# Supplement 2008-2010 (no. 48) to the White-Kauffmann-Le Minor scheme.

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In memory of Prof. Michel-Yvan Popoff (1945-2013) who headed the WHO Collaborating Centre for Reference and Research on *Salmonella* at the Pasteur Institute between 1989 and 2003

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## Abstract

This supplement (no. 48) of the White-Kauffmann-Le Minor scheme reports on the characterization of 63 new *Salmonella* serovars and 25 new variants of previously described *Salmonella* serovars recognized by the WHO Collaborating Centre for Reference and Research on *Salmonella* between 2008 and 2010. Forty-four new serovars were assigned to *Salmonella enterica* subspecies *enterica*, 12 to subspecies *salamae*, two to subspecies *arizonae*, two to subspecies *diarizonae* and three to subspecies *houtenae.* All these new serovars or new variants are described with their multilocus sequence type.



*Keywords*: *Salmonella;* Serovars; Taxonomy; MLST; White-Kauffmann-Le Minor scheme

34 The genus *Salmonella* consists of only two species, *Salmonella enterica* and *S. bongori. S.*
35 *enterica* is divided into six subspecies: *S. enterica* subsp. *enterica*, *S. enterica* subsp. *salamae*,
36 *S. enterica* subsp. *arizonae*, *S. enterica* subsp. *diarizonae*, *S. enterica* subsp. *houtenae*, and *S.*
37 *enterica* subsp. *indica.* This nomenclature reflects present understanding of *Salmonella*
38 taxonomy [1, 2]. The species called *S. subterranea* [3] does not belong in the genus
39 *Salmonella* (Table 1, Figure).
40 Serovars belonging to *S. enterica* subsp. *enterica* are typically designated by a name usually
41 related to the geographical place where the serovar was first isolated [7]. The serovar name is
42 written in non-italicized Roman letters and the first letter capitalized. Serovars belonging to
43 other subspecies are designated by their antigenic formulae, following the subspecies name.
44 The antigenic formulae of *Salmonella* serovars are available in the White-Kauffmann-Le
45 Minor scheme [7] at: http://www.pasteur.fr/sante/clre/cadrecnr/salmoms/WKLM_En.pdf
46 Updating this scheme is the responsibility of the WHO Collaborating Centre for Reference
47 and Research on *Salmonella* (WHO-Salm), Institut Pasteur, Paris, France. The current edition
48 (9th) issued in 2007 comprises antigenic formulae validated as of January 1st 2007. In 2010,
49 Supplement 47 reported the characterization of 70 new *Salmonella* serovars recognized
50 between January 1st 2003 and December 31th 2007 [8].
51 Supplement 48 reports the characterization of 63 new *Salmonella* serovars recognized
52 between January 1st 2008 and December 31th 2010 by the WHO-Salm: 44 were assigned to
53 *S. enterica* subsp. *enterica*, 12 to subsp. *salamae*, two to subsp. *arizonae*, two to subsp.
54 *diarizonae* and three to subspecies *houtenae* (Table 2).
55 It is useful to note that strain 9736/07, erroneously described in the Supplement 47 [8] as
56 the reference strain of *S. bongori* serovar 1,9,12:d:e,n,x has been reassigned to *S. enterica*
57 subsp. *enterica* on the basis of its biochemical characteristics, its diphasic nature, *rpoB*
58 sequence (Figure 1), and multilocus sequence type [6]. This strain is now considered as the

reference strain of the new serovar Viikki.

Among the 63 new serovars identified, 21 were received from the Gastrointestinal Bacteria Reference Unit of Public Health England (PHE), Colindale, UK. These 21 new serovars were isolated between 1994 and 2004 and correspond to all potential new serovars identified at PHE during this period.

New variants of previously described *Salmonella* serovars are provided in Table 3

For the first time, the multilocus sequence type has been indicated for all the 63 new serovars as well as for the 25 new variants of previously described *Salmonella* serovars. Multilocus sequence typing (MLST) has been performed both at the WHO-CC or at the PHE according to Achtman *et al.* [6]. The data have been submitted to the *Salmonella enterica* MLST database (http://mlst.warwick.ac.uk/mlst/dbs/Senterica).

The present number of serovars per species and subspecies is given in Table 4.

The next issue of the White-Kauffmann-Le Minor scheme, which will contain MLST data, is expected in December 2015.

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**Table 1.** Atypical characteristics of the reference strain of "*Salmonella subterranea"* (strain CIP 109002)

| | Strain CIP109002 |
|---|---|
| Biochemical tests[a] | Indole$^{+}$, citrate$^{-}$, LDC$^{-}$, H2S$^{-}$ |
| Serotyping[b] | No agglutination |
| *rpoB* sequencing[c] | Not clustered with *Salmonella* strains |
| MLST[d] | Not typable |

[a] This strain was not pigmented in yellow in classical culture media as described by the authors
[b] Performed with antisera produced according to reference 4
[c] See Figure
[d] Performed according to reference 6. More than 2,300 strains belonging to >650 serotypes of *S. enterica* subsp. *enterica* (n=1,765), *salamae* (n=227), *arizonae* (n=51), *diarizonae* (n=165), *houtenae* (n=63), *indica* (n=15), and *S. bongori* (n=31) have been MLST typed at the WHO-CC without encountering not typable *Salmonella* strains

**Table 2.** New *Salmonella* serovars recognized by the WHO Collaborating Centre for Reference and Research on *Salmonella*, 2008-2010.

| Serovar name | Antigenic formula | Other characters[b] | Source | Area of isolation (or contamination) | Year | IP strain number | Received from[c] | MLST type |
|---|---|---|---|---|---|---|---|---|
| ***Salmonella enterica* subsp. *enterica*** | | | | | | | | |
| Viikki[a] | 1,9,12:d:e,n,x | ONPG$^+$, Gal$^+$ | Cattle | Finland | 2007 | 9736/07 | NPHI | ST1743 |
| Bruxelles | 41:y:- | | Spice | Belgium | 2007 | 9764/08 | ISSP | ST1735 |
| Forges | 47:$z_4$,$z_{23}$:1,2 | | Human feces | France | 2007 | 9765/08 | IP | ST1700 |
| Trumersee | 1,6,14,25:k:e,n,x | | Rosemary herb | Austria | 2008 | 9789/08 | IMED | ST1701 |
| Pajala | 13,23:$z_{41}$:e,n,$z_{15}$ | | Bird | Sweden | 2008 | 9806/08 | SMI | ST1704 |
| Chapuri | 13,23:i:$z_6$ | | Human feces | USA | 2007 | 9811/08 | CDC | ST1705 |
| Baltimore | 35:y:l,w | | Human feces | USA | 2008 | 9812/08 | CDC | ST1706 |
| Landeskrone | 39:-:1,6 | | Human | Germany | 2007 | 9814/08 | IHU | ST1707 |
| Rosslyn | 51:y:1,2 | | Snake | Niger | 2008 | 9817/08 | PHAC | ST1708 |
| Kakikoka | 30:b:$z_6$ | | Human feces | Benin | 2008 | 9829/08 | RKI | ST627 |
| Parabiago | 28:c:l,w | | Human feces | Italy | 2008 | 9837/08 | ISS | ST1709 |
| Durance | 13,22:z:$z_6$ | | Human feces | France | 2008 | 9843/08 | IP | ST1710 |
| Santaclara | 3,10:$z_{35}$:1,5 | Mal$^+$, Sal$^+$, Gal$^+$ | Human feces | USA | 2007 | 9847/08 | CDC | ST1711 |
| Capetown | 3,15,34:y:1,6 | Dtar$^-$, Gal$^+$ | Human feces | USA | 2008 | 9848/08 | CDC | ST1712 |
| Fortbend | 1,3,19:$z_{41}$:e,n,$z_{15}$ | | Human feces | USA | 2008 | 9850/08 | CDC | ST1713 |
| Mali | 51:r:e,n,x | | Human | Germany (West Africa) | 2009 | 9879/09 | RKI | ST1714 |
| Bergerac | 44:c:e,n,x | | Human feces | France (Guinea) | 2009 | 9970/09 | IP | ST1715 |
| Salpetriere | 21:k:1,6 | | Human feces | France | 2009 | 9992/09 | IP | ST1716 |
| Wembleypark | 17:g,m:- | H2S$^-$ | Human feces | UK | 1994 | 9997/09 | PHE | ST1761 |
| Noho | 13,23:k:1,6 | | Human feces | UK | 1996 | 9999/09 | PHE | ST1762 |
| Ashford | 6,7:k:$z_{35}$ | ONPG$^+$ | Spice | UK | 1996 | 10000/09 | PHE | ST1760 |
| Elmdon | 51:i:1,2 | | Human feces | UK | 1996 | 10002/09 | PHE | ST1763 |
| Torbay | 3,10:l,$z_{28}$:1,5 | | Human feces | UK (Gambia) | 1997 | 10004/09 | PHE | ST1764 |
| Colchester | 8,20:r:1,6 | | Sausage | UK | 1997 | 10005/09 | PHE | ST1765 |
| Sandbanks | 6,8:k:1,7 | | Human feces | UK | 1997 | 10006/09 | PHE | ST1766 |
| Cork | 9,46:y:1,2 | | Sausage | Republic of Ireland | 1998 | 10008/09 | PHE | ST1767 |
| Frimley | 39:r:1,5 | | Human feces | UK (Nigeria) | 1999 | 10010/09 | PHE | ST1769 |
| Harrow | 4,12:$z_{10}$:1,7 | | Human feces | UK | 1999 | 10011/09 | PHE | ST1811 |
| Goodmayes | 44:z:e,n,$z_{15}$ | | Human feces | UK | 1999 | 10012/09 | PHE | ST1770 |
| Poole | 9,46:a:1,6 | | Human feces | UK (East Africa) | 2001 | 10017/09 | PHE | ST1773 |
| Kingslynn | 3,10:z:e,n,$z_{15}$ | | Human feces | UK (Gambia) | 2004 | 10018/09 | PHE | ST877 |
| Maybush | 11:z:e,n,$z_{15}$ | | Human feces | UK | 2004 | 10019/09 | PHE | ST878 |
| Carshalton | 47:g,m,s:- | | Human feces | UK (Nigeria) | 2004 | 10020/09 | PHE | ST1774 |
| Stafford | 6,14,24:z:l,$z_{13}$,$z_{28}$ | | Human feces | UK | 2004 | 10023/09 | PHE | ST557 |
| Coppettswood | 30:b:l,$z_{13}$,$z_{28}$ | | Human feces | UK (Ghana) | 2004 | 10024/09 | PHE | ST1775 |
| Welwyn | 11:l,$z_{13}$,$z_{28}$:e,n,$z_{15}$ | | Dried ugu leaves | UK | 2004 | 10026/09 | PHE | ST887 |
| Zollikerberg | 6,7:$z_4$,$z_{24}$:1,5 | | Human feces | Switzerland | 2007 | 10031/09 | IFSH | ST1717 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Yverdon | 1,4,12:$z_{38}$:1,5 | | Human feces | Switzerland (Burkina Faso) | 2009 | 10033/09 | IFSH | ST1718 |
| Nuorikkala | 8:$z_4$,$z_{24}$:e,n,x | | Feed factory environment | Finland | 2010 | 10084/10 | NPHI | ST1719 |
| Gostenhof | 1,42:d:$z_6$ | | Human feces | Germany | 2009 | 10085/10 | IHU | ST1720 |
| Owerri | 6,14,25:l,$z_{13}$,$z_{28}$:1,6 | | Human feces | Norway (Nigeria) | 2010 | 10105/10 | NIPH | ST1721 |
| Braeswood | 47:c:$z_6$ | | Human feces | USA | 2009 | 10113/10 | CDC | ST1722 |
| Saintes | 13,23:d:e,n,x | | Human feces | France (Guinea) | 2010 | 10142/10 | IP | ST1723 |
| Perrosguirec | 4,12:$z_4$,$z_{23}$:e,n,$z_{15}$ | | Human feces | France (Cote d'Ivoire) | 2010 | 10146/10 | IP | ST1724 |
| **subsp. *salamae*** | | | | | | | | |
| | 3,15:$z_{87}$:e,n,x,$z_{15}$ | $Sal^+$, $ONPG^+$ | Reptile | Germany | 2007 | 9822/08 | BfR | ST1349 |
| | 11:$z_{41}$:e,n,x | $ONPG^+$ | Chamaeleon | Germany | 2008 | 9827/08 | BfR | ST1365 |
| | 3,10:a:$z_{87}$ | | Human feces | USA | 2008 | 9849/08 | CDC | ST1348 |
| | 9,12:g,m,t:$z_{39}$ | | Tea leaves | Germany | 2008 | 9880/09 | IHU | ST1725 |
| | 13,23:g,s,t:e,n,x | | Human | Germany | 2009 | 9944/09 | IHU | ST1726 |
| | 17:d:$z_6$ | $Dul^-$ | Human | Germany | 2009 | 9991/09 | RKI | ST1727 |
| | 6,7:z:e,n,x,$z_{15}$ | | Spice | France | 2009 | 9994/09 | IP | ST1728 |
| | 35:g,$z_{62}$:e,n,x | | Human feces | UK | 1994 | 9996/09 | PHE | ST1812 |
| | 6,7:b:1,5 | | Human feces | UK | 2000 | 10014/09 | PHE | ST1772 |
| | 13,22:g,m,t:$z_{42}$ | | Human feces | UK | 2001 | 10016/09 | PHE | ST1813 |
| | 1,9,12,46,27:b:$z_{39}$ | | Lizard | Germany | 2010 | 10090/10 | BfR | ST1729 |
| | 43:m,t:- | $ONPG^+$ | Chamaeleon | Germany | 2010 | 10134/10 | BfR | ST1730 |
| **subsp. *arizonae*** | | | | | | | | |
| | 51:$z_{36}$:- | | Human sputum | USA | 2008 | 9813/08 | CDC | ST1414 |
| | 17:g,$z_{51}$:- | | Bobcat lung | USA | 2007 | 9846/08 | CDC | ST1375 |
| **subsp. *diarizonae*** | | | | | | | | |
| | 48:k:$z_{57}$ | | Human | Poland | 2007 | 9785/08 | MUG | ST1731 |
| | 11:i:z | | River | USA | 2007 | 9809/08 | CDC | ST1265 |
| **subsp. *houtenae*** | | | | | | | | |
| | 30:g,m,t,$z_{51}$:-[d] | $Sal^-$ | Sea water | Bolivia | 1978 | 2193/78 | INLASA | ST1200 |
| | 48:$z_4$,$z_{24}$:- | | Human feces | USA | 2007 | 9810/08 | CDC | ST1732 |
| | 21:$z_{38}$:- | | Toucan bird | Brazil | 2008 | 9828/08 | BfR | ST1733 |

[a]Serovar previously described as belonging to *S. bongori* in Supplement 47 of the White-Kauffman-Le Minor scheme [8] but reassigned to *S. enterica* subsp. *enterica*

[b]The differential phenotypical characters of *Salmonella* species and subspecies are indicated in reference 7. Only the atypical results are mentioned. Tests used : β-galactosidase, ONPG ; galacturonate, Gal ; malonate, Mal ; salicin, Sal ; dulcitol, Dul ; L(+) tartrate (= *d*-tartrate), Dtar ;

h□□□□□□□□□□□□□□□□□, H2S . +, positive reaction ; -, negative reaction

[c]The National Reference Centres that sent the isolates are indicated in the acknowledgments section

[d]The reactivity to H:m and H:t factors depends on the brand of the antisera. The gelatinase test might be lately positive (5 days) or negative

**Table 3**. New variants of previously described *Salmonella* serovars recognized by the WHO Collaborating Centre for Reference and Research on *Salmonella*, 2008-2010.

| IP strain number | Antigenic formula | Other character[a] | Source | Area of contamination or isolation | Year | Received from[b] | Serovar name | MLST type | Updated antigenic formula |
|---|---|---|---|---|---|---|---|---|---|
| ***S. enterica* subsp. *enterica*** | | | | | | | | | |
| 9763/08 | 1,13,23:$z_4$,$z_{23}$:- | | Human feces | France | 2008 | IP | Ajiobo | ST1065 | 1,13,23:$z_4$,$z_{23}$:- |
| 9766/08 | 3,10:g,s,t:-:$Rz_{27}$ | | Poultry environment | La Réunion[c] | 2008 | IP | Westhampton | ST185 | 3,{10}{15}{15,34}:g,s,t:-:[$Rz_{27}$], [$Rz_{37}$] |
| 9768/08 | 1,4,5,12:z:1,2 | | Human feces | France | 2007 | IP | Shubra | ST1394 | 1,4,[5],12:z:1,2 |
| 9815/08 | 6,14,25:k:e,n,x | | Rosemary herb | Germany | 2008 | IHU | Trumersee | ST1701 | 1,6,14,25:k:e,n,x |
| 9838/08 | 45:m,t:-:$Rz_{45}$ | | Poultry | Senegal | 2008 | IP | Apapa | ST1049 | 45:m,t:-:[$Rz_{45}$] |
| 9957/09 | 1,3,19:d:l,w:$Rz_{45}$ | | Environment | France | 2009 | IP | Tilburg | ST1736 | 1,3,19:d:l,w:[$Rz_{45}$], [$Rz_{49}$] |
| 9959/09 | 4,12:b:e,n,$z_{15}$ | | Human feces | France | 2009 | IP | Wagenia | ST1667 | 1,4,12,[27]:b:e,n,$z_{15}$ |
| 10035/09 | 4,5,12:i:e,n,x | Dtar$^-$, Gas$^-$ | Poultry environment | France | 2009 | IP | Farsta | ST886 | 4,[5],12:i:e,n,x |
| 10087/10 | 3,15,34:d:e,n,x | | Horn | Germany | 2010 | RKI | Souza | ST1737 | 3,{10}{15}{15,34}:d:e,n,x |
| 10088/10 | 35:$z_{29}$:-:$Rz_{58}$ | | Lizard | Germany (Ghana) | 2010 | BfR | Widemarsch | ST1739 | 35:$z_{29}$:-:[$Rz_{58}$] |
| 10104/10 | 6,7:g,m,s:-:$Rz_{82}$ | | Poultry environment | Mayotte | 2009 | IP | Montevideo | ST195 | {6,7,14},{54}:g,m,[p],s:[1,2,7]:[$Rz_{82}$] |
| 10110/10 | 1,4,12,27:l,v:e,n,$z_{15}$ | | Human feces | France | 2010 | IP | Brandenburg | ST241 | 1,4,[5],12,[27]:l,v:e,n,$z_{15}$ |
| ***S. enterica* subsp. *salamae*** | | | | | | | | | |
| 10007/09 | 35:m,t:e,n,x | | Human feces | UK | 1997 | PHE | | ST1642 | 35:m,t:[e,n,x] |
| 10036/09 | 30:g,t:1,5 | | Human | Germany | 2009 | IHU | | ST1466 | 30:g,t:[1,5] |
| 10089/10 | 9,12:b:e,n,x | | Reptile | Germany | 2010 | BfR | | ST1843 | 1,9,12:b:e,n,x[d] |
| 10106/10 | 1,40:$z_{10}$:e,n,x | ONPG$^+$ | Chameleon | Germany | 2010 | RKI | | ST1636 | 1,40:$z_{10}$:e,n,x |
| ***S. enterica* subsp. *diarizonae*** | | | | | | | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 9780/08 | 47:c:e,n,x,$z_{15}$:$Rz_{84}$ | Snake | Canada | 2007 | PHAC | 47:c:e,n,x,z15: [$Rz_{57}$], [$Rz_{84}$] |
| 9874/09 | 48: l,v:1,5,7:$Rz_{90}$ | Reptile | Germany | 2009 | BfR | 48:l,v:1,5,(7): [$Rz_{47}$], [$Rz_{50}$], [$Rz_{70}$], [$Rz_{89}$], [$Rz_{90}$] |
| 9965/09 | 47:r:z:$Rz_{50}$ | Human feces | Korea | 2009 | KCDC | 47:r:z:[$Rz_{50}$] |
| 9973/09 | 60:r:e,n,x,$z_{15}$:$Rz_{55}$ | Snake | Germany | 2009 | BfR | 60:r:e,n,x,$z_{15}$:[$Rz_{55}$] |
| 9974/09 | 61:i:z:$Rz_{54}$ | Snake | Germany | 2009 | BfR | 61:i:z:[$Rz_{54}$] |
| 9993/09 | 48:r:z:$Rz_{50}$ | Poultry environment | La Réunion[c] | 2009 | IP | 48:r:z:[$Rz_{50}$] |
| 10028/09 | (6),14:$z_{10}$:z:$Rz_{57}$ | Poultry | France | 2009 | IP | (6),14:$z_{10}$:z:[$Rz_{56}$], [$Rz_{57}$], [$Rz_{90}$] |
| 10082/10 | 38:k:$z_{35}$:$z_{65}$ | Human feces | Finland | 2010 | NPHI | 38:k:$z_{35}$:[$z_{65}$] |
| 10112/10 | 48:l,v:1,5,7:$Rz_{70}$ | Snake | USA | 2009 | CDC | 48:l,v:1,5,(7): [$Rz_{47}$], [$Rz_{50}$], [$Rz_{70}$], [$Rz_{89}$], [$Rz_{90}$] |

[a]The differential phenotypical characters of *Salmonella* species and subspecies are indicated in reference 7. Only the atypical results are mentioned. Tests used : Gas production from glucose, Gas ; β-galactosidase, ONPG ; L(+) tartrate (= *d*-tartrate), Dtar ; +, positive reaction ; -, negative reaction

[b]The National Reference Centres that sent the isolates are indicated in the acknowledgments section

[c]French island in the Indian Ocean

[d]This antigenic formula was erroneously mentioned in the 9th edition of the White-Kauffmann-Le Minor scheme

1. **Table 4.** Present number of serovars in each species and subspecies of *Salmonella*.

| *S. enterica* | *n* |
|---|---|
| subsp. *enterica* | 1586 |
| subsp. *salamae* | 522 |
| subsp. *arizonae* | 102 |
| subsp. *diarizonae* | 338 |
| subsp. *houtenae* | 76 |
| subsp. *indica* | 13 |
| | |
| *S. bongori* | 22 |
| | |
| Total | 2 659 |

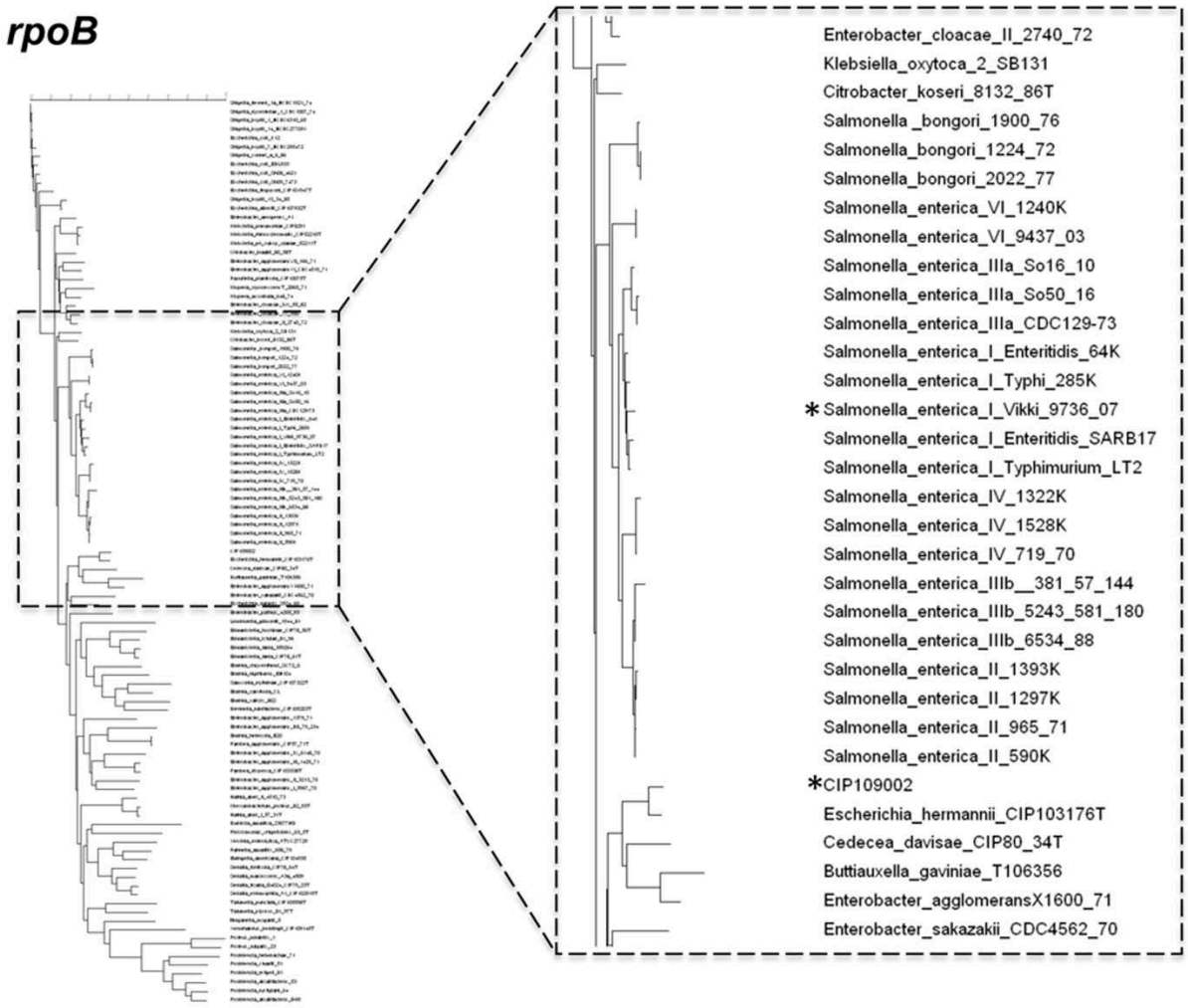


**Figure. Phylogenetic analysis of partial *rpoB* sequences of 103 strains of Enterobacteriaceae, including strains 9736/07 and CIP109002.** The analysis was done by the neighbour-joining method using BioNumerics version 6.6 software package (Applied Maths, Sint-Martens-Latem, Belgium). The partial *rpoB* sequences (about 1000 bp) were obtained by PCR using primers VIC4 (5'GGCGAAATGGCDGARAACCA-3') and VIC6 (5'-GGTTACAACTTCGARGAYTC-3') with conditions (annealing at 50°C) described previously [5]. The different *S. enterica* subspecies are indicated by symbols, I (subsp. *enterica*), II (subsp. *salamae*), IIIa (subsp. *arizonae*), IIIb (subsp. *diarizonae*), IV (subsp. *houtenae*), and VI (subsp. *indica*). The strains 9736/07 and CIP109002 are indicated with an asterisk.