersiniosis in various countries in West- and Northern Europe coincides with a high pork consumption [Kapperud *et al.* 1995], and several case-control studies and surveys in these countries have elucidated pork consumption as a risk-factor for catching yersiniosis [Ostroff *et al.* 1994]. In Moslem countries on the other hand, and among other religious groups or cultures that traditionally do not consume pork, yersiniosis is rare [Haghighi 1979; Samadi *et al.* 1982; Jegathesan *et al.* 1984].

Finally, direct contact with raw pork, especially in the setting of food preparation, was also shown to be a risk factor. In 1969, yersiniosis, although being very rare in North-Africa, was suggested as being transmitted by raw meat, since butchers appeared to be healthy carriers of the bacterium [Makulu *et al.* 1969]. More recently, some culturally determined habits, such as consumption of foods containing raw pork (a habit quite common in Belgium) or the household preparation of swine intestines (as is usual at Thanksgiving among certain populations in the USA), were shown to be highly associated with yersiniosis [Tauxe *et al.* 1987; Lee *et al.* 1990 1991; DeBuono 1995; Bien 1998]. Handling of raw pork appeared to be the ultimate cause of infection in the first reported case of yersiniosis due to serotype O:8 outside the USA [Ichinohe *et al.* 1991].

1.6.2 Drinking Water

Y. enterocolitica's wide distribution in nature and its ability to grow at low temperatures have led to the suspicion that drinking water could also be a reservoir for man. Indeed, the organism has frequently been isolated from drinking water, but in most cases only non-pathogenic variants. Nevertheless, several reports describe a coincidence between gastro-enteritis and consumption of water contaminated with *Y. enterocolitica*. In Norway, for example, a serotype O:13 strain was isolated from a human patient as well as from the well-water she had been drinking [Lassen 1972]. Similarly, an outbreak of gastrointestinal illness in a ski-resort in the USA in 1974/1975 was most likely caused by consumption of well-water contaminated with

Y. enterocolitica serotypes O:3 and O:5 [Eden *et al.* 1977]. In addition, one of the earliest cases of yersiniosis reported in the United States, due to serotype O:8, was traced to consumption of water from a mountain stream, and wild animals were suggested to have played a role in contamination of the water [Keet 1974]. It was therefore suggested that the commonly reported seasonal variation of yersiniosis outbreaks, peaking in autumn and winter, could be due to specific outgrowth of *Y. enterocolitica* in the cold season, after spread into the waterways in the summer months [Hurvell 1981]. More recently, the organism was indeed shown to be able to proliferate in water stored at 4°C [Karapinar & Gönül 1991]. In Japan, *Y. enterocolitica* serotype O:3 was isolated from surface water in the vicinity of a piggery that raised Ye O:3 positive pigs [Fukushima *et al.* 1984], and sporadic cases of human O:8 infection have been attributed to the drinking of mountain stream water that was likely contaminated with the faeces of wild rodents carrying this strain [Ohtomo *et al.* 1995]. In Italy, serotype O:7,8, which had previously been associated with gastro-intestinal infection in this country, was isolated from river water [Massa *et al.* 1988], and in Australia, pathogenic *Yersinia* were detected, by means of PCR, in an environmental water reservoir [Sandery *et al.* 1996].

Indirect consumption of environmental waters has also been implicated in yersiniosis: water used in the manufacturing process was identified as the source of outbreaks linked to the consumption of tofu and bean sprouts in the USA [Tacket *et al.* 1985; Cover & Aber 1989], and water used to dilute buttermilk was the cause of the first reported foodborne outbreak of yersiniosis in India [Abraham *et al.* 1997]. Furthermore, drinking water in a medical residence was found to contain *Y. enterocolitica* after *Y. frederiksenii* had been isolated from several, ill as well as asymptomatic, members of the hospital staff [Cafferkey *et al.* 1993].

1.6.3 Live Animals

Pets

Because of their close contact with humans, pet animals have long been suspected to be a reservoir for human infections with *Y. enterocolitica*. Dogs and cats have occasionally been found to harbour pathogenic serotypes, particularly O:3, O:5,27 and O:9 [Fukushima *et al.* 1987; Chiesa *et al.* 1987; Fenwick *et al.* 1994], and outbreaks in breeding kennels as well as infection-transmission studies showed that these animals might be asymptomatic carriers [Fantasia *et al.* 1985; Fantasia *et al.* 1993; Fenwick *et al.* 1994]. Several sporadic cases and small scale outbreaks of human yersiniosis have been described in which ill dogs or cats were most likely the source of infection. On some occasions, identical pathogenic serotypes (O:20, O:3 or O:9) were isolated from ill or asymptomatic pets and human contacts [Ahvonen *et al.* 1973; Gutman *et al.* 1973; Wilson *et al.* 1976], but transmission to man could not be proven, or seemed at least doubtful. Some observations in Japan suggested involvement of wild animals in the spread of yersiniosis: the presence of *Y. enterocolitica* serotype O:8 in wild-living rodents in a restricted period coincided with the occurrence of sporadic cases of human yersiniosis, due to identical

strains, in the same period and area [Hayashidani *et al.* 1995; Ohtomo *et al.* 1995]. Similarly, wild rodents seem to play an active role in the spread of yersiniosis in Kazakhstan: peaks in human yersiniosis due to serotype O:5 (in 1992 and 1995) followed epizootic manifestations of infection with the same serotype in rats in 1991 and 1994 [Necrasova *et al.* 1998a]. In addition, a Danish study showed that wild rats and mice living on swine-breeding farms are potential reservoirs of *Y. enterocolitica* O:3, too [Bech-Nielsen *et al.* 1998]. Indirect support for possible spread through wild animals also comes from the observed carriage of serotypes O:5,27 and O:3 by hares in Germany [Wuthe *et al.* 1995], but a possible relation with human yersiniosis has not been investigated.

Farm animals

Suspicion has also been directed at contact with domestic animals in the food industry, especially swine, a common risk for farm- or abattoir-workers. After a labourer on a pig farm in South Africa died of septicemia due to *Y. enterocolitica* O:3, animals from this farm were inspected, and the identical strain was found in rectal swabs of 50% of the pigs [Rabson & Koornhof 1973]. At the same time, increased anti-*Y. enterocolitica* titres were found among healthy pig-slaughterers, suggesting past contact with the organism and occupational risk from exposure to pigs. The involvement of swine in putting humans in contact with this bacterium is also supported by data obtained from serological studies in Scandinavia and Italy [Merilahti-Palo *et al.* 1991; Seuri & Granfors 1992; Franzin & Curti 1993; Nesbakken *et al.* 1991; Franzin *et al.* 1998].

1.6.4 Humans

Epidemiological studies concerning many small scale familial outbreaks of yersiniosis suggest that the disease can easily be spread in contacts with infected people, possibly via highly contaminated stool [Ahvonen & Rossi 1970; Gutman *et al.* 1973; Szita *et al.* 1973; Marks *et al.* 1980; Martin *et al.* 1982]. Communicability of the illness is also evidenced by the large scale outbreaks that occurred among school populations [Asakawa *et al.* 1973; Olšovský *et al.* 1975; Kasatiya 1976], as well as by several hospital-acquired episodes, affecting both in-patients, staff and their relatives [Toivanen *et al.* 1973; Ratnam *et al.* 1982; McIntyre & Nnochiri 1986; Cannon & Linnemann 1992].

1.6.5 Blood-transfusions

Even more worrisome than the direct transmission between humans, is the indirect person-to-person transmission of *Y. enterocolitica* which may occur during blood transfusions. This is a rare but easily fatal complication arising from contaminated blood products, especially red blood cell concentrates [Prentice 1992]. The rate of *Yersinia*-associated adverse transfusion reactions has been estimated to lie between 0.1 and 2 in one million transfusions [Högman & Engstrand 1996; Halpin *et al.* 1997]. As is to be expected, this type of infection does not result in gastro-enteritis; it usually leads to septic shock, a severe disorder with a high mortality rate.

Since the first published case of *Y. enterocolitica* sepsis, which occurred in the Netherlands in 1975 [Bruining & De Wilde-Beekhuizen 1975], more than 50 cases of transfusion reaction caused by this organism - with a mortality rate higher than 60% - have now been described in the English and German literature [Högman & Engstrand 1996; Höher 1996]. In addition to the common pathogens O:3, O:9 and O:5,27, which were causative agents in most cases of transfusion-acquired *Yersinia* infection with fatal outcome [Högman & Engstrand 1996; Neumeister *et al.* 1997; Theakston *et al.* 1997; Mewis *et al.* 1997], more rare serotypes as O:20 and O:1,2,3 have also been involved [Tipple *et al.* 1990]. In several transfusion-acquired cases, stool culture and/or serology revealed overt *Yersinia* infections in the blood donor [Bjune *et al.* 1984; Brown & White 1988; Haverly *et al.* 1996; Kuehnert *et al.* 1997] or asymptomatic carriage of the bacterium [Stenhouse *et al.* 1982; Brown & White 1988; Elrick 1988; McDonald *et al.* 1996]. In other cases, however, donors were negative for *Y. enterocolitica* in blood and stool cultures, as well as in antibody-serology [Neumeister *et al.* 1997]. The opposite result has also been observed: *Y. enterocolitica* serotype O:3 was cultured from blood containing a high antibody titre against Ye O:3, donated by a donor with a history of surgically treated pseudo-appendicitis, but the recipient of the erythrocyte concentrate did not experience any adverse effects from the transfusion [Jacobs *et al.* 1989]. Nevertheless, most reports of transfusion-acquired septicemia include serological evidence of donor infection with *Y. enterocolitica*, with or without a history of diarrhoea at the time of donation [CDC 1991; Högman & Engstrand 1996]. Thus, there is strong evidence for a link between the increase of transfusion-associated fatalities and an increased incidence of *Y. enterocolitica* gastroenteritis [CDC 1991]. This suggestion was recently supported by a report from New Zealand in which a high incidence of transfusion-transmitted *Y. enterocolitica* infections has been correlated with a rise in the number of faecal isolations [Theakston *et al.* 1997].

1.7 INFLUENCE OF COLD STORAGE

Effects in foods

A number of studies have shown that *Y. enterocolitica* is able to multiply in many types of refrigerated foods, especially raw and cooked meat [Hanna *et al.* 1977; Garcia de Fernando *et al.* 1995; Greer *et al.* 1995; Shenoy & Murano 1996], but also in dry sausages [Kleemann & Bergann 1996]; in dairy products, such as milk [Stern *et al.* 1980a, 1980b; Kendall & Gilbert 1980], butter [Slavchev 1989; Lanciotti *et al.* 1992], and wet, soft as well as dry cheeses [Sims *et al.* 1989; Little & Knochel 1994; Sarigiannidou *et al.* 1997]; in fresh and boiled eggs [Erickson 1995]; in boiled rice and potatoes [Kendall & Gilbert 1980]; in raw and smoked fish [Hudson & Mott 1993; Davies & Slade 1995]; and in shell-fish [Hudson & Avery 1994]. It has also been reported that only serotypes O:3, O:8 and O:9 grow well at 4°C, while other serotypes did not [Eiss 1975]. Freezing conditions may have an adverse effect on the survival of the bacterium [Hanna *et al.* 1977; Asakawa *et al.* 1979], but freezing tolerance has also been reported [Leistner *et al.* 1975; Kendall & Gilbert 1980; Slavchev 1989]. On the other hand, the

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ability of *Y. enterocolitica* to compete with other psychrotrophic organisms normally present in food may be poor [Fukushima & Gomyoda 1986; Kleinlein & Untermann 1990], and growth may also be inhibited by components of the product itself, such as minced meat exudates [Doherty *et al.* 1995]. At retail level, pathogenic serotypes have been found in various refrigerated foods of animal origin, including cooked meat products and fish fillets [Velázquez *et al.* 1993; Velázquez *et al.* 1996]. In addition, significantly higher amounts of pathogenic strains were found, in Taiwan, in refrigerated or frozen stored pork products compared to non-refrigerated products [Tsai & Chen 1991]. These observations indicate that cold proliferation of the bacterium is not just a laboratory bound-phenomenon.

Effects in blood products

From retrospective investigations in cases of transfusion-acquired *Yersinia* infections, it was concluded that extended storage at low temperature might have a disastrous influence on the quality of blood products, and laboratory studies support this conclusion. In almost all cases of transfusion-acquired septicemia, the donated whole blood or red cell concentrates had been stored for over three weeks before transfusion, and a number of laboratory studies have shown that under conditions of cold storage and iron enrichment from aging erythrocytes, *Y. enterocolitica* can proliferate after a lag phase of 10-20 days [Arduino *et al.* 1989; Franzin & Gioannini 1992]. Obviously, those serotypes with a high iron requirement, i.e. those which do not produce endogeneous siderophores, will benefit most from the iron overload. The difference in relative advantage from iron enrichment, in combination with a difference in serum resistance, might explain why serotype O:8 has never been found in cases of transfusion-associated bacteraemia, while serotype O:3 is the most common cause of this type of *Y. enterocolitica* infection [Neumeister *et al.* 1997]. It has also been suggested that, during temperature fall after blood donation, the organism might utilize its invasive capacity by expressing the *inv* gene, to reach a protective side inside a cell. Resistance to intracellular killing mechanisms is low at 37°C but increases with decreasing temperatures, which might explain why pre-storage leucocyte depletion has a protective effect on contamination with the bacterium during prolonged storage of blood products [Högman & Engstrand 1996; Neumeister *et al.* 1997].

1.8 ISOLATION & IDENTIFICATION

1.8.1 Selective Media

Y. enterocolitica strains show a marked degree of variability in ability to grow and appearance on commonly used enteric isolation media. On such media, the usually very small and unspecific colonies can easily be overlooked, especially when surrounded by an abundant growth of heterogenous native flora. This has possibly accounted for its initially delayed

recognition and has led to the development of several specific media and enrichment techniques [Pee and Stragier 1979; Head *et al.* 1982]. For isolation of pathogenic strains from the heavily contaminated faecal samples of symptomatic persons, direct plating on specific media such as Cefsoludin-Irgasan-Novobiocin (CIN) and Desoxycholat agar is satisfactory [Wauters 1973; Butler 1981]. For the recovery of *Y. enterocolitica* from less contaminated samples such as foods, cold preincubation, specific enrichments, e.g. with Irgasan-ticarcillin-potassium chlorate (ITC), and polycarbonate surface adhesion have proven to be valuable techniques [Wauters *et al.* 1988b; Sheridan *et al.* 1998]. However, polycarbonate surface adhesion is non-selective and cold enrichment also favours growth of the non-pathogenic strains, so these isolation techniques do not take away the need of methods to differentiate between pathogens and non-pathogens.

1.8.2 Classical Virulence Tests

The differentiation between virulent and non-virulent strains has, until the onset of the 1990s, mainly relied upon bio- and serotyping, based on the strong association of pathogenic significance with only a few serogroup-biovar combinations. In addition, a number of different in-vitro and in-vivo tests have been used to distinguish between pathogens and non-pathogens. These tests include various animal models, using either gerbils, mice, rabbits or guinea pigs [reviewed by Carter 1981 and Schiemann 1989]; in-vitro invasiveness [Une 1977; Prpic *et al.* 1985]; resistance to the bactericidal action of blood serum [Pai & DeStephano 1982]; autoagglutination and calcium-dependent growth at 37°C [Laird & Cavanaugh 1980; Gemski *et al.* 1980]; binding of dyes like Congo red or Crystal violet [Prpic *et al.* 1983; Dziezak 1991]; and pyrazinamidase-activity [Kandolo & Wauters 1985]. However, many of these tests are based on properties associated with the virulence plasmid, and/or are subject to problems of gene expression in vitro, which make their sensitivity and selectivity questionable [Wachsmuth *et al.* 1984; Farmer *et al.* 1992].

1.8.3 DNA-based Methods

Several molecular genetic typing methods have been used for detection and/or identification of virulent strains. Applying DNA-hybridizations, the presence of pYV could easily be detected, independent of gene-expression [Hill *et al.* 1983; Jagow & Hill 1986], and after 1989, when the polymerase chain reaction (PCR) technique appeared on the scene, much progress was gained in sensitivity and specificity of the pYV-detection methods [Miliotis *et al.* 1989; Wren & Tabaqchali 1990; Kapperud *et al.* 1990, Nesbakken *et al.* 1991]. However, neither of these pYV-targeted methods overcame the problem of false negative results that might occur due to the easy loss of the virulence plasmid during the isolation procedure. An escape from this dilemma was found in the development of DNA-based methods that target chromosomal virulence associated sequences: distinguishing virulent and non-virulent strains was shown to be possible

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et al. 1992] or *yst* [Delor *et al.* 1990]. These probes have successfully been applied to detect pathogenic strains in clinical specimens, raw meat samples, foods and environmental waters [Ibrahim *et al.* 1992a 1992b 1997; Harnett *et al.* 1996; Thisted Lambertz *et al.* 1996; Sandery *et al.* 1996]. Excellent results in detection, as well as in distinguishing pathogenic and non-pathogenic strains, have also been obtained with DNA-probe- and/or PCR-based tests that simultaneously target both chromosomal and plasmid-borne virulence genes [Nakajima *et al.* 1992; Thisted Lambertz *et al.* 1996; Fliss *et al.* 1995; Harnett *et al.* 1996; Weynants *et al.* 1996; Nilsson *et al.* 1998]. In addition, genetic relatedness among strains, a tool useful in epidemiological studies, has successfully been studied by combining various DNA-based methods, including whole-cell DNA RFLP analysis by hybridizations with rRNA-based probes ('ribotyping') [Iteman *et al.* 1996; Lobato *et al.* 1998]; random amplified polymorphic DNA (RAPD)-fingerprinting [Odinot *et al.* 1995]; and pulsed-field gelelectrophoresis (PFGE) analysis of restriction endonuclease profiles obtained from plasmid (REAP) or chromosomal (REAC) DNA [Buchrieser *et al.* 1994; Najdenski *et al.* 1994; Asplund *et al.* 1998].

Good results in detection of (antigens from) virulent strains has also been obtained by applying specific immunofluorescent antibodies [Viitanen *et al.* 1991, Sheridan *et al.* 1998] and by in-situ hybridizations with fluorescently tagged oligonucleotide probes [Trebesius *et al.* 1998].

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2

The Cold Chain

**food preservation in
historical perspective**

ABSTRACT

Refrigeration, although not a recent discovery, has, in our era, become a general means of keeping foods from spoilage at all stages between production and consumption. However, chilling is not enough to restrain certain micro-organisms, i.e. those which are known as 'psychrophiles' or 'psychrotrophs' because of their ability to multiply at temperatures near zero. Among these are not only many spoilage bacteria, such as *Pseudomonas* spp., but also several bacteria that are pathogenic for humans, especially *Yersinia enterocolitica* and *Listeria monocytogenes*. Infection with these latter organisms has emerged as an important cause of foodborne disease in the last four decades. This undesirable development has presumably been favoured by the enormous increases that have occurred in the application of refrigeration for the preservation of perishable foods. In addition, refrigeration is not without danger in modern medical technology. Rare, but not to be neglected, are fatalities which occur in blood transfusions, due to bacterial growth during extended chilled storage of the administered blood-products. *Yersinia enterocolitica* is the major organism involved in this latter type of infection.

2.1 TRADITIONAL METHODS OF FOOD PRESERVATION

2.1.1 'Natural' Methods: Drying and Freezing

When life was largely nomadic, food preservation was not under discussion because man literally lived from hand to mouth: food was gathered and eaten where and when it could be found. But when life became sedentary, approximately 10,000 years ago, keeping some of the harvest bounty for use during the non-productive season became a vital necessity for survival [Baumgartner 1978]. Whilst our ancestors must have experienced that almost all raw foods are liable to spoilage at some rate or other, they will not have failed to notice too that the deterioration process was sometimes delayed by climatic factors ¹.

Early man must have been aware that naturally dried products such as nuts and seeds hardly go bad: witness the storage-pits for dried grains that have been found in the valleys of the Indus and Euphrates-Tigris, the cradle of our civilization [Borgstrom 1968]. In extremely low temperature regions, on the other hand, early man will have noticed that captured fish or game could be preserved by freezing, just by hanging it outdoors. When learning, probably by chance, how to use utilize these factors, early man started to imitate nature. Thus, by just taking advantage of the sun's heat, wind and frosty cold, he (or she) 'invented' drying and freezing as the first methods of food preservation.

2.1.2 First 'Artificial' Methods: Smoking, Salting, Chilling

As time went on, other more or less natural resources, such as smoke, salt, snow and ice, were also adopted to keep food surpluses edible for longer periods. Whether or not they were combined with drying, new techniques such as smoking, salting, curing and fermenting became widely used for long-range preservation of highly perishable foods, such as meat, fish

1. Drying was most probably the first method adapted by man to enlarge the storage-life of food surpluses. Presumably, sun-dried seeds served as a model for solar drying of more perishable foodstuffs. Anyhow, dried foodstuffs have been used for centuries, all over the world: ranging from sun-dried fruits in ancient Mesopotamia and Palestine to dried, salted fish with the Phoenicians, and from freeze-dried potato tubers with the pre-Columbian Indians in Peru and Bolivia to sun- or wind-dried meat as the typical travelling food of hunting and migratory people from Central Asia, Africa and the American continent. Similarly, man must have learned by experience that foodstuffs also kept better in the cold. Prehistorians think that in the lower Old Stone Age (100,000 B.C.) caves, such as those in Altamira in Spain, were used for cool storage of food, especially game. Old written documents also testify that man was positively aware of the benefit of cool storage: in 40 A.D., the Latin agronomist Columella gives advice on the orientation of buildings so as to obtain a cool ambience for keeping cheese, fruit and vegetables. In Spain, around 1200, recommendations and prescribed rules concerning the cooling of carcasses after slaughter were given, and around 1600, summer storage of game in caves was recorded in alpine regions of Austria and Switzerland.

and milk. To keep less vulnerable products such as fruits, cabbages and tubers from precocious spoilage, man in general took advantage of natural cold in caves, cellars and cold springs [Jobsevan Putten 1989; Reinink & Vermeulen 1981; Plank 1960; Thévenot 1979]. In addition, snow and ice were sometimes used for cooling purposes, especially during long-distance transport of perishables such as fish and fruit [Legge 1876; Mez 1922; Forbes 1966; Tannahill 1988; Toussaint-Samat 1992]². This latter habit, however, mainly served the tables of the rich and was not used for common people's food supply. In general, chilling by ice played a minor role in food preservation.

2.1.3 Mechanisms of Effectiveness

For ages, the factual action of the empirically developed preservation methods was veiled in mysteries: when the Spanish doctor Nicolas Monardes reviews in 1574 the means of cooling of foodstuffs which were in use at that time, he sighs that the delaying effect of snow on the rotting of fruits, fish and meat is "... *something which human intelligence can neither understand nor explain...*" [Thévenot 1979]. In fact, the mechanisms of the effectiveness of preservation methods were not understood before the end of the 19th century, after Louis Pasteur in the 1860s had established the relationship between microbial activity and putrefaction.

Nevertheless, all the empirically developed methods to arrest or retard the natural processes of decay were based on sound microbiological principles. These were either suppression of unwanted bacterial growth, by reducing water activity and/or temperature, or, on the contrary, favouring the growth of advantageous types of organisms by adding them deliberately and/or providing an optimal environment (Table 2.1, upper part)

2. Food preservation by refrigeration hasn't just sprung up overnight. Almost four thousand years ago, snow and ice were harvested and stored for later use as refrigerants, as may be concluded from inscriptions on Mesopotamian clay tablets and from passages in the 'Shi-King', the classic Chinese 'Book of Poetry', in which Confucius recorded aspects of daily life in the period between 1800 and 1300 B.C. Born in the Far East, storage of snow and ice became widespread in the Old World, wherever cold winters or mountain altitudes permitted its harvest: ice-pits, -cellars and -houses have left their traces in Japan and India, as well as all over the Mediterranean and Black Sea regions.

In many cases, the snow and ice had to be carried down from distant mountains, and it was initially mainly used for luxury applications: cooling of wine and drinking water, as was common practice amongst the privileged people of ancient Rome, or preparation of fruit-sorbets, which were very popular in the Arab world of the Middle Ages.

But ice was also used as a preservative agent during food-transports in the hot season. The markets of ancient Rome, for example, were provided with fish from the Rhine and the North Sea, packed round with ice and transported under layers of insulating furs. Much later, in the 10th century, watermelons were sent from northern Iran to Baghdad in ice-cooled lead containers. And in the 16th century, plums and bamboo shoots were being transported to the palaces of the Chinese emperors in Peking by keeping them fresh in ice.

Table 2.1 Methods of food preservation, adapted from [Adams & Moss 1995]

TREATMENT	TEMP. RANGE	AIMED EFFECT
Drying, curing, and concentration	< 100°C	Inhibition of growth by reducing wateractivity
Fermentation, and addition of preservatives	RT *	Arrest of unwanted growth by addition of inhibitory factors
Freezing and chilling	-20 to 4°C	Arrest of growth by reducing metabolic activity
Sterilization	> 100°C	Complete elimination of viable micro-organisms
Cooking	± 100°C	Destruction of pathogenic micro-organisms
Pasteurization	60 - 80°C	Elimination of pathogens & spoilage organisms
Vacuum- & Modified-atmosphere-packaging	-20°C to RT	Arrest of growth by imposing of inhibitory factors
Ionizing radiation	-20°C to RT	Elimination of viable micro-organisms by damaging of DNA

* RT = room temperature

2.1.4 Nutritional Drawbacks

Just as people were unaware of microbiological principles, so the basics of wholesome food were misunderstood. Food was largely thought of as containing a single element to sustain life, and a possible decrease in nutritional value during extended storage was not under discussion. The traditional methods of drying, smoking, salting, curing and fermenting stood undisputed for ages, in spite of their apparent drawbacks with respect to loss of attractiveness and taste. Besides, common people relied heavily on such preserved foods, from sheer necessity. The resulting monotonous diets, which were usually short of essential nutrients, contributed greatly to reduced public health, but it took until the 1830s before the connection between malnutrition and unhealthiness was recognized [Borgstrom 1968; Hartog 1980]. The alimentary situation, however, was not to be altered before a drastic reform had taken place in the field of food preservation.

2.2 REVOLUTIONS IN FOOD PRESERVATION

2.2.1 New Heat-treatments

With the onset of the industrial era, heat was discovered to be a useful tool to realize an increase in the storage life of perishable foodstuffs. Heat-preservation was invented by the French chef Nicolas Appert who described, in 1811, a procedure of boiling combined with

hermetic closure as the "... *Art of Conserving all kinds of Animal and Vegetable Matter for several Years*", by which canning was born [Adams & Moss 1995]. Initially, the success of this technique was erroneously ascribed to the exclusion of air from the product. It took fifty years more before Louis Pasteur recognized that microbial inactivation was in fact the essential event. He developed a milder heat-processing technique, by which harmful micro-organisms could be destroyed without deactivating the useful ones. When the mechanisms of effectiveness of 'appertization' and 'pasteurization' were established, their value in protecting public health was also recognized, and they became increasingly used in food preservation.

2.2.2 Revaluation of Cold

Ice-houses

From the 16th century onwards, cold became revalued as a useful 'additive' in the human diet. Strictly speaking, the application of cold was not new, since ice and snow had been used for the cooling of spices and drinks in ancient times (see also footnote 2). For ages, however, the icing of foods was unusual and the application of ice and snow had been mainly restricted to the cooling of wine and drinking water, in addition to use for nursing and air-conditioning(!) [Plank 1954]. A change started to set in when, in the 16th and 17th centuries, sorbets and ice-creams came into fashion in Europe and North-America [Tannahill 1988; Adams & Moss 1995]. By the 18th century, special ice-houses or -cellars had become a common feature at Europe's stately homes: huge amounts of ice were stored yearly, especially for the cooling of wine and the preparation of luxury refreshments [Reinink & Vermeulen 1981]. The preservative qualities of ice remained, of course, not unnoticed, but the ice-houses were as yet scarcely used for food preservation, since the well-to-do, in their situation of comfort, had little interest in preserved foods. Ordinary people, on the other hand, could not afford such stores, nor the labour-intensive harvesting of large quantities of ice. Only in Spain, where the very hot summers provoked early research into the benefits of natural cold, was trade in snow a public affair in those days, and refrigeration generally adapted to foods [Thévenot 1979]. Until the end of the 18th century, the icing of foods for preservation purposes was in most other countries a private and small scale phenomenon that was mainly restricted to the cooling of milk, butter and meat products on farms [Reinink & Vermeulen 1981].

The victory march of ice

At the end of the 18th century, almost simultaneously with the invention of heat-preservation, the application of cold as a preservative agent received a new impetus: the harvesting and storage of ice started to become rationalized, which meant that it came within the reach of common people. When, at the turn of the century, the collection of natural ice became further mechanized, ice-houses mushroomed at farms all over North America. Similar progress was made in the ways of transport and storage, a process that went hand in hand with

commercialization of the ice-trade, especially in the USA and Scandinavia (Figure 2.1)³.

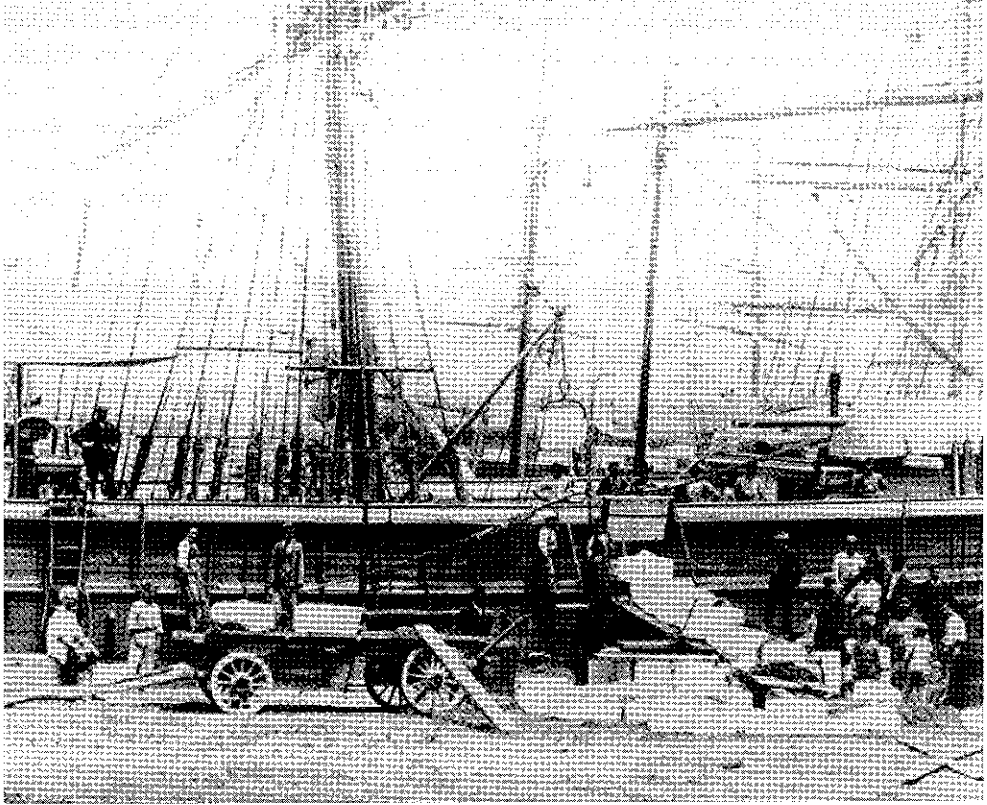


Figure 2.1 The sailing ship '*Tenax Propositi*' from Kragerø (Norway) in the harbour of Philippeville (Algeria), in 1886, delivering Norwegian ice. Copied from [Reinink & Vermeulen 1981], with permission.

3. The real breakthrough of refrigeration as a food-preservation method took place in the course of the 19th century, and its triumphal progress was initiated in North America and Europe. Here, the industrialization of harvesting, storage and transport of natural ice was realized, which was a prerequisite for the enormous expansion of ice-consumption that was, in its turn, the driving force for the development of mechanical refrigeration. Some figures may illustrate the scope of cooling by ice at the end of the 19th century: yearly, five million tonnes of ice were harvested in the United States, mainly for use in the meat- and fish-trade. Annually, some 8000 tonnes of fish from the North American Great Lakes was frozen in salt/ice mixtures, and 30,000 tonnes of iced beef were shipped from the United States to Great Britain. Private consumption also reached enormous proportions, as is evident from the 700 kg of ice that were used yearly per head by the citizens of a large town like New York. Some 200,000 tonnes of American ice were exported to destinations as far away as Rio de Janeiro, Calcutta and Australia, and the export of Norwegian ice to Great Britain and Germany was even larger, reaching levels of half a million tonnes per year.

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These developments cleared the way for a more general utilization of ice in food preservation [Thévenot 1979]: a boom followed in ice-consumption and in the 1830s, the application of ice had become common practice in the meat- and fish-trade in both North America and Europe [Papworth 1832; Thévenot 1979; Jobse-van Putten 1996]. To meet the growing needs of the market, the ice-business was quickly industrialized, which mutually stimulated further expansion of refrigeration as a means of food preservation. When, halfway through the 19th century, special cooling cabinets for private use made their entry, the refrigeration of perishable foodstuffs became generally adopted in big towns, where it was distributed by doorstep deliveries at hotels, restaurants and well-to-do households (Figure 2.2).



Figure 2.2 Street scene in the Netherlands, in the 1930s: blocks of ice are delivered at a restaurant (*Fotoarchief Spaarnestad*)

Following the improvements in the meat- and fish-trade, large-scale application of refrigeration spread to other commodities: cold stores for apples were built, and ice-cooled as well as ice/salt-refrigerated rail transport of fruits and butter started in the last quarter of the 19th century [Plank 1954; Thévenot 1979].

Mechanization of refrigeration

Natural ice as a cooling medium, however, had many drawbacks, from which contamination during its formation and handling formed the main problem for direct application on foods. So much effort was devoted to realizing a cleaner (and less space-occupying) production of cold. In the second half of the 19th century, when the industrial revolution was in full swing, the principles of thermodynamics were established and a wide range of new mechanical devices for all kinds of techniques, including power supply, became available. Simultaneously, the utilization of liquefiable gases was mastered and before the turn of the century, mechanical refrigeration was a fact. Breweries, and ships for the international transport of meat, were the first to be equipped with refrigerating machines [Thévenot 1970; Plank 1962]. In the first decades of the 20th century, refrigeration machines were installed in dairy plants and in public cold stores, and the capacity of mechanically refrigerated transport expanded enormously.

2.2.3 Development of the 'Cold Chain'

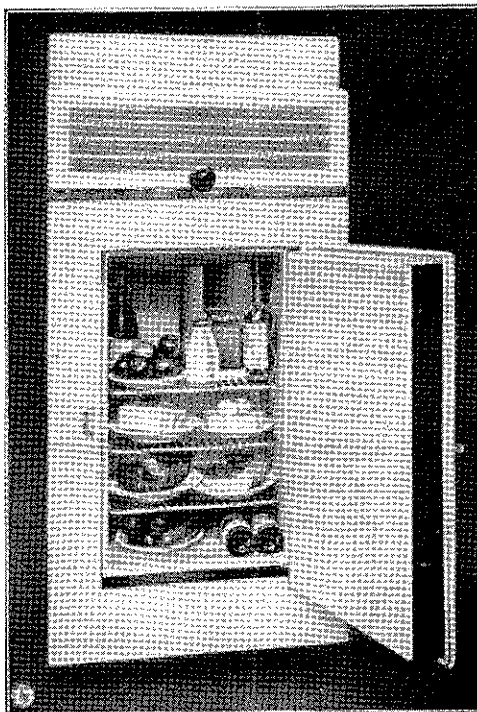


Figure 2.3 The 'Protos-Frigor': one of the first mechanical house-hold refrigerators in the Netherlands, (copied from 'Koeltechniek', 1932)

Although natural ice had paved the way, the mechanization of refrigeration was essential for the development of the 'Cold Chain'. In the 1930s, the world-wide commercial refrigeration of all types of foodstuffs grew in size, favoured by both internal and external factors, such as use of the newly developed freons and completion of the electricity grid in the industrialized countries. In the first half of the 20th century, mechanical refrigeration integrated also into the private sector. The household refrigerator was launched in 1918, spread in the USA in the Interbellum, and became current in the other industrialized countries after the second world war [Thévenot 1979; Plank 1962; Jobse-van Putten 1996].

The maturation of the 'Cold Chain' was beginning to take shape in the middle of the 20th century, when trade became more and more centralized and refrigerating equipment was incorporated in retail food

distribution systems in most developed countries, a development that was speeded up by the introduction of supermarkets. When, finally in the 1960s, the household refrigerator had become an integral part of kitchen furniture in all industrialized countries, the ultimate link in the 'cold chain' was closed. Actually, a continuous cold chain from producer to consumer has evolved, and nowadays cooling is an indispensable factor in the commerce of foodstuffs [Gac 1992].

2.3 THE ALIMENTARY REVOLUTION

2.3.1 Healthier Diets

As a result of the changing nutritional insights, a clear concept of the superiority of fresh products prevailed throughout the last half of the 19th century and interest grew for cooling of various foodstuffs. Canning and pasteurization had already brought about a nutritional revolution, but the mechanization of refrigeration initiated a second, even more drastic breakthrough in food-handling and dietary patterns. First, the age-long dominant position of vegetable food in the ordinary man's diet was finally broken down when 'fresh' meat which everybody could afford became available: in fact, chilled and frozen meat imported from Argentina, Australia and New Zealand fed the rapidly increasing populations of Europe and North-America in the first decades of the 20th century. Second, large scale trans- and intercontinental transports enabled delivery of fresh fruits and vegetables for longer periods and to wider geographical areas, which consequently enlarged nutritional diversity, especially in the industrialized countries.

2.3.2 New Products and Changing Preferences

By the maturation of the 'cold chain' in the second half of our century, and the simultaneous expansion of the agro-alimentary industry, chilling and freezing became the keystones of the world food supply. As a result, our food and eating habits were changed more in the fifty years after the second world war than in the previous nineteen centuries [Fenton & Kisbán 1986; Otterlo 1990; Jobse-van Putten 1989].

Convenience foods

New commodities such as ready-to-eat meals and other convenience foods appeared upon the scene and, in addition, a tremendous growth was seen in the consumption of quick-frozen foods. In the last decades, stress has been laid not only on ease of preparation, but also on maximum retention of the original qualities of foodstuffs with respect to appearance, flavour, and dietetic values [Gould 1996]. Through the consumer's preference for foods that are more

convenient but at the same time less heavily processed and not loaded with additive preservatives, refrigeration has become even more important because it is, in general, the gentlest method of food preservation, having relatively few adverse effects upon taste, texture and nutritional value [Potter & Hotchkiss 1995].

Chilled products with extended shelf life

To meet the consumers demands for more 'natural' and fresh products, new food processing technologies have been developed to extend the shelf life of refrigerated products. These methods include mild heating, pH reduction, and vacuum- or modified atmosphere packaging, resulting in 'Sous-Vide'-products, and so-called REPFEDs (i.e. Refrigerated Pasteurized Foods of Extended Durability) [Lechowich 1988; Sofos 1993; Gould 1996]. To keep the microbial population of such foods under control, several relatively mild preservative factors are combined, creating a so-called hurdle effect [Leistner 1995; Gould 1996]. The hurdle technology is aimed at optimization of the safety and quality of products by adjustment of the different preservative factors (= 'hurdles') applied. Nevertheless, evidence is growing that even the introduction of these new technologies may not completely expel the risks of food spoilage or food poisoning [Mossel & Struijk 1991; Notermans *et al.* 1990]. After all, a wide range of homeostatic mechanisms have evolved in micro-organisms, which enable them to survive various types of extreme environmental stresses. Exposure to one type of stress can induce resistance to other environmental extremes, the so-called Global Stress Response [Gould *et al.* 1995]. Some of these adaptations may be just the thing needed to leap one or more hurdles in modern food-preservation, and the ability to survive and proliferate at low temperatures might very well be one of these features.

2.4 RISKS OF COLD PRESERVATION

2.4.1 Cold-tolerant Food Spoilage Organisms

With the advent of the refrigeration era, the idea took form that refrigeration could probably be enough to keep foods from precocious spoilage. In 1936, for example, it was recommended that foods should be stored below 10°C and preferably at 4°C, "... to prevent growth of pathogens or toxin development..." [Prescott & Geer 1936]. By the mid-1950s, however, it became evident that cooling, though it indeed greatly retarded microbial growth and production of undesirable metabolites, could not completely prevent the growth of food spoilage organisms [Walker & Stringer 1990]. Various bacteria, yeasts and molds appeared to grow in a wide range of food products held at 5°C. Coincidental with improved refrigeration over the years, a change in the spoilage flora of many types of food occurred, and cold-tolerant organisms became an escalating problem for the food-industry [Tompkin 1973; Palumbo 1986; Sørhaug & Stepaniak 1997].

2.4.2 Cold-tolerant food-borne Pathogens

Cold-loving 'Psychrophiles' and 'Psychrotrophs'

From the 1950s onwards, it was taken into account that a decreased storage temperature only retards food spoilage, but refrigeration was still considered adequate to prevent growth and/or toxin formation by foodborne pathogens. In the early 1960s, however, it became evident that refrigeration is not enough to restrain foodborne pathogens, since several 'cold-loving' organisms, called psychrotrophs or psychrophiles, appeared to be amongst them. Since then, several human pathogenic bacteria have been shown to grow and/or produce toxins in foods held at 5°C or less, in particular *Listeria monocytogenes*, *Yersinia enterocolitica*, *Aeromonas hydrophyla* and certain types of *Clostridium botulinum* (Table 2.2) [Olsvik & Kapperud 1982].

Table 2.2 Psychrotrophic* bacteria involved in foodborne disease. Adapted from [Kraft 1992; Adams & Moss 1995]

ORGANISM	GRAM-TYPE	OXYGEN TOLERANCE	MOTILITY
<i>Aeromonas hydrophyla</i>	-	facultative	+
<i>Clostridium botulinum</i>	+	aneuroob, (sporeforming)	+
<i>Listeria monocytogenes</i>	+	facultative	+ at 25°C, - at 37°C
<i>Yersinia enterocolitica</i>	-	facultative	+ at 25°C, - at 37°C

* Able to grow at temperatures <4°C

Between 1973 and 1987, bacterial infections accounted for 66% to 87% of all foodborne disease of known origin in the USA. In this 15-year period, several bacteria emerged that were not previously recognized as important foodborne pathogens, including *L. monocytogenes* and *Y. enterocolitica* [Bean & Griffin 1990]. Whilst these pathogens were increasingly involved in outbreaks of foodborne intoxications, refrigerated foods have, in many cases, been incriminated as the vehicles for these bacteria [Rocourt 1994; Bottone 1997; Kraft 1992]. Just like many mesophilic pathogens, these psychrotrophs appeared to be associated primarily with foods of animal origin. Extended refrigerated storage of raw and underprocessed foods of animal origin, as well as cross-contamination of other foods, have all played a role in outbreaks of both yersiniosis and listeriosis.

Cold-tolerant mesophiles

In addition to the expansion of these natural psychrotrophic species, recently some more or less cold-tolerant strains have also popped up in some typical mesophilic organisms, such as *Bacillus cereus*, *Escherichia coli* and *Salmonella* spp. [Palumbo 1986; d'Aoust 1991]. Such strains,

although not involved in human disease so far, may pose new problems for maintaining food safety.

2.4.3 Cold-tolerant Pathogens in Blood Products

Refrigeration has not been restricted to foods; amongst its numerous other applications, preservation of blood-products for transfusion is to be mentioned in view of it posing a risk to human health. Bacterial contamination of blood for transfusion is uncommon, but when such an event occurs, morbidity and mortality per individual may be significant [Mhyre 1985]. Among the micro-organisms involved in transfusion-associated bacteremia, *Y. enterocolitica* and *Pseudomonas fluorescens* have emerged to play an important role, undoubtedly favoured by their ability to grow at the common blood storage temperature of 4°C [Jacobs *et al.*, 1981; Tipple *et al.* 1990].

2.5 FUTURE PERSPECTIVES

The present importance of refrigeration for the preservation of perishable foods can hardly be overestimated: the food supply to all our densely populated areas is nowadays, to a large extent, dependent upon chilling and freezing. This dependence is expected to be even further enhanced by ongoing urbanization, as the distance between production and consumption grows larger and larger [Persson 1987]. At the same time, foodborne disease is increasingly being recognized as a major cause of morbidity, and reduced economic productivity, in both industrialized and developing countries [Todd 1989; Archer 1985, Bean & Griffin 1990; Knöchel & Gould 1995] and cold-tolerant micro-organisms are jointly responsible for this.

Finally, cold-tolerant pathogens also pose a problem in modern medical technology, especially with regard to the safety of blood products.

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3

Bacteria in the Cold

**adaptation & acclimation
to low temperatures**

ABSTRACT

Temperature has a profound influence on the metabolism and composition of most bacteria. Based on their upper and lower temperature limits of growth, four main groups can be distinguished, i.e. thermophiles, mesophiles, psychrotrophs and psychrophiles. In response to a sudden decrease in growth temperature, many bacteria modify the fatty acid composition of their structural lipids. Although this modification is not a prerequisite for growth at low ambient temperatures, cold-adapted bacteria tend to have a higher degree of fatty acyl unsaturation in their membranes. In general, bacteria which are able to grow at temperatures near zero, the psychrophiles and psychrotrophs, seem to have developed the genetic ability to synthesize quantitatively or qualitatively more fluid lipids at low temperature than meso- or thermophiles, whose lower temperature limits for growth are around 7°C or 25°C, respectively. However, the relationship between the resulting phenotypic adaptations and the lower temperature limit for growth is still unclear.

The psychrophiles and psychrotrophs differ also from the meso- and thermophiles in their protein composition and -synthesis at reduced temperatures. Most bacteria, being either psychro-, meso- or thermophiles, produce a set of specific proteins, called 'cold-shock' proteins after an abrupt temperature down shift. According to the Cold-Shock Ribosomal Adaptation model, these cold-shock proteins enable them to adjust their mRNA translation machinery, especially their ribosomes, to reduced temperatures. The level of adjustment, however, seems to be species-specific. Meso- or thermophiles apparently fail to modify their ribosomes adequately to temperatures below 7°C or 25°C, respectively. Cold-adapted bacteria, on the other hand, are able to maintain efficient initiation of translation, even at temperatures near zero. During growth at such low temperatures, psychrophiles and psychrotrophs also synthesize another set of specific proteins, the so-called 'cold-acclimation' proteins, and these might be responsible for a far-reaching cold-adaptation of the translation machinery. Still, it is unclear to what extent these features contribute to setting the lower temperature limits for growth.

3.1 TEMPERATURE LIMITS FOR GROWTH

3.1.1 Restricted Growth Range

Bacteria as a group can grow over a wide temperature range that seems to be limited only by the availability of liquid water. Generally speaking this is between approximately -10 and +110°C. Individual species, however, show a much more limited growth range: their maximum and minimum temperatures are seldom more than 40 degrees apart (Figure 3.1).

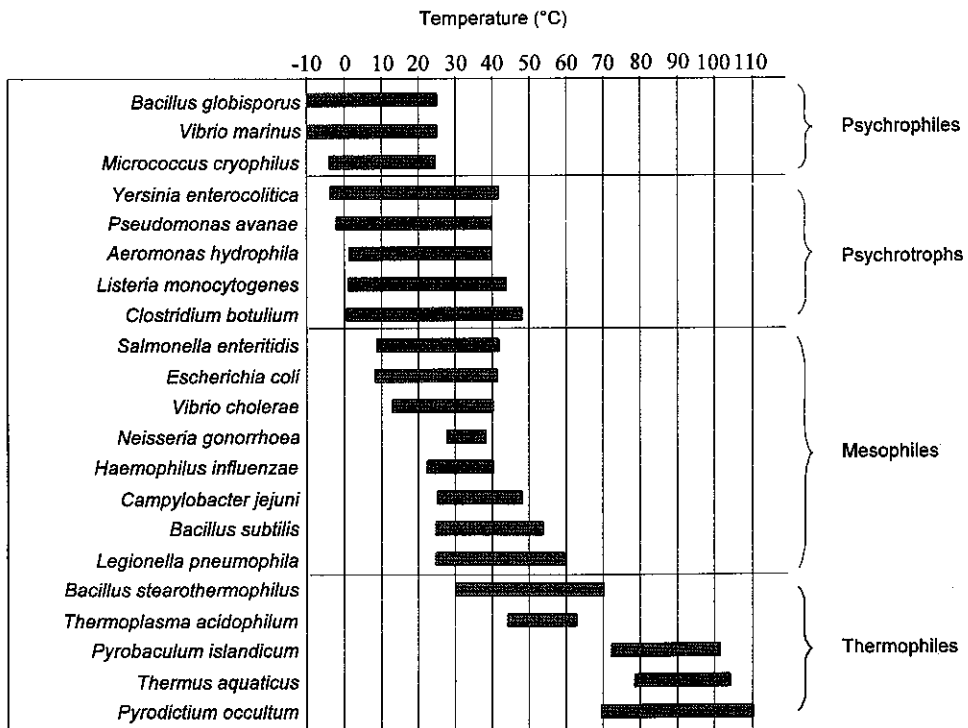


Figure 3.1 Growth temperature range of various bacteria, adapted from [Neidhardt *et al.* 1990]

According to their ability to grow at high, intermediate or low temperatures, micro-organisms have been divided into three broad classes: thermophiles, mesophiles and psychrophiles, respectively. The 'cold-loving' organisms, which can grow at temperatures close to zero, have been further subdivided into obligate and facultative psychrophiles, on the basis of their

optimum and upper growth temperatures [Morita 1975]. The optimum growth temperature of obligate psychrophiles lies below 16°C, whereas facultative psychrophiles, or psychrotrophs, grow best at around 20-25°C. Similarly, psychrotrophs have a higher upper temperature limit (up to 40°C) than psychrophiles (around 20°C).

3.1.2 Few Mutants with Dropped Lower Limits

Numerous studies have been carried out to determine why psychrophiles and psychrotrophs can grow at low temperature, or, from another point of view, why mesophiles and thermophiles cannot. To tackle this problem, there have been many attempts to isolate mutants from the group of mesophiles that have an extended lower temperature range. Such mutants, however, appeared to be extremely difficult to obtain. Despite numerous attempts, real psychrotrophic mutants of *E. coli* have never been isolated; the lowest minimum growth temperature obtained in some 'cold-resistant' mutants was 7.5°C [Kawamoto *et al.* 1989]. A mutant of the cyanobacterium *Anacystis nidulans* has been described, which had acquired enhanced tolerance to a temporary chilling stress but an extended growth range was not reported [Wada *et al.* 1994]. The only successful conversion of a mesophile into a psychrotroph reported so far concerns *Pseudomonas aeruginosa* [Azuma 1962; Olsen & Metcalf 1968].

The relative ease by which these mutants were obtained prompted the authors to suggest that the growth temperature range is prescribed by a limited number of genetic loci. However, this ease may only reflect the particular situation in *P. aeruginosa*: this organism probably requires a small number of mutations to gain psychrophily, since it is almost unique among Pseudomonads in not being itself a psychrotroph. The virtual inability to generate psychrotrophic mutants in other mesophilic species rather suggests that this would require mutations in a great number of genes.

3.1.3 Many Mutants with Raised Lower Limits

Reduced ability to grow near zero

In contrast to the apparent impracticability of a simultaneous 'upgrading' of all the key-genes for psychrotrophy in mesophiles, it is obviously less difficult to switch off one or more of these genes in psychrophiles.

'Cold-sensitive' mutants of psychrophiles, showing a reduced ability to grow at 0-10°C, have been frequently isolated. Such mutants appeared to be affected in various cellular processes. (Table 3.1, upper part). Growth-range-shifted mutants of *Micrococcus cryophilus* for example, which had swapped the ability to grow at 0°C for the ability to grow at elevated temperatures, showed changes in several metabolic pathways, such as oxidation and transamination routes [Tai & Jackson 1969]. On the other hand, no changes in metabolism, nor in ribosomal stability, were observed in certain mutants of *Bacillus psychrophilus*, which showed a similar shift in

growth range [Kim & Larkin 1973]. Some mutations seemed to have disordered membrane functioning, such as in a pure cold-sensitive mutant of *B. psychrophilus* [Murray & Innis 1980]: in this mutant, the ATPase synthesis is cold-inactivated and this might lead to an inability to energize membrane transport systems. In view of this, it is very interesting that various psychrotrophic bacteria of Antarctica, including *Pseudomonas*, *Micrococcus*, *Planococcus*, *Arthrobacter* and *Sphingobacterium* species, show temperature-dependent phosphorylation of membrane proteins and/or lipopolysaccharides [Ray *et al.* 1994a, 1994b]. It was suggested from this observation that these membrane components might either function as sensors of external temperature or as modulators of membrane-permeability and transport activity. Membrane function is probably also affected in cold-sensitive mutants of the cyanobacterium *Synechocystis*, because their altered growth ranges coincide with dramatic changes in membrane lipid composition [Wada & Murata 1989]. More recently, three affected genes were isolated from cold-sensitive mutants of *Listeria monocytogenes*, but their products have not been identified [Zheng & Kathariou 1994, 1995].

Table 3.1 Affected cellular processes in various Cold-Sensitive mutants

AFFECTED CELLULAR PROCESSES	GENES	ORGANISMS	REFERENCES
oxidation and transamination	?	<i>Micrococcus cryophilus</i>	110
ATPase synthesis	?	<i>Bacillus psychrophilus</i>	74
membrane lipid desaturation	<i>desA</i>	<i>Synechocystis spec.</i>	116 - 119
Protein export	<i>secY</i>	<i>Escherichia coli</i>	4
DNA-precursor synthesis	<i>tmk</i>	<i>Escherichiacoli</i>	25
mRNA elongation	<i>nusA, nusB</i>	<i>Escherichia coli</i>	18, 32
Ribosome assembly	?	<i>Salmonella typhimurium</i>	111
Ribosome assembly	<i>rpsE</i>	<i>Escherichia coli</i>	102

'Cold-Sensitive' mesophiles

In addition to cold-sensitive mutants in psychrophilic species, mutants with raised lower temperature limits can also be found among meso- and thermophiles. Such mutants are generally also referred to as 'cold-sensitive' (CS), although their parent strains were never able to grow below 7°C. CS-mutants of *E. coli* and *Salmonella typhimurium*, for example, have lost the ability to grow below 20°C or even 30°C. Like the cold-sensitive mutants of psychrophiles, these CS-mutants also appear to be affected in diverse cellular processes, such as protein export, biosynthesis of DNA precursors, mRNA elongation, or ribosome assembly (Table 3.1, lower part).

3.1.4 Determinants of Minimum Growth Temperature

The coincidence of cold-sensitivity with the occurrence of disturbances in various biosynthesis-pathways suggests that adaptation to lower temperatures requires specific synthesis of macromolecules with particular characteristics. In addition, there are both physical [Russell 1990] and biochemical [Feller & Gerday 1997] reasons to suppose that the lower temperature limit for growth of a micro-organism is given by the sum of the characteristics of its macromolecules¹.

In other words, proteins and lipids are most likely the determinants of the minimum growth temperature. Indeed, numerous studies which were focused on the growth and physiology of micro-organisms have revealed that (i) temperature downshifts induce the production of specific macromolecules and (ii) there are quantitative and qualitative temperature-dependent differences in the cellular lipid- and protein compositions.

3.2 LIPID ADAPTATIONS

When micro-organisms are subjected to low temperatures, a variety of changes in lipid composition may occur, depending on the species involved [McElhanev 1976; Herbert 1986, 1989; Russell 1984a, 1984b, 1990, 1992; Gounot, 1991]. In response to cold, many micro-organisms, including *Y. enterocolitica* [Abbas & Card 1980; Nagamachi *et al.* 1991], accumulate lipids with a

1. **First**, the physics of aqueous solvent systems cannot explain why so many organisms are unable to grow at temperatures much above zero. Clearly, there is a physical restriction on growth at sub-zero temperatures: while between 0°C and -10°C many cells remain unfrozen, cytoplasmic waters begin to freeze when the temperature drops below -10°C. This results in toxic effects that will either prevent the organism from growing or possibly kill it. Thus, the minimum growth temperature of psychrotrophs and psychrophiles (-12°C) is fixed by the physical properties of aqueous solvent systems. The minimum growth temperatures of meso- (8°C) and thermophiles (25°C), however, is not given by such effects and must therefore reside in the chemical and/or structural properties of their cellular macromolecules. **Second**, thermodynamics also fails to explain why psychrophiles but not mesophiles can grow near zero. Certainly, temperature influences growth rates by the rate of enzyme reactions. Following the Arrhenius equation, which describes the exponential relationship between temperature and reaction rate, a drop in temperature of 10 degrees will usually produce a 2 to 3-fold decrease in enzyme rate constant. This means that a temperature shift from 37°C to 0°C will result in a 16 to 80-fold (2⁴ to 3⁴) lowering of enzyme activity. As a consequence, the velocity of all biochemical reactions may fall considerably when the temperature is lowered, but a definite standstill is not to be expected. Nevertheless, mesophilic and thermophilic enzymes usually completely lose their activity at lower temperatures, while psychrophilic proteins maintain their catalytic function. Apparently, cold-adapted bacteria have changed the properties of essential enzymes, whereas mesophiles have not. **Third**, when living organisms are subjected to temperature downshifts, many of them respond by implementing significant changes in their lipid- and protein compositions. This, too, indicates that adaptation to low temperature requires drastic quantitative and qualitative modifications in the macromolecules that are responsible for the cellular structure, organization and metabolism.

lower gel-to-liquid-crystalline transition temperature, thereby keeping membrane fluidity relatively constant [McElhanev 1976; McElhanev 1982; Herbert 1986; Cronan *et al.* 1987]. This phenomenon is called 'homeoviscous adaptation' [Russell 1984a; Herbert 1989]².

3.2.1 Maintaining Membrane Fluidity

Homeoviscous adaptation has its origin in changes in the relative proportions of the various fatty acid classes present. It is brought about most commonly by an increase in the proportion of unsaturated residues and/or a decrease in the average fatty acyl chain length.

Increased fatty acid unsaturation

The major mechanism for regulation of the degree of unsaturation in *E. coli* is via anaerobic *de novo* synthesis of mono-unsaturated fatty acids [Mendoza & Cronan 1983; Cronan & Rock 1987]. Temperature dependent changes are mediated solely by the differential heat-sensitivity and relative activity of two enzymes with almost identical functions, but diverging precursor-affinities in the cyclic elongation pathway. The branching point between the synthesis of saturated and monounsaturated fatty acids is at the C10-phase, but the increase of unsaturation in *E. coli* at reduced temperature is completely brought about at the C16-phase, by an increased elongation of C16:1 (*palmitoleate*) compared to C16:0 (*palmitate*). This elongation step is catalyzed by either β -ketoacyl-ACP synthase I or II, from which the latter enzyme does elongate C16:1 much more effectively than C16:0. In addition, synthase II is more temperature labile than synthase I. Consequently, the activity of the synthase II increases relative to that of the synthase I at reduced temperatures, and the amount of C18:1 (*cis-vaccenate*) will rise compared to its saturated counterpart C18:0 (*stearate*).

Reduced fatty acid chain length

The reduction of the average fatty acyl chain length is, in *E. coli*, also achieved by *de novo*

2. The classical phospholipid bilayer that forms the cytoplasmic and outer membranes of bacteria and other prokaryotes is not a rigid or unassailable barrier, but a fairly loosely packed, fluid and relatively permeable structure, which harbours embedded and traversing intrinsic proteins. When temperature falls, this flexible structure can undergo a reversible liquid-crystalline to gel phase transition, which blocks correct membrane function. However, important characteristics such as the efficiencies of electron transport, ion pumping and nutrient uptake (which have all often been mooted as determinants of psychrophily) depend, either directly or indirectly, on both membrane-lipid fluidity and -protein activity. For this reason, maintaining the liquid-crystalline state - and thus keeping membranes fluid and functional - is essential for microbial growth. Although quite wide variations in membrane fluidity are tolerated to sustain growth, micro-organisms have developed a number of strategies to ward off the imminent danger of membrane solidifying at low ambient temperatures. Membrane fluidity is profoundly affected by the fatty acid composition of the phospholipids: the shorter or less saturated the carbon chain is, the lower the 'melting point' of a fatty acid. Hence, the process of temperature-dependent membrane modification, termed 'homeoviscous adaptation' usually involves changes in the fatty acid moieties of the phospholipids.

synthesis of membrane phospholipids, and it is mediated by a temperature-regulated activity of the membrane-bound elongase enzyme. This enzyme can interconvert C16 and C18 fatty acids, and the conversion from C18:0 to C16:0 is maximal at low temperature.

Branched and cyclic fatty acids

Changes in the proportions or types of branched and cyclopropane fatty acids may also contribute to maintaining membrane fluidity, but are less frequently observed. Cyclopropane fatty acids are synthesized by addition of a methyl group across the cis-double bond of an unsaturated fatty acid acyl chain. Hence, C16:1 is the precursor of C17:0°. In contrast to the synthesis of the straight-chain fatty acids, cyclopropane fatty acids are formed by modification of their precursors in the phospholipids, residing in the inner and outer membranes. In general, the amount of cyclopropane fatty acids rises when batch cultures enter stationary phase. However, at low pH, exponentially growing *Y. enterocolitica* cells were shown to synthesise rather large amounts of cyclic fatty acids, which was thought to increase the chance of survival under these conditions, by toughening the cellular membrane [Bodnaruk & Golden 1996]. The role of cyclopropane fatty acids in thermal adaptation, however, is questioned since their molecular packing properties are very similar to those of the monounsaturated precursors [Cronan & Rock, 1987].

Combinations of fatty acid modifications

None of these different types of fatty acid modifications is unique for any class of micro-organism, either thermo-, meso- or psychrophilic, and all kinds of combinations are seen. These observations have led to the conclusion that a large variety of fatty acid compositions can apparently give the same thermal properties [Russell 1990].

3.2.2 High Unsaturation in Psychrotrophs and Psychrophiles

Despite the above conclusion, there is much evidence to show that the level of fatty acid unsaturation contributes to the lower temperature limit at which a bacterium can sustain growth. The mesophiles *E. coli* and *Arthrobacter globiformis*, for example, require a temperature-dependent minimum proportion of unsaturated fatty acids to sustain growth at reduced temperatures [Cronan & Gelman 1973; Canillac 1982]. However, the factual membrane lipid unsaturation levels are generally considerably in excess of the required minima [Herbert 1989; Russell 1990]. This might explain some rather confusing early observations that temporary starved, cold-shocked cells of *E. coli* resume growth at 10°C, while still having a fatty acid profile typical for cells grown at 37°C [Shaw & Ingraham 1965]. In fact, the fatty acid profiles of psychrotrophs and psychrophiles are often characterized by high degrees of unsaturation over their whole growth temperature range: e.g. >70% in certain *Pseudomonas* and *Vibrio* species, and even >95% in *Micrococcus cryophilus* [Russell 1984b, 1990; Herbert 1986]. The fatty acid profiles in these organisms are almost invariable with temperature, or only show a further

decrease in the, still low, average chain length. It has therefore been suggested that such high unsaturation levels provide a sufficiently fluid membrane throughout the whole growth temperature range, and chain length changes only represent a redundant control process or a 'fine-tuning' mechanism to regulate membrane-bound enzyme activity [Russell 1984b].

3.2.3 Specific Types of Unsaturation

In certain cyanobacteria, temperature affects not only the level but also the type of unsaturation: in *Synechocystis* species, temperature downshifts from 38°C to 22°C induce accumulation of tri- and tetraunsaturated fatty acids at the expense of mono- and diunsaturated residues [Wada & Murata 1990]. Recently, it was shown that this shift in fatty acid profile is preceded by an increase in the mRNA levels of *desA*, *desB* and *desC* genes, which encode desaturases that introduce double bonds at particular positions in C18 fatty acids [Sakamoto *et al.* 1997]. Conversely, genetic manipulation of the extent and type of desaturation in *Synechocystis*, by means of mutations in one or more of the *des* genes, leads to aberrant growth patterns and shows that growth at low temperature requires either a certain level or a certain type of poly-unsaturation, or both [Wada & Murata 1989; Wada *et al.* 1992; Tasaka *et al.* 1996]. In addition, the tolerance of the photosynthetic machinery of *Synechocystis* to chilling stress was shown to depend on adaptational unsaturation of its membrane lipids [Gombos *et al.* 1994], and introduction of the cloned *desA* gene in the *desA*⁻, chilling-sensitive cyanobacterium *Anacystis nidulans* increases the tolerance of the recipient to low temperature [Wada *et al.* 1990, 1994].

3.3 PROTEIN ADAPTATIONS

Temperature influences the protein composition of micro-organisms in three different ways: (i) proteins may undergo conformational changes, (ii) the rate of protein synthesis is down-regulated, or (iii) the protein synthesis is affected in a qualitative manner.

3.3.1 Changes in Protein Structure

At low temperatures, the rate of enzymatic reactions and the affinity of uptake- and transport systems decreases, while the requirement for organic substrates increases [Grauman & Marahiel 1996]. Thus, the structure of all the proteins in a cold-adapted micro-organism must be adjusted, such that conformational flexibility and catalytic efficiency are maintained for substrate conversions at low temperature. Obviously, this information must be fixed in the gene base-sequence of psychrophiles and psychrotrophs [Russell 1992]. A survey of the adaptive traits of various enzymes in psychrophilic organisms reveals that conformational flexibility, as well as catalytic efficiency, is certainly improved in comparison to their mesophilic

counterparts. This is mainly accomplished via the elimination of salt bridges and hydrophobic clusters, by a diminished interaction among aromatic side chains, or by an increase in the number of interactions between the enzyme surface and the solvent [Jaenicke 1990; Davail 1994; Marshall 1997]. At the molecular level, the determinants of the expected flexibility range from a single mutation in a functional site (but not the active one), to a large number of altered weak interactions, distributed in the whole structure [Feller & Gerday 1997].

3.3.2 Quantitative Downregulation of Protein Synthesis

When mesophiles like *E. coli* and *Pseudomonas aeruginosa* are subjected to temperatures that are below their minimal growth temperatures ($\pm 8^{\circ}\text{C}$), their protein synthesis slows down progressively and eventually ceases [Das & Goldstein 1968]. This cessation of protein synthesis is accompanied by an accumulation of ribosomal subunits and 70S ribosomal particles, which are no longer capable of attaching to mRNA [Das & Goldstein 1968; Broeze *et al.* 1978]. Thus, these organisms are unable to grow at low temperatures due to a cold-induced block in initiation of translation. Such a block does not occur in the psychrotroph *Pseudomonas fluorescens* [Broeze *et al.* 1978] nor in a psychrophilic *Vibrio* species [Oshima *et al.* 1987], indicating that the translational capacity of their ribosomes is not affected by cold. This might be due to some positive conformational change of the ribosomes, or because a negative change fails to occur. Interestingly, a protein factor washed from a psychrotrophic *Pseudomonas putida* strain reactivated the translational capacity at 0°C of *E. coli* ribosomes [Szer 1970], suggesting a regulatory role for some initiation factor. Other studies revealed that cold-sensitivity does not reside in inactivation of initiation factors but is due to some feature of the ribosomal 30S subunit itself [Oshima *et al.* 1987]. Recently it was shown that the cold-sensitive phenotype of a certain *E. coli* mutant is caused by the absence of a protein that specifically interacts with 16S rRNA during 30S maturation [Dammel & Noller 1995].

The rate of protein turnover might also play a role in psychrotrophy, since it was observed that protein breakdown is much greater in the psychrotrophic bacterium *Arthrobacter* S155 than in the mesophil *E. coli* [Potier *et al.* 1985]. Maybe, rapid protein turnover is an energy-saving mechanism to provide amino acids during the synthesis of new proteins, which are required for adaptation.

3.3.3 Qualitative Upregulation of Protein Synthesis

With respect to the intracellular protein composition, two types of cold-induced qualitative changes can be distinguished, i.e. 'cold-acclimation', which is observed during acclimatized growth at low temperature, and a 'cold-shock' response, which occurs after an abrupt temperature downshift.

Cold-acclimation-proteins: CAPs

Although the steady-state levels of most cellular proteins do not change greatly at different growth temperatures, some are synthesized at a greater level when a micro-organism is subjected to temperatures near the edge of its normal growth range. In *E. coli*, for example, three proteins are markedly increased during growth at 13.5°C, as compared with 37°C [Herendeen *et al.* 1979]. Similarly, many psychrophiles and psychrotrophs contain enhanced levels of certain proteins during continuous growth at low temperatures ($\leq 7^\circ\text{C}$). This phenomenon is generally referred to as 'cold-acclimation', and the proteins of this specific class are called 'cold-acclimation' proteins or CAPs. CAPs have been detected in bacteria that belong to various genera, including *Aquaspirillum arcticum* [Roberts & Inniss 1992]; *Arthrobacter globiformis* [Potier *et al.* 1990] and *A. protophormiae* [Berger *et al.* 1996]; *Bacillus cereus* [Mayr *et al.* 1996], *B. psychrophilus* [Whyte & Inniss 1992] and *B. subtilis* [Graumann *et al.* 1996]; *Lactococcus lactis* [Panoff *et al.* 1994]; *Listeria monocytogenes* [Bayles *et al.* 1996]; *Pseudomonas fluorescens* [Ray *et al.* 1994c; Colucci & Inniss 1996], *P. fragi* [Hébraud *et al.* 1994] and *P. putida* [Gumley & Inniss 1996]; *Rhizobium* species [Cloutier *et al.* 1992]; and *Vibrio* species. [Araki 1991]. Recently, it was shown that CAPs are also produced (at 8°C) by *Enterococcus faecalis*, a bacterium that is generally described as a mesophil, although it is commonly present in cold environments [Panoff *et al.* 1997].

Cold-shock-proteins: CSPs

When bacteria are subjected to abrupt temperature down-shifts that do not exceed their normal growth range, their protein synthesis does not come to a halt, but is affected in a more subtle way: the production of house-keeping proteins is temporarily reduced in favour of a transient induction of a specific subset of proteins called 'cold-shock proteins' or CSPs. This specific pattern of gene-expression, which is generally referred to as the 'cold-shock-response', was first observed in the mesophile *E. coli* [Jones *et al.* 1987]. To date, the induction of cold-shock-proteins is known to occur in many other micro-organisms [Jones & Inouye 1994] and the phenomenon has been monitored in psychro-, meso-, and/or thermophilic species of the genera *Aquaspirillum* [Roberts & Inniss 1992], *Arthrobacter* [Ray *et al.* 1994c; Berger *et al.* 1996], *Bacillus* [Whyte & Inniss 1992; Willimsky *et al.* 1992; Lottering & Streips 1995; Graumann *et al.* 1996], *Enterococcus* [Panoff *et al.* 1997], *Lactobacillus* [Mayo *et al.* 1997], *Lactococcus* [Panoff *et al.* 1994], *Listeria* [Phan-Thanh & Gormon 1995; Bayles *et al.* 1996], *Pseudomonas* [Ray *et al.* 1994c; Colucci & Inniss 1996; Gumley & Inniss 1996], *Rhizobium* [Cloutier *et al.* 1992], *Salmonella* [Jeffreys *et al.* 1998] and *Vibrio* [Araki 1991]. Very recently, a cold shock response has also been reported for *Yersina enterocolitica* [Dickinson *et al.* 1998] and *Y. pseudotuberculosis* [Tafelshtein *et al.* 1998].

Most of the CSPs produced by *E. coli*, as well as the cellular processes in which they are involved, have now been identified (Table 3.2).

Chapter 3

Table 3.2 The Cold Shock response in *E. coli* :
Cold shock proteins, their corresponding genes, and the (supposed) affected cellular processes

COLD SHOCK PROTEINS	GENES	AFFECTED CELLULAR PROCESSES	REF.
CspA (or CS7.4)	<i>cspA</i>	Transcription initiation	56
NusA	<i>nusA</i>	Transcription termination	56
Initiation factor 2 α , β	<i>infB</i>	Translation initiation	54
Ribosomal binding factor A (P15)	<i>rbfA</i>	Ribosomal maturation,	54
CsdA (or DeaD)	<i>csdA</i>	mRNA unwinding,	59
Polynucleotide phosphorylase	<i>pnp</i>	mRNA degradation	56
Pyruvate dihydrogenase	<i>aceE,F</i>	Pyruvate-decarboxylation	56
RecA	<i>recA</i>	DNA repair	56
H-NS	<i>hns</i>	DNA structuring	64
DNA gyrase α -subunit	<i>gyrA</i>	DNA structuring	58
Trigger factor	?	Ribosomal modification & Polypeptide folding	47

The *E. coli* cold-shock protein with the highest induction level (200-fold increase following a shift from 37°C to 10°C) is CspA (or CS7.4). The induction of most other *E. coli* CSPs is thought to be under transcriptional control of CspA, and the transcription enhancement of the cold-shock genes is most likely mediated by a specific recognition site in, or nearby, their promoters [LaTeana 1991; Jones *et al.* 1992b; Qoronfleh *et al.* 1992; Jones & Inouye 1994; Brandi *et al.* 1994]. This recognition site comprises the 5-base motif ATTGG, or its inverted repeat CCAAT, and is identical to the so-called 'Y-box', the recognition site for eukaryotic homologs of CspA [Wolffe 1994; Jones *et al.* 1992b]. These motifs are now generally referred to as 'cold-shock motifs'. In addition, CspA shares the binding capacity to the cold-shock motif with a whole family of homologs in *E. coli*, three of which, CspB, G and I, are also cold-inducible [Lee *et al.* 1994; Nakashima *et al.* 1996; Wang *et al.* 1999].

Overlap CAPs and CSPs

Comparative studies have shown that there is considerable, but not complete, overlap between the proteins that are specific for cold-acclimation and the cold-shock-response. This overlap is seen in several cold-adapted organisms, including *Aquaspirillum arcticum* [Roberts & Inniss 1992]; *Bacillus psychrophilus* [Whyte & Inniss 1992]; *Pseudomonas fluorescens* [Ray *et al.* 1994c] and *P. putida* [Gumley & Inniss 1996]; *Enterococcus faecalis* [Panoff *et al.* 1997] and *Vibrio spec.* [Araki 1991]. Interestingly, CAPs which are structurally highly homologous to the major *E. coli* cold-shock-protein CspA have been found in various, phylogenetically unrelated microorganisms (Table 3.3).

Table 3.3 CAPs and CSPs which are homologs of the major *E. coli* cold shock protein CspA, in various psychrotrophic (*) or mesophilic bacteria.

ORGANISMS	COLD ADAPTATION PROTEINS	COLD SHOCK PROTEINS	REFERENCES
<i>Arthrobacter globiformis</i> *	CspA-like	CapA	7
<i>Bacillus cereus</i> *	CspA-like	---	69
<i>Escherichia coli</i>	---	CspB, CspG, CspI	65, 76, 121
<i>Lactococcus lactis</i> *	---	CspB	15, 63
<i>Lactobacillus plantarum</i>	---	CspL, CspP	68
<i>Listeria monocytogenes</i> *	CspA-like	---	6
<i>Bacillus subtilis</i>	---	CspB, CspC, CspD	38, 39, 123
<i>Pseudomonas fluorescens</i> *	CspA-like	---	93
<i>Pseudomonas fragi</i> *	---	C7.0, C8.0	43
<i>Salmonella enteritidis</i>	---	CspA	49
<i>Yersinia enterocolitica</i> *	---	CspB	27

* --- = not investigated, or not detected

Extracellular anti-freeze proteins

Some bacteria are reported to produce extracellular anti-freeze proteins. Such proteins are synthesized and secreted by numerous species of fish, insects and plants, especially those from cold habitats, to protect their body-tissues from freezing/thawing damage. This protection is accomplished by the control of extracellular ice-formation in their body-fluids, through a process called thermal hysteresis. With bacteria, the thermal hysteresis activity of anti-freeze proteins might likewise function to regulate the growth of ice-crystals outside the bacterium, thereby protecting it from freezing-damage. Thermal hysteresis activity has been observed in extracts from the common soil bacterium *Rhodococcus erythropolis* and the psychrotroph *Micrococcus cryophilus* [Duman & Olsen 1993], and an anti-freeze protein has been isolated from the rhizobacterium *Pseudomonas putida* [Sun *et al.* 1995]. However, the thermal hysteresis activity was not observed until after 3 to 4 weeks of cold growth. This suggests that the anti-freeze proteins are not linked with the processes which enable these bacteria to function at low temperatures.

3.4 REGULATION OF COLD-ADAPTATION

3.4.1 Cold Shock Proteins: Effectors of Cold-Adaptation?

Several lines of evidence suggest that the cold-shock response is essential for bacterial

adaptation to low temperature. **First**, the lag period of cell growth upon cold shock corresponds to the period of transient expression of the cold-shock genes [Jones *et al.* 1992a]. **Second**, there is a reciprocal relationship between the production of cold-shock proteins and the production of other cellular proteins [Jiang *et al.* 1996a]. **Third**, the absence of certain cold-shock proteins frequently leads to reduced viability, especially at low temperatures. *E. coli* mutants with a truncated *hns* gene, for example (which are devoid of a functional DNA-binding protein H-NS), proliferate more slowly than the wild type at 12°C, but not at 37°C [Dersch *et al.* 1994]. Similarly, *rbfA* knock out mutants, which lack the ribosomal binding factor RbfA, can't grow at 26°C and below [Dammel & Noller 1995]. Likewise, the intracellular amounts of the initiation factors IF2 α and IF2 β , encoded by *infB*, seem to be crucial at reduced temperatures, since *E. coli* mutants lacking one of these forms can't grow at 30°C and below [Sacerdot *et al.* 1992]. In addition, a minimum of one *csp* gene (B, C or D) is essential for viability of *B. subtilis*, although this effect seems not to be restricted to low temperatures [Graumann *et al.* 1997]. **Fourth**, over-expression of cold-shock genes also has profound effects on viability: plasmid-mediated over-production of RbfA results in faster resumption of growth after a temperature downshift [Jones & Inouye 1996]. Overproduction of truncated *cspA* mRNAs (which retain translational ability), on the other hand, completely blocks cell growth at low temperatures [Jiang *et al.* 1996b].

3.4.2 Ribosomes: Sensors for Cold-Adaptation?

On the basis of various observations with respect to ribosomal assembly, functioning and maturation [Das 1968; Nashimoto & Nomura 1970; Broeze *et al.* 1978; Har-El *et al.* 1979], a sensor function was postulated for the ribosome in various bacterial stress-responses, including the heat- and cold-shock responses [VanBogelen & Neidhardt 1990]. This idea was supported by more recent studies, in which was shown that (i) several cold-sensitive mutants of *E. coli* are defective in proper assemblage of ribosomes [Yano & Yura 1989]; (ii) various cold-shock proteins, such as RbfA, CsdA and IF2, have functions associated with the ribosome [Dammel & Noller 1995; Jones *et al.* 1996]; and (iii) antibiotics which target the prokaryotic ribosome, such as chloramphenicol, tetracycline and erythromycin can mimic temperature shifts, including the corresponding induction of heat- or cold-shock proteins [Jiang *et al.* 1993; VanBogelen *et al.* 1990]. Moreover, various 'cold'-sensitive mutants of *E. coli* have been described that were affected in either transcription termination, translation initiation, or polypeptide elongation at 20°C or below [Nashimoto *et al.* 1985; Shiba *et al.* 1986a; Shiba *et al.* 1986b; Schauer *et al.* 1987]. Finally, the mRNA of *cspA* is very unstable at 37°C, but is transiently stabilized at 15°C [Tanabe *et al.* 1992; Goldenberg *et al.* 1996]. Thus, several pieces of evidence suggest that inhibition of translation is setting the minimal temperature of bacterial growth, and the adaptive role of the cold-shock response is in the adequate modification of the translation machinery.

3.4.3 The 'Cold Shock Ribosomal Adaptation' model

To explain the induction and function of the cold-shock -response, the 'cold-Shock Ribosomal Adaptation model' was proposed [Jones & Inouye 1996] (Figure 3.2).

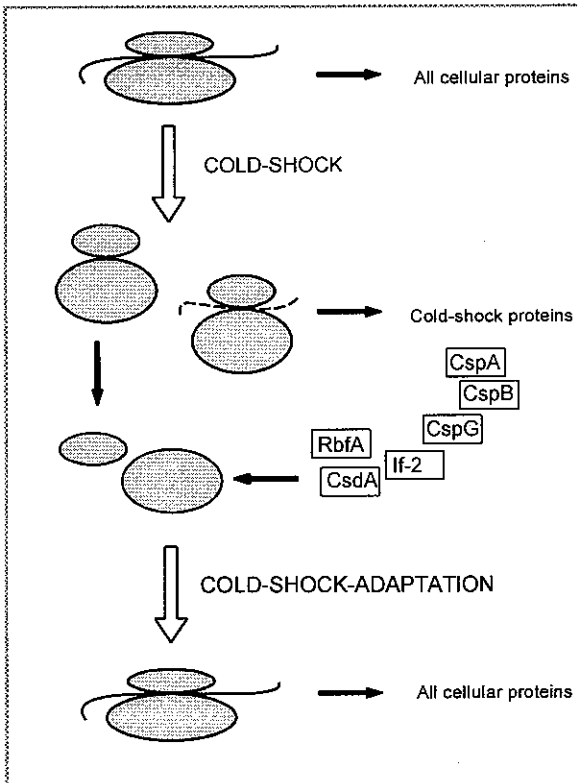


Figure 3.2 The Cold Shock Ribosomal Adaptation model, adapted from [Jiang *et al.* 1996b]

In this model, ribosomes are translatable at high and moderate temperatures, but become defective in initiation of translation of most mRNAs after a temperature downshift. The mRNA of *CspA* and other cold-shock genes, by contrast, can still be efficiently translated. Thus, the cold-induced change in translational efficiency of the ribosomes triggers the synthesis of *CspA*, which snowballs into enhanced transcription and synthesis of Initiation Factor 2, RbfA, and CsdA. These CSPs associate with 70S monosomes and with 30S or 50S ribosomal subunits. Through this interaction, the ribosomes are converted to a renewed translatable, cold-resistant state.

By this, adaptation to the lower temperature has been accomplished: the synthesis of house-keeping proteins will resume, and the cell can start growing again.

3.4.4 Onset and Shutdown of the Cold Shock Response

The likelihood of the above scenario is supported by several new observations with respect to mechanisms of onset and shutdown of the cold-shock response. It was shown, for example, that cold-shocked ribosomes translate the *cspA* mRNA much more efficiently compared to ribosomes from 37°C-grown cells [Brandi *et al.* 1996]. Furthermore, the cold-shock induction of

CspA appeared to be promoter-independent, i.e. the *cspA* gene is efficiently transcribed even at 37°C, but the translation of the *cspA* mRNA is blocked because of its extreme instability at 37°C [Fang *et al.* 1997]. Moreover, a possible explanation was found for the temperature-independent maintenance of the ribosome's translation efficiency with respect to the *cspA* mRNA's: the cold-shock induction of CspA required the presence of a certain 14-base stretch in the 5'-terminus of the coding region [Mitta *et al.* 1997]. This stretch, which is called the Downstream Box, is complementary to a 16S rRNA region, and was previously shown to act as an efficient translation initiation signal in *E. coli* [Sprengart *et al.* 1996]. It now appeared to be highly conserved in the m-RNA of all cold shock proteins. Comparably, another conserved sequence is supposed to play a role in the ending of the cold-shock response. This concerns an 11-base motif in the 5' untranslated region (5'-UTR) of the many CSP's mRNA's [Jiang *et al.* 1996a]. This motif is designated the 'cold box', and it may act as a repressor binding site [Jiang *et al.* 1996b; Yamanaka *et al.* 1998; Fang *et al.* 1998].

3.4.5 Cold Shock Proteins: mRNA-chaperones?

In addition to the major problems that result from a temperature fall, i.e. the reduction of membrane fluidity and the impaired protein synthesis, cold-shocked cells are also confronted with an increase in the stability of secondary structures in DNA and mRNA [Thieringer *et al.* 1998]. Stable secondary structures affect the efficiencies of transcription, translation and DNA-replication. CSPs are, for several reasons, now thought to play a role in counteracting these effects. First, CSPs prevent formation of secondary structures within the 5'-end of mRNA [Graumann *et al.* 1997]; second, CsdA was shown to be exclusively associated with ribosomes and to exhibit dsRNA unwinding activity [Jones *et al.* 1996]; and third, CspA was shown to bind cooperatively to ssRNA and ssDNA, thus protecting it from denaturation [Jiang *et al.* 1997]. Furthermore, PNPase, which is one of the two 3'-5' exoribonucleases and, at the same time, one of the minor cold shock proteins in *E. coli*, can degrade secondary-structured mRNAs more efficiently than its counterpart RNaseII [Guarneros & Portier 1990]. Moreover, PNPase was found to act in concert with several other enzymes, including the endonuclease RNaseE, which is involved in the general degradation of the bulk of cellular mRNAs, and the RNA-helicase RhlB [Carpousis *et al.* 1994; Braun *et al.* 1996; Pye *et al.* 1996]. This multi-enzyme complex, which was designated 'degradosome', is thought to co-ordinate two processes, i.e. the decay of intermediates that would encode non-functional polypeptides on the one hand, and the efficient recycling of ribonucleotides, on the other [Pye *et al.* 1994]. Recently, another cold-shock protein was detected, called Trigger Factor, that appeared to be associated with ribosomes and nascent polypeptides [Hesterkamp *et al.* 1997]. This protein is also thought to be a molecular chaperone, probably engaged in proper folding at low temperature [Kandror & Goldberg 1997].

3.4.6 Insufficient Cold Shock Response in Mesophiles?

The striking omnipresence of CspA-like proteins in cold-adapted micro-organisms has led to the idea that proteins of this family might play a role in protecting cells from damage due to cold [Goldstein *et al.* 1990]. In line with this, it has been speculated that mesophilic bacteria fail to restore harmonious growth at low temperatures because their cold-shock response is probably only a part of the total response of psychrotrophs and psychrophiles [Berger *et al.* 1996]. This hypothesis is supported by the results of comparative studies addressing the CSP-profiles of wild-type and mutant strains of *Bacillus psychrophilus*, since two CSPs of the parental strain are not induced in a cold-sensitive mutant [Whyte & Inniss 1992]. On the other hand, studies on the CSP-profile of *Listeria monocytogenes* showed no obvious differences between the wild type and a cold-sensitive mutant [Bayles *et al.* 1996]. Introduction of CSP- or CAP-genes from psychrotrophs into mesophiles might shed light on the physiological role of the cold-shock-response and the cold-acclimation proteins, but such experiments have not been described so far.

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4

Detection & Identification

this chapter is based on the following publication:

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**Digoxigenin-labelled *inv*- and *ail*-probes for the detection
and identification of pathogenic *Yersinia enterocolitica*
in clinical specimens and naturally contaminated pig samples**
R.L.J. Goverde, J.G. Kusters, and J.H.J. Huis in 't Veld

ABSTRACT

A non-radioactive colony hybridization method has been developed for rapid detection of *Yersinia enterocolitica* in primary isolates, and for differentiation between pathogenic and non-pathogenic strains. The analysis is based on the previous observations [Miller et al. 1989] that the *inv*-locus is present in all *Yersinia* species, while the *ail*-gene is only found in pathogenic *Yersinia*. A panel of 132 *Y. enterocolitica* strains was tested for hybridization with digoxigenin-labelled *ail*-probes, and tested for in vitro invasiveness in a tissue culture invasion assay (TCI). The results of both the hybridization and TCI-test were in good agreement with pathogenicity phenotypes as indicated by serotyping. All 39 strains that were positive in the TCI-test were also positive by hybridization with *ail*, whereas 91 out of 93 strains that were negative in the TCI-test were also negative in hybridization with *ail*. Two strains appeared to hybridize with *ail* although they were negative in the TCI-test. The practicability of the method was investigated by testing 86 primary isolates of human, animal, or slaughterhouse origin for hybridization with *inv*- and/or *ail*-probes and comparison of the results with those of conventional methods to detect and identify *Y. enterocolitica*. *Yersinia* species and pathogenic *Yersinia* were detected in 19 and 16 samples, respectively, by cultivation and bio/serotyping. In hybridization with *ail*-probes, positive signals were obtained with 15 out of 16 samples in which pathogenic *Yersinia* had been detected (one sample was not tested). Hybridization with *inv*-probes was tested in four of the 19 samples from which *Yersinia* species had been isolated, and these also produced positive hybridization signals. On the other hand, *Yersinia* species could not be isolated from 67 samples, and 60 of these were negative in hybridizations with both *ail* and *inv*-probes. Hybridization results that were distinct from the results of cultivation were found only with slaughterhouse swab-samples, i.e. two out of 51 cultivation-negative samples produced strong positive signals with *ail* and/or *inv*, while five samples produced weak signals with one or both of the probes.

These results indicate that the described method can be used for (i) the identification of pathogenic *Y. enterocolitica* isolates and (ii) the detection of *Yersinia* species in primary isolates of naturally contaminated samples.

4.1 INTRODUCTION

'Yersiniosis' is a, mainly food-borne, gastro-intestinal human disease [Lee 1977; Black *et al.* 1978; Tacket *et al.* 1984; Tauxe *et al.* 1987] which is often accompanied by other, wide-ranging, clinical manifestations [Bottone 1977; Stern & Pierson 1979; Bos *et al.* 1985]. It is caused by pathogenic strains of *Yersinia enterocolitica*, which can be distinguished from non-pathogenic strains by *in vivo* virulence tests in animals, or on the basis of their serotype and/or biotype [Bottone 1977; Wauters 1981; Cornelis *et al.* 1987; Wauters *et al.* 1987]. As animal tests are less desirable and sero- and biotyping is time-consuming and not always reliable [Zink *et al.* 1982; Cornelis *et al.* 1987; Miller *et al.* 1989], alternative methods to distinguish between pathogenic and non-pathogenic strains have been sought.

Research on the genetic basis of the phenotypic differences between *Y. enterocolitica* serotypes has resulted in the discovery of a virulence-associated plasmid [Lee *et al.* 1977; Gemski *et al.* 1980] and the presence or absence of this plasmid has been used to discriminate between virulent and non-virulent strains [Bölin *et al.* 1982; Hill *et al.* 1983; Jagow & Hill 1986; Milliotis *et al.* 1989; Kapperud *et al.* 1990; Nesbakken *et al.* 1991]. However, methods based on the detection of the virulence plasmid may lead to false negative results, because the plasmid is easily lost during repeated subculturing of the bacteria [Zink *et al.* 1980; Portnoy *et al.* 1981; Portnoy & Falkow 1981]. More recently, plasmid independent properties were shown to be involved in *Y. enterocolitica* pathogenicity [Heesemann *et al.* 1984; Isberg & Falkow 1985; Isberg *et al.* 1987; Isberg 1989], especially adhesion and invasion features encoded by a chromosomal gene called *ail* (adhesion-invasion-locus) [Miller & Falkow 1988; Miller *et al.* 1990]. Hybridization with radioactive *ail*-probes and invasion into HEp-2 cells, as determined in an *in vitro* tissue culture invasion (TCI) assay, was shown to be restricted to strains of serotypes associated with disease [Miller *et al.* 1989]. Whereas *ail* was thus found uniquely in pathogenic strains of *Y. enterocolitica*, a second gene involved in invasion, designated *inv*, appeared to be specific for the whole genus *Yersinia* [Miller *et al.* 1989; Robins-Browne *et al.* 1989]. It has been suggested that *inv*-genes present in non-pathogenic strains were most likely not functioning [Pierson & Falkow 1990]. Based on these observations, *inv*-probes can be used to identify *Yersinia* species, and *in vitro* invasion (a TCI⁺-phenotype) or the presence of *ail* can both be used to classify a particular *Y. enterocolitica* strain as pathogenic.

In this paper, we describe the development of a method based on digoxigenin (DIG) labelled *ail*- and *inv*-probes, which can be used to identify pathogenic and non-pathogenic *Yersinia* isolates. Since non-radioactive probes are used, the method is fit to detect virulent and non-virulent *Y. enterocolitica*, as a routine laboratory analysis, in primary cultures of environmental, human or animal origin. The sensitivity of DIG-labelled *ail*-probes was investigated by hybridizations using various types of DNA-blot. The specificity of the *ail*-probe was tested by hybridizations of culture dot-blot and colony blot from *Y. enterocolitica*

strains of 17 different serotypes. TCI-phenotypes of these strains were used to correlate hybridization results with potential for pathogenicity. The specificity of two *inv*-derived probes was tested on colony blots of a panel of bacterial species. Finally, *ail*- and *inv*-derived probes were used to detect, respectively, pathogenic *Y. enterocolitica* or *Yersinia* species in naturally contaminated samples, by means of colony blot hybridizations of primary cultures.

4.2 MATERIALS & METHODS

4.2.1 Bacterial Strains, Media, Growth Conditions

Yersinia enterocolitica, *Y. intermedia*, *Y. frederiksenii* and *Y. pseudotuberculosis* were sero- and biotyped collection-strains, isolated from human and non-human sources, from the National Institute of Public Health and the Environment (RIVM), Bilthoven, The Netherlands. The strains were maintained at 4°C on nutrient agar slopes. For DNA-isolations, TCI-assays or blotting procedures, cultures were grown overnight at 30°C in nutrient broth or on Plate Count Agar (PCA, Oxoid), Tryptic Soy Broth (TSB, Oxoid) or Salmonella-Shigella-Deoxycholate-Calcium (SSDC, Oxoid) agar plates. *Escherichia coli* DH5 α (BRL, Maryland, USA) competent cells and transformants were stored at -70°C in nutrient broth containing 25%(v/v) glycerol. For plasmid isolation, strains were grown at 37°C in nutrient broth supplemented with ampicillin (200 μ g/ml). Type strains used to determine the specificity of the *inv*-probes were: *Listeria monocytogenes*, serotypes 1/2A (NCTC cat.no.7973) and 4B (NCTC cat.no.10527); *Escherichia coli* O:128 [Orskov *et al.* 1977]; *Salmonella typhimurium*, phage types 20 and 150 [Guinée *et al.* 1974]; and *Salmonella enteritidis*, phage types 1 and 2 (RIVM no.88-8859 and no.88-8993).

4.2.2 Plasmids & Probes

Standard DNA-techniques were used for DNA-isolations, restriction enzyme digestions, ligations, and plasmid transformations [Maniatis *et al.* 1982]. The restriction enzymes were obtained from Boehringer Mannheim (Germany). Plasmids pVM103 and pVM101, containing *Yersinia*-fragments with the *ail*- and *inv*-sequences, were kindly donated by Dr. V. Miller (University of California, Los Angeles, USA). Plasmid pVM103 was used to construct two plasmids which contained smaller *ail*-bearing *Yersinia* fragments, i.e. pRG101 and pRG102 (Figure 4.1).

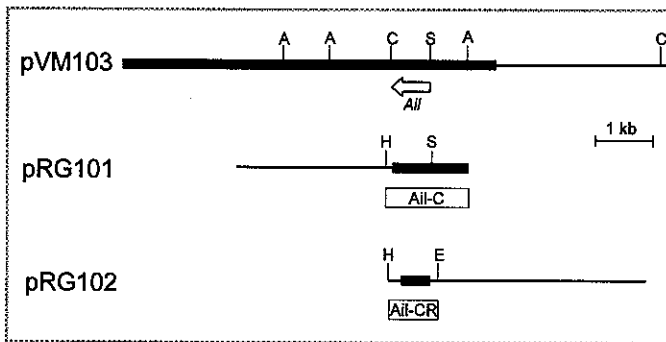


Figure 4.1

Plasmids and probes which harbour *ail*-sequences from *Y. enterocolitica*. Bold lines: *Y. enterocolitica* DNA, thin lines: vector DNA. The position of the *ail*-gene is indicated by an arrow. Probes are depicted as open boxes. Relevant restriction sites are: A = *Ava*I, C = *Cl*aI, E = *Eco*RI, H = *Hind*III, and S = *Sca*I.

Plasmid pRG101 was constructed by ligation of Ail-C, a 1.2 kb *Ava*I/*Cl*aI fragment of pVM103 [Miller *et al.* 1989], into the *Ava*I/*Acc*I-linearized vector pUC19 [Yanisch-Perron *et al.* 1985]. Plasmid pRG102 was obtained by ligation of a 0.65 kb *Sca*I/*Hind*III fragment of pRG101 into the *Hind*III/*Sma*I-linearized vector pEMBL8 [Dente *et al.* 1983]. Fragments of pRG101 (*Ava*I/*Hind*III digest, 1.2 kb) and pRG102 (*Eco*RI/*Hind*III digest, 0.65 kb) were used to prepare the DIG-labelled probes Ail-C and Ail-CR, respectively. Both Ail-C and Ail-CR contained the complete *ail* gene. The probes differed in the length of the flanking sequence upstream of *ail*, i.e. 0.7 kb in Ail-C and 0.1 kb in Ail-CR [Miller *et al.* 1989; Miller *et al.* 1990]. Plasmid pVM101 was used to obtain probes Inv-D and Inv-B. Inv-D was prepared from the 3.6 kb *Cl*aI-fragment of pVM101. This fragment had previously been designated Inv-ent [Miller & Falkow 1988] and had been used as a [³²P]-labelled probe for identification of *Yersinia* species. The probe Inv-B was prepared from a 3.2 kb *Pvu*I/*Mlu*I-fragment of pVM101. Inv-B comprised almost the whole coding sequence of *inv*, plus a 0.7 kb sequence downstream of the gene [Young *et al.* 1990], whereas Inv-D contained only the 1.2 kb C-terminal part of the *inv*-gene, plus a 2.4 kb downstream sequence (Figure 4.2).

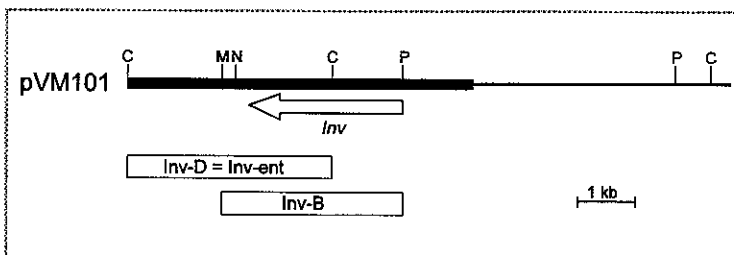


Figure 4.2

Plasmid and probes which harbour *inv*-sequences from *Y. enterocolitica*. Symbols as used in Figure 4.1. Relevant restriction sites are: C = *Cl*aI, M = *Mlu*I, N = *Nco*I, and P = *Pvu*I.

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All DNA-fragments were purified by means of gel-electrophoresis and treatment with 'GeneClean' (Bio101, La Jolla, Cal., USA), prior to labelling with the non-radioactive marker digoxigenin, applying a ready-to-use kit (DIG, Boehringer Mannheim, Germany) according to the manufacturer's instructions.

4.2.3 Sample Preparations

Human faeces

Approximately 1 g of sample was suspended in 2 ml of phosphate-buffered saline. Equal volumes (0.1 ml) were plated directly on Cefsulodin-Irgasan-Novobiocin agar (CIN, Oxoid) and plates were incubated for 48 or 96 h at 30°C. Duplicate plates were incubated at 22°C, which was meant to favour psychrotrophic *Yersinia*-like organisms [Schiemann 1982]. The remaining suspension was mixed with 25 ml of modified Rappaport-broth [Wauters 1973] and then split into two portions. One portion was incubated for 48 h at 30°C and the other one at 22°C. After this enrichment procedures, 0.1 ml volumes from both cultures were plated in duplicate onto Deoxycholate agar (DC, Oxoid) and further incubated for 48 h at both 30°C and 22°C. All plates showing bacterial growth were stored at 4°C, prior to subculturing and colony blotting.

Pig slaughterhouse samples

Various samples collected in a pig slaughterhouse (i.e. pig's tongues, contents of pig's ileum and rectum, swab-samples of carcasses, and swab-samples of machinery and employees hands) were investigated for the presence of *Yersinia* species by applying semi-cold enrichment in Irgasan-Ticarcillin-Potassiumchlorate (ITC) broth [Wauters *et al.* 1988], followed by incubation on selective CIN or SSDC agar [Boer *et al.* 1989]. All plates were stored at 4°C, prior to subculturing and colony blotting.

4.2.4 Subculturing and Identification

From all plates with primary isolates, colonies resembling *Yersinia* species on the basis of their morphological appearance (very small, colourless and translucent on SSDC; small, cream-coloured and with a red centre on CIN and DC) were subcultured. *Yersinia* strains were identified, serotyped and biotyped according to established criteria [Bercovier *et al.* 1980; Wauters 1981; Wauters *et al.* 1987].

4.2.5 Blotting Procedures and DNA-fixation

Southern blots with digested genomic DNA

Chromosomal DNA was isolated from *Y. enterocolitica* by means of proteinase-K/SDS lysis of the cells and subsequent CTAB/NaCl treatment and chloroform/isoamylalcohol extraction

of the lysate, as described elsewhere [Maniatis *et al.* 1982]. Portions of the DNA were digested to completion with either *EcoRV*, *EcoRV+ScaI*, *SauIIIA1* or *SauIIIA1+CfoI*, and the fragments were separated by agarose-gel electrophoresis. Southern blot transfer of the fragments on Hybond-N⁺ membranes (Amersham/Life Sciences, Amersham, UK) was performed with {3.6 M NaCl, 0.2 M NaH₂PO₄, 0.02 M EDTA} blotting buffer, using a vacuum-blot apparatus (Millipore, Bedford, USA).

Spot-blot with purified total genomic DNA

DNA-concentrations of genomic and plasmid preparations were determined spectrophotometrically (OD₂₆₀/OD₂₈₀), and dilution series in 0.25 M NaOH were prepared containing either 0.005-10 ng/μl of plasmid pVM103, or 5-5000 ng/μl of purified genomic DNA. Equal volumes (1 μl) of the dilutions were pipetted in rows onto Genescreen-Plus membranes (Biotechnology Systems, 's-Hertogenbosch, the Netherlands) and on Hybond-N⁺ membranes, producing well defined spots of immobilized DNA after air-drying .

Dot-blot with cell suspensions

Y. enterocolitica strains were grown overnight at 30°C, and the cell density was estimated spectrophotometrically (OD₆₀₀). Cells were pelleted by low speed centrifugation (5000 g, 10 min, 4°C). The supernatants were removed and the pellets were resuspended in sterile distilled water. From each suspension, a volume containing approximately 10⁸ cells was mixed with NaOH to a final concentration of 0.25 M, and the cells were lysed by incubation at room temperature for 10 min. The lysates were transferred to a Genescreen-Plus membrane, using a 96-well dot-blot apparatus (Millipore, Bedford, USA), and the released DNA was fixed by air-drying of the membrane.

Colony blots

Small aliquots of freshly broth-cultured *Yersinia* reference strains and reference strains of other species were spotted onto agar plates and incubated overnight at 22°C or 37°C, to obtain distinct colonies on the plates. From these plates, as well as from those which had been obtained from clinical specimens and slaughterhouse samples, as described above, colonies were lifted onto circular membranes (Genescreen NEF-978X), according to the protocol provided by the manufacturer. Cell-lysis and simultaneous DNA-fixation was done by alkaline steaming [Maas 1983]. Briefly, a hybridization membrane disc was placed onto the agar plate, left for 3 min, peeled off carefully, and transferred - with colony side up - to a piece of 3MM Whatman filter paper, that had previously been saturated with 0.5 M NaOH, in a pyrex petri dish. The dish (without lid) was placed in a steaming water bath for 10 min. Subsequently, the hybridization membrane was neutralized by soaking it (still with colony side up) on a pool of 0.75 ml 1M Tris-HCl buffer (pH=7.5). After 3 min, the neutralizing step was repeated once, with a fresh pool of buffer solution. Next, the membrane disc was transferred to {0.3 M NaCl, 0.03 M sodium citrate} wash buffer. Any excessive cellular debris was removed by rubbing

the membrane with a piece of wet paper towel. Finally, the rinsed membrane was air dried at room temperature.

4.2.6 Hybridization Conditions

Several preliminary experiments with blots of purified plasmid- and genomic DNA were performed, according to the hybridization- and detection protocol of the ready-to-use DIG-kit provided by the manufacturer. However, it was observed that, after finishing of the experiments, the stored GenescreenPlus membranes frequently attained, within a few days, an overall purple colouring, which overwhelmed the signals. Obviously, this colour development hindered the comparison of results of successive hybridizations. To eliminate this problem, we introduced several modifications in the composition of the hybridization solution.

Eventually, the modifications comprised the increase of the concentrations of both SDS and blocking agents (from 0.02 to 0.2% and from 0.5 to 2%, respectively), and the addition of heterologous DNA to a final concentration of 1µg/ml hybridization buffer. These modifications resulted in a better durability of finished membranes, a better signal-to-noise ratio, and a better reproducibility. For this reason, the modified hybridization solution was used in all subsequent experiments.

4.2.7 Tissue Culture Invasion Assay

The invasion capacity of all *Yersinia* strains was investigated by a tissue culture invasion (TCI-) assay, which was performed essentially as described by Falkow and co-workers [Miller & Falkow 1988]. HEp-2-cells used for this assay were obtained from Flow Laboratories (Rockville, Maryland, USA, cat. no. 0-26410).

4.3 RESULTS

4.3.1 Tissue Culture Invasion

TCI-phenotypes of two hundred European *Y. enterocolitica* strains of fifteen different serotypes were established, and the results are shown in [Table 4.1](#). *In vitro* invasiveness (a TCI⁺ phenotype) was found in all 26 strains of serotypes O:3 and O:9, which are commonly associated with disease. These results agreed with earlier findings for American strains [Miller *et al.* 1989] and supported the assumption that pathogenicity of *Y. enterocolitica* is coupled to invasiveness. With 42 serotype O:5 strains, both TCI-phenotypes were observed, and only two out of 132 strains of serotypes which are usually not associated with disease also showed a TCI⁺ phenotype.

Table 4.1 Correlation between serotype, origin, *in vitro* invasiveness and DNA-hybridization with an *ail*-probe, of various strains of *Y. enterocolitica*.

SEROTYPES	ORIGIN		INVASIVENESS ¹			HYBRIDIZATION ²	
	human	animal	+	-	nm	+	-
O:3	12	3	15	0	0	15	0
O:9	6	5	11	0	0	11	0
O:5	7	6	13	0	0	13	0
O:5	22	7	0	29	0	0	29
O:4,33	5	5	0	10	0	1	9
O:6,30	16	10	0	26	0	1	25
O:6,31	10	7	0	7	10	0	17
O:7,8	10	2	0	2	10	0	12
O:7,13a,b	11	5	0	4	12	0	16
O:10,34	6	5	0	3	8	0	11
O:12,25	2	1	0	2	1	0	3
O:14	3	0	0	0	3	0	3
O:16a,b	1	1	0	0	2	0	2
O:16a,58	5	10	0	1	14	0	15
O:27,41,43	3	2	0	3	2	0	5
O:40	2	0	0	2	0	0	2
O:41,43	3	0	0	3	0	0	3
O:47	1	6	0	1	6	0	7
Total number of strains	125	75	39	93	68	41	159
			132		68		
	200		200			200	

¹ *In vitro* invasiveness of strains, as measured in a Tissue Culture Invasion assay [Miller & Falkow 1988]: + = invasive, - = non-invasive, nm = not measured

² Signals obtained in culture dot-blot hybridization with a DIG-labelled *ail*-probe, as described in this paper: + = hybridization, - = no hybridization.

4.3.2 Sensitivity and Specificity of DIG-labelled Probes

Sensitivity

Southern blots of *EcoRV*-digested DNA from four TCI⁺ strains and two TCI⁻ strains were hybridized with *Ail-C* by the prescribed protocol. Single positive signals were obtained with 7.2 and 10.5 kb fragments from the TCI⁺ strains of serotype O:9 and O:3, respectively, while no hybridization was observed with DNA from the TCI⁻ strains (results not shown). These results were in agreement with those obtained with [³²P]-labelled *ail*-probes [Miller & Falkow 1988; Miller *et al.* 1989], and indicated that the sensitivity of the method using DIG-labelled probes was

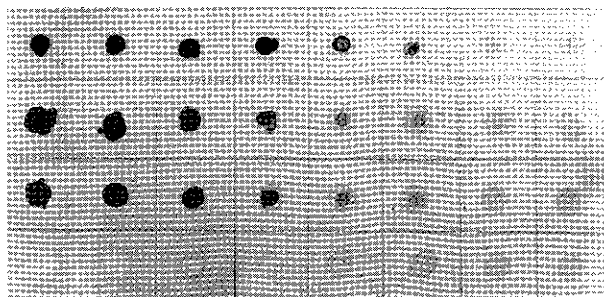
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sufficient to detect homologous fragments of DNA in Southern-blot. The detection limit for *ail* DNA was investigated with 1 µl spot-blot of purified plasmid and genomic DNA, obtained from pVM103 and four different serotypes of *Y. enterocolitica*, respectively. When using the modified hybridization buffer, and probe Ail-C in the recommended concentrations (1-10 ng/ml), the lower detection limit of Ail-C homologous DNA, as present in pVM103, appeared to rank between 0.001 and 0.005 ng (Figure 4.3, upper row). Signals of similar intensity were obtained with spots containing ca. 25 ng of purified genomic TCI⁺ *Y. enterocolitica* DNA, which originated from approximately 5x10⁶ cells (Figure 4.3, middle rows). In contrast, up to 1 µg of TCI⁻ DNA, originating from up to 10⁹ cells, only produced background signals (Figure 4.3, lower row). No differences were found between the results obtained with Hybond-N⁺, Genescreen-Plus or NEF-978X membranes (results not shown).

plasmid-derived DNA: Ail-C	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005
genomic DNA, TCI ⁺ , serotype O:9	5000	2500	500	250	50	25	5	2.5
genomic DNA, TCI ⁺ , serotype O:3	5000	2500	500	250	50	25	5	2.5
genomic DNA, TCI ⁻ , O:6,30	5000	2500	500	250	50	25	5	2.5

Figure 4.3

Inoculation scheme, and finished membrane, of a spot-blot-experiment. Spots contain 0.005-1 ng Ail-C DNA (as present in pVM103) or 2.5-5000 ng total genomic DNA of *Y. enterocolitica* (as purified from 5x10⁵ - 10⁹ cells). The blot was hybridized with DIG-labelled Ail-C (1 ng/ml). Shaded inoculation sites are known, or presumed, to contain *ail* DNA



Specificity of *ail*-probes in culture-blot

Culture dot-blot of 200 strains were hybridized with Ail-C, and 61 of them also with Ail-CR. Figure 4.4 shows the inoculation scheme and the results of one of the membranes. The results are summarized in Table 4.1, and show that all TCI⁺, but only two TCI⁻, strains hybridized with the *ail*-probe. No differences in sensitivity or specificity were observed using either Ail-C or Ail-CR.