## Intra- and Interspecies Relatedness of Yersinia pestis by DNA Hybridization and Its Relationship to Yersinia pseudotuberculosis

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Abstract. The biochemical characteristics of Yersinia pestis are presented and compared with those of Y. pseudotuberculosis. Motility at 28°C, urease, fermentation of rhamnose, and growth rate on nutrient agar are the best means of separating these organisms. DNA hybridization studies demonstrated that Y. pestis strains are 90% or more interrelated and that Y. pestis and Y. pseudotuberculosis are indistinguishable by DNA relatedness. On the basis of DNA data and biochemical and antigenic similarity, these organisms should be treated as two separate subspecies of the same species. Y. pseudotuberculosis was described before Y. pestis and therefore has priority. Y. pseudotuberculosis subsp. pseudotuberculosis and Y. pseudotuberculosis subsp. pseudotuberculosis and Y. pseudotuberculosis subsp. pseudotuberculosis and Y. pseudotuberculosis and

Yersinia pestis was first described in Hong Kong by Yersin in 1894 [29]. Since then, the "plague bacillus" was frequently transferred from one genus to another until, with general agreement, it was finally placed in the genus Yersinia Van Loghem [28]. It is described as such in the eighth edition of Bergey's Manual [21]. The isolation of Yersinia pseudotuberculosis in Europe in 1883 is credited to Malassez and Vignal [15]. Y. pseudotuberculosis has also undergone frequent nomenclatural changes [18].

Taxonomists considered these two organisms to be separate species; the main problem for the bacteriologists who isolated Y. pestis from throughout the world during the third pandemic was to differentiate it from Y. pseudotuberculosis. The consequence for a country in which the plague bacillus was isolated—i.e., in terms of quarantine, vaccination, prophylaxis, etc.—were so important that between 1910 and 1950 an enormous amount of scientific literature was devoted to that topic [24]. Y. pestis and Y. pseudotuberculosis are still considered separate species, but in the field, it is difficult to differentiate between them, especially with nonhuman isolates.

Since it was difficult to separate these organisms, our approach was to determine the extent to which they were similar. In this report, we present biochemical and DNA relatedness data, and review antigenic and epidemiological findings to define the relationship between Y. pestis and Y. pseudotuberculosis and the relatedness of these two organisms to other Yersinia species.

## Materials and Methods

Organisms. The Yersinia pseudotuberculosis and Y. pestis strains used for DNA hybridization are listed in Table 1. Other Yersinia species [7] and species of Enterobacteriaceae [26] used for DNA hybridization have been described previously. Some fifty strains each of Y. pseudotuberculosis and Y. pestis from the collection of the National Yersinia Center (Institut Pasteur, Paris) were studied biochemically.

Biochemical and genetic characterization. Biochemical reactions were done at 28°C, unless otherwise indicated. Tellurite reduction was done according to Brzin [8]. Reference to the other methods used has been previously cited [1]. Methods used for the separation of single- and double-stranded DNA on hydroxyapatite (HA), and thermal elution chromatography on HA have been described [2,3,4,6]. DNA from Y. pseudotuberculosis and Y. pestis strains was labeled in vitro with tritium using John Johnson's modification of the methods described in references [10] and [23]. G+C content was determined by the optical thermal denaturation method [16].

Species	Strain designation*	Serogroup	Source	Country of origin (sender)	
Yersinia pseudotuberculosis	(P P)	TI.	Human	France	
Y. pseudotuberculosis	IP P3 (55.85), NCTC 10275, Thal 14-1	I		Sweden (Thal)	
Y. pseudotuberculosis	P62				
Y. pseudotuberculosis	P105		Mink	Denmark (Thal)	
Y. pseudotuberculosis	P320		Human	Germany (Thal)	
Yersinia pestis	IP P1. Harbin			USSR	
Y. pestis	IP P2, PKR 288		Rodent	lran	
Y. pestis	IP P3, Kenya 129			Kenya	
Y. pestis	IP P4, Kenya 102			Kenva	
Y. pestis	IP P5. Congo Belge Lita			Zaire	
Y. pestis	IP P6, PKR 292		Rodent	Iran	
Y. pestis	IP P7, Madagascar 6/69		Human	Madagascar	
Y. pestis	IP P8. Dalat 286		Human	Vietnam	
Y. pestis	IP P9, Madagascar 8/70		Human	Madagascar	
Y. pestis	IP P10, Dalat 317		Human	Vietnam	
Y. pestis	IP ₽11, Kenya 147			Kenya	
Y. pestis	JP P12, Turquie 10/5			Turkey	
Y. pestis	1122			(Corwin)	

Table 1. Bacterial strains.

" IP, Institut Pasteur, Paris, France: NCTC, National Collection of Type Cultures, Colindale, England.

## **Results and Discussion**

Conventional biochemical tests as well as API 20E and API 50E tests were done on about 50 strains each of Yersinia pseudotuberculosis and Y. pestis. The API tests were done according to the manufacturer's instructions (Analytab Products Inc.)<sup>1</sup> except that incubation was at 28°C. Conventional biochemical tests were also carried out at 28°C. Good agreement was obtained with all three methods. The one exception was with D-sorbitol. Both Y. pestis and Y. pseudotuberculosis were uniformly sorbitol negative by the conventional test in peptone water or the API 50E. With the API 20E, most Y. pestis strains gave a sorbitol-positive reaction at 16 h and became negative after 24 h.

Strains of both Y. pestis and Y. pseudotuberculosis show very little biochemical heterogeneity. The biochemical reactions that both organisms exhibit are listed in Table 2. Biochemical and cultural characteristics useful in separating Y. pestis from Y. pseudotuberculosis are shown in Table 3. Motility at 28°C, urease activity, fermentation of rhamnose, growth rate, and colony size on nutrient agar remain the best way to differentiate these organisms. Problems related to the choice of suitable media for Y. pestis biochemical reactions have been reviewed elsewhere [24]. Differential characters have also been discussed elsewhere [9,24]. In addition to having comparable physiological and biochemical characteristics, the two organisms are very similar in other respects. Eleven of the 18 antigens studied by Lawton, Fukui, and Surgalla are found in strains of both Y. pestis and Y. pseudotuberculosis [14]. Even the lipid composition in these organisms was shown to be highly related [27].

G+C content averaged 46.5 mol% for Y. pseudotuberculosis and 46.0 mol% for Y. pestis (Table 4). These G+C percentages confirm previous values already in the literature [12,17]. The 0.5 mol% difference in the G+C values obtained for strains of Y. pestis and Y. pseudotuberculosis is not meaningful. This kind of minimal difference in G+C percentage is within the technical limits of the optical denaturation method and well within the variability in G+C found among different strains of the same species [3]. Other Yersinia species contain slightly more G+C in their DNA [7,13]. The values usually obtained for Y. enterocolitica and Y. ruckeri are 47–49% G+C.

Hybridization reactions with labeled DNA from Y. pestis 1122 and Y. pseudotuberculosis strains P62 and P3 and unlabeled DNA from Yersinia strains are presented in Table 5. By reacting DNA from a single strain of Y. pestis with labeled DNA from Y. pseudotuberculosis, two laboratories reported a high degree of relatedness between these organisms [22,25]. Brenner et al. [5] pointed out the intraspecies homogeneity in Y. pseudotuberculosis and its close relation to Y. pestis. We now report results of DNA relatedness obtained using 13 strains of Y. pestis reacted with both labeled Y. pestis DNA and two labeled Y. pseudo-

<sup>&</sup>lt;sup>1</sup>Use of trade name is for identification only and does not constitute endorsement by the Public Health Service or by the U.S. Department of Health and Human Services.

Table 2. Biochemical characteristics of Yersinia pseudotuberculosis and Y. pestis.<sup>a</sup>

	Y. pseudotuberculosis			Y. pestis			
Test	Reac- tion		Neo- type strain NCTC 10275	Reac-		Refer- ence strain NCTC 5923	
Motility (28°C)	+	98	+	-	0	_	
Urease	+	100	+	-	$0^{h}$	_	
Indole	-	0	_	_	0	_	
Simmons' citrate (28°C)	_	1.	-	-	0	-	
Malonate	v	٧r	-		υ	_	
NO <sub>2</sub> reduction to NO <sub>2</sub> /Type	+	99/B	+/B	v	V <sup>a</sup>	+/B	
Tetrathionate	-	0	-	v	15	-	
Deoxyribonuclease Acid production from:	v	85	+	+	91	+	
Glycerol	+	99	+	v	$\mathbf{V}^{d}$	_	
L-Arabinose	+	100	+	+	98	+	
Adonitol	_	5	_	_	0	_	
D-Mannose	+	97	+	+	100	+	
L-Rhamnose	+	99	+	_	3	_	
Maltose	+	100	+-	v	84	+	
D-Melibiose	+	99	+	v	$\mathbf{V}^d$	-	
D-Raffinose	٧	£1	-	-	2	_	
D-Melizitose	-	0		_	2	_	
D-Sorbitol	—	2	-	-	0	-	
Salicin	v	65	+	v	88	+	
Arbutin	v	88	+	+	100	+	
Dextrin	-	5	-	v	62	+	

" All incubations, except where indicated, were done at 28°C. +, 90.0% or more positive within 7 days; V, 10.1-89.9% positive; -, less than 10% positive after 7 days. The following tests gave positive reactions for all strains of Y. pseudotuberculosis and Y. pestis tested: catalase, methyl red (28°C and 37°C), fermentation in O-F test, β-galactosidase (ONPG; 37°C), β-xylosidase (PNPX; 37°C), polypectate, and acid production from D-glucose, ribose, D-xylose, galactose, D-fructose, D-trehalose, D-mannitol, esculin, N-acetylglucosamine, and starch. The following tests gave negative reactions for all strains tested: oxidase, motility (37°C), Voges-Proskauer (28°C and 37°C), Simmons' citrate (37°C), mucate, Christensen's citrate, KCN, gas from D-glucose, H<sub>2</sub>S (Kliegler's), phenylalanine deaminase, tryptophan deaminase, lysine decarboxylase, arginine dihydrolase, ornithine decarboxylase, lipase (Tween 80), gelatin (film), and acid production from erythritol, Darabinose, L-xylose, L-sorbose, dulcitol, D-cellobiose, lactose, sucrose, *i*-inositol, amygdalin,  $\alpha$ -methyl-xyloside,  $\alpha$ -methyl-D-mannoside, a-methyl-D-glucoside, inulin, amylose, and glycogen.

<sup>b</sup> Some strains give positive reactions when first isolated [20]. <sup>c</sup> Serogroup IV strains of *Y. pseudotuberculosis* are positive.

"Reaction varies in different biotypes of Y. pestis [19].

tuberculosis DNAs. Our results confirm and extend the previous observations. Y. pestis strains representing the three described varieties (orientalis, medievalis, and antiqua) were included in these studies [11]. All varieties were essentially identical by DNA relatedness.

Table 3. Differentiation between Yersinia pestis and Y. pseudotuberculosis.<sup>a</sup>

	Y. pestis	Y. pseudo- tuberculosis
Motility 28°C	-	+
Urease	_ <sup>h</sup>	+
L-Rhamnose	_*	+
Colony size on nutrient agar in mm	≤1	≥2
Nutritional requirement for amino acids	+	_
Tellurite reduction	_ <i>d</i>	+
Glycerol (oxidative) <sup>e</sup>	V	+
D-Melibiose <sup>e</sup>	v	+
Adonitol	_	-(5%+)
Maltose	V(84%+)	· + ′
	-	

<sup>4</sup> See Table 1 for explanation of +, -, and incubation conditions.

<sup>b</sup> Rare strains are urease positive on primary isolation. They become negative after subculture [20].

<sup>c</sup> Rare strains ferment rhamnose but never in 24 h.

<sup>d</sup> Weak; a few black specks if heavy inoculum is used.

<sup>e</sup> Variable characters used for the classification of Y. pestis biogroups [19].

<sup>7</sup> Variable reaction, more than 10% and less than 90% of strains are positive.

Table 4. G+C content in DNA from strains of Yersinia pestis and Y. pseudotuberculosis.

Source of DNA	G+C (mol%)			
Y. pseudotuberculosis Pl	46.5			
Y. pseudotuberculosis P2	46.5			
Y. pseudotuberculosis P3	46.5			
Y. pestis P1	46.0			
Y. pestis P2	46.0			
Y. pestis P3	46.0			
Y. pestis P10	46.5			
Y. pestis PIL	46.0			

Intra- and interspecies DNA relatedness values for Y. pestis and Y. pseudotuberculosis are virtually identical. They are 90% or more related in reactions done at 60°C and this percentage does not decrease in 75°C reactions. Percent divergence (%D) is zero to 1% in interspecies reactions. Other Yersinia species (Y. enterocolitica, Y. intermedia, Y. frederiksenii, Y. kristensenii) are at most 48% related to Y. pestis and Y. pseudotuberculosis, with %D values greater than 10. Reciprocal hybridization reactions using the different labeled strains did not show any differences in DNA relatedness values. This suggests not only that Y. pestis and Y. pseudotuberculosis are highly related, but also that their genome size is very similar.

The DNA data support the two following conclusions: First, biochemical distinctions between Y. *pestis* varieties should be considered only as epidemiological markers, not as criteria for subspeciation.

Y. pseudotuberculosis		V a satis				
P62	Y. pestis 1122			Y. pseudotuberculosis P3		
60°C 75°C	60°C RBR	%D	75°C RBR	60°C RBR	%D	75°C RBR
Source of unlabeled DNA RBR <sup>a</sup> %D <sup>a</sup> RBR						
Y. pseudotuberculosis P62 100 0 100						
Y. pseudotuberculosis P3 92 4 79				100	0	100
Y. pseudotuberculosis P1				89	1	
Y. pseudotuberculosis P320 92 0 93						
Y. pseudotuberculosis P105 91 0 98						
Y. pestis P1	98	0		96	1	89
Y. pestis P2	97	0		93	0.5	91
Y. pestis P3 87 0 85	97	0	97	94	0	94
Y. pestis P4 87 0	94	0		96	0	98
Y. pestis P5				97	0	95
Y. pestis P6 90 0	99	0	100	95		95
Y. pestis P7 89 0	99	0	99	100	0	97
Y. pestis P8 89 0	99	0	100	98	0.5	95
Y. pestis P9 91 0				100		100
Y. pestis P10 89 0 84				95		99
Y. pestis P11 87 1				98		
Y. pestis P12				97	1	
Y. pestis 1122 86 0	100	0	100			
Y. enterocolitica 497-70 48 12 15						
Y. enterocolítica 3953 (Bottone 48) 44 12						
Y. enterocolítica 867 44 11						
Y. enterocolítica 1474 44 11						
Y. enterocolítica 4052				40		14
Y. enterocolitica 6005 (X2)						
Y. ruckeri 4535-69 33 13 7				44	14	16

Table 5. DNA relatedness of Yersinia pseudotuberculosis and Y. pestis.

" RBR, relative binding ratio = % (heterologous DNA bound to HA)/(homologous DNA bound to HA)  $\times$  100. RBR is a convenient way to express percent relatedness.

<sup>b</sup> %D, percent divergence. D is calculated on the assumption that a 1°C decrease in thermal stability of a heterologous DNA duplex compared to that of the homologous DNA duplex is caused by each 1% of the bases within the duplex that are unpaired [2]. For example, consider organisms A and B which are 50% related (RBR = 50%). The thermal stability of an A-A duplex is 91°C, and the thermal stability of an A-B duplex is 76°C; the %D of the related DNA is 15, %D is given to the nearest 0.5%.

Second, in addition to being very similar biochemically, antigenically, and structurally, Y. pestis and Y. pseudotuberculosis genetically belong to the same species. This is certainly true if we agree with the definition of Enterobacteriaceae species cited in a previous paper on Yersinia [7].

Epidemiological data and the clinical aspects of infections due to these two organisms are notably different. Y. pseudotuberculosis is found frequently, at least in Europe, among Lagomorpha and birds, which can be considered its reservoir. In contrast, Y. pestis infects and is often epizootic in different genera of rodents (Citellus, Meriones, Rattus, etc.). The two organisms grossly share the same ecology in that they are mainly pathogenic for rodents and occasionally for man. The route of human infection and the consequences of infection are, however, quite different.

Humans are usually infected by oral ingestion of Y. pseudotuberculosis, which causes a mesenteric lymphadenitis. The bacteria rarely reach the bloodstream to cause septicemia. On the other hand, Y. pestis is generally transmitted from animals to humans by a bite from infected fleas. A peripheral adenitis (bubo) develops in the lymph nodes, draining the site where the bacteria entered. Without treatment, bubonic plague will evolve to septicemia or pneumonic plague, which, as a rule, are fatal. Thus, plague must be considered as an epidemic and fatal disease; Y. pseudotuberculosis, on the other hand, causes sporadic disease in man and infections are rarely fatal.

We, and most taxonomists, have long believed that no single property, even pathogenicity, is a sufficient basis for designating species. Therefore, on the basis of the data presented and cited here we believe that these two organisms should be treated as a single species, differentiated at the level of subspecies. From a strictly taxonomic point of view, we recommend that Y. pseudotuberculosis subsp. pseudotuberculosis be the type species of the genus Yersinia, since it was described before Y. pestis and therefore has priority. Y. pestis would then become Y. pseudotuberculosis subsp. pestis. It would still be perfectly acceptable for clinical bacteriologists and public health officers to refer to Y. pseudotuberculosis and Y. *pestis.* In fact, we strongly recommend this approach. Thus, the taxonomy of these organisms would be consistent with available scientific knowledge and the need of the medical community for practical designations would be met. Strain NCTC 10275 (=ATCC 29833= Thal 14.1) is proposed as the neotype strain for pseudotuberculosis subspecies pseudotuberculosis. It belongs to serogroup 1. Strain NCTC 5923 (= ATCC 19428) is the type strain for Y. pseudotuberculosis subspecies pestis. Biochemical reactions for strains NCTC 10275 and ATCC 19428 are given in Table 2.

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