**Serratia glossinae Geiger et al. 2010 is a later synonym of *Serratia fonticola* Gavini et al. 1979**

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*Serratia glossinae* DSM 22080\(^T\) was compared with *Serratia fonticola* ATCC 29844\(^T\) to clarify the taxonomic relationship of both species. 16S rRNA gene sequence comparisons demonstrated that these species share 99.6 % sequence similarity. Investigation of substrate utilization profiles displayed no striking differences from the type strains of both species. DNA–DNA hybridizations between both strains showed 100 % (99.9 %) similarity. Therefore, the reclassification of *S. glossinae* as a later synonym of *S. fonticola* is proposed, based upon the estimated phylogenetic position derived from 16S rRNA gene sequence data, biochemical data and DNA–DNA hybridization results.

*Serratia glossinae* was proposed by Geiger et al. (2010) for a bacterium isolated from the midgut of the tsetse fly *Glossina palpalis gambiensis*, one of the vector insects responsible for transmission of the trypanosomes that cause sleeping sickness in sub-Saharan African countries. *Serratia fonticola* had already described by Gavini et al. (1979) for a group of strains isolated from water. The two species were shown to be very similar on the basis of 16S rRNA gene sequence similarities, which was later supported by the close affiliation of the species obtained by a four protein coding gene based multilocus sequence analysis (MLSA) (Brady et al., 2013).

Comparison of the 16S rRNA gene sequences of both strains, *S. glossinae* DSM 22080\(^T\) (acc. no. FJ790328) and *S. fonticola* LMG 7882\(^T\) (= ATCC 29844\(^T\); acc. no. AVAH01000293), showed that the strains shared a sequence similarity of 99.6 %. A further comparative phenotypic analysis supported the close relationship.

Physiological/biochemical tests were performed with methods as described previously (Kämpfer, 1990; Kämpfer et al., 1991). On the basis of the methods according to Kämpfer et al. (1991), both strains were positive for acid production from D-glucose, lactose, sucrose, D-mannitol, dulcitol, salicin, adonitol, myo-inositol, sorbitol, L-arabinose, raffinose, L-rhamnose, maltose, D-xyllose, trehalose, methyl D-glucoside, erythritol, melibiose, D-arabitol and D-mannose. Acid production from cellobiose was negative. Both strains were positive for the hydrolysis of p-nitrophenyl (pNP) *α*--*D*-glucopyranoside, pNP *β*--*D*-glucopyranoside, aesculin, pNP *β*--*D*-galactopyranoside, pNP *β*--*D*-xylopyranoside, pNP-phosphorycholine, L-glutamate-gamma-3-carboxy-p-nitroanilide (NA), L-proline-pNA, bis-pNP-phosphate, 2-deoxythymidine-5'-thymidine-pNP-phosphate and L-alanine-pNA. Neither strain hydrolysed pNP *β*--*D*-glucuronide. The following compounds were utilized as a sole source of carbon by both strains: *N*-acetylglucosamine, *N*-acetylgalactosamine, cellobiose, D-galactose, gluconate, D-glucose, L-arabinose, maltose, salicin, D-mannose, D-fructose, glycerol, D-mannitol, maltitol, L-rhamnose, D-ribose, D-salicin, D-xyllose, adonitol, myo-inositol, D-sorbitol, acetate, putrescine, cis-aconitate, trans-aconitate, fumarate, DL-lactate, citrate, L-alanine, L-phenylalanine, L-serine, L-aspartate, L-histidine, L-proline, L-prolylalanine and phenylacetate. The following compounds were not utilized as a sole source of carbon by both strains: *α*-melibiose, sucrose, propionate, 4-aminobutyrate, adipate, azelate, glutarate, DL-3-hydroxybutyrate, mesaconate, itaconate, 2-oxoglutarate, pyruvate, suberate, *β*-alanine, L-ornithine, L-leucine, 3-hydroxybenzoate and 4-hydroxybenzoate.

*S. glossinae* DSM 22080\(^T\) produced urease and very weakly acetoin, and did not form acid from L-rhamnose, characteristics also reported by Geiger et al. (2010) as differentiating this strain from *S. fonticola*. *S. fonticola* ATCC 29844\(^T\) did not produce urease or acetoin and formed acid from L-rhamnose, as reported by Gavini et al. (1979). Lysine decarboxylase, ornithine decarboxylase, and alkalization of malonate and citrate were positive, while arginine dihydrolase, indole production and hydrogen-sulphide production were negative.

These results were essentially in accordance with those of Gavini et al. (1979) who studied 20 strains of *S. fonticola*, and who also reported variability in acid production from L-rhamnose.

DNA–DNA hybridization experiments were performed with strains *S. glossinae* DSM 22080\(^T\) and *S. fonticola* ATCC 29844\(^T\). DNA isolation and DNA–DNA hybridization were done as described by Ziemke et al. (1998). Results of the
DNA–DNA cross-hybridization yielded a similarity of 100 % and 99 % in the reciprocal analysis.

The MLSA sequence data published by Brady et al. (2013) were investigated with respect to sequence similarity comparisons (Table 1). *S. glossinae* CCUG 57457\(^T\) and *S. fonticola* LMG 7882\(^T\) shared 98.3 % sequence similarity of the concatenated partial gyrB, rpoB, infB and atpD nucleotide sequences (evolutionary distance 0.017); in contrast, the two strains shared \(\leq 92\) % sequence similarity (evolutionary distance \(\geq 0.08\)) with type strains of other species of the genus *Serratia*. At the level of amino acid sequences, *S. glossinae* CCUG 57457\(^T\) and *S. fonticola* LMG 7882\(^T\) shared identical amino acid sequences of the four housekeeping genes, except one amino acid exchange in the partial ATPD sequence. Amino acid sequence similarities to other species of the genus *Serratia* were much lower, 95.7–97.6 % amino acid sequence similarity for concatenated sequences. A universal species cut-off value based on MLSA data is not given, and need to be evaluated separately for each taxa and applied MLSA scheme (Tindall et al., 2010; Kämpfer & Glöser, 2012). Here the MLSA data support the data obtained by DDH analysis.

Table 1. Pairwise nucleotide and amino acid sequence distances and similarities of *S. fonticola* LMG 7882\(^T\) and *S. glossinae* DSM 22080\(^T\) to each other and to type strains of other species of the genus *Serratia* based in concatenated nucleotide and translated amino acid sequences of four housekeeping genes, gyrB, rpoB, infB and atpD (partial sequences)

Sequence data were taken from Brady et al. (2013). Phylogenetic distances were calculated in the MEGA 5 software package (Tamura et al., 2011). p-distances: only count nucleotide or amino acid sequence distances without counting evolutionary changes; evolutionary distances including an evolutionary model for base exchanges of nucleotide position were calculated using the Kimura two-parameter model (K2P; Kimura, 1980).

![Table 1](http://ijs.sgmjournals.org)

<table>
<thead>
<tr>
<th>Distances</th>
<th><em>S. glossinae</em>–<em>S. fonticola</em></th>
<th>To other <em>Serratia</em> type strains*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nucleotide sequence distances (p-distances)</td>
<td>0.017</td>
<td>0.078–0.116</td>
</tr>
<tr>
<td>Nucleotide sequence distances (K2P)</td>
<td>0.017</td>
<td>0.083–0.127</td>
</tr>
<tr>
<td>Amino acid sequence distances (p-distances)</td>
<td>0.002</td>
<td>0.024–0.043</td>
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<tr>
<th>Similarities†</th>
<th><em>S. glossinae</em>–<em>S. fonticola</em></th>
<th>To other <em>Serratia</em> type strains*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nucleotide sequence similarities (p-distances)</td>
<td>98.3 %</td>
<td>88.4–92.2 %</td>
</tr>
<tr>
<td>Nucleotide sequence similarities (K2P)</td>
<td>98.3 %</td>
<td>87.3–91.7 %</td>
</tr>
<tr>
<td>Amino acid sequence (AA) p-similarities</td>
<td>99.8 %</td>
<td>95.7–97.6 %</td>
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</table>

*Serratia nematodiphila* DSM 21420\(^T\), *Serratia liquefaciens* LMG 7884\(^T\), *Serratia plymuthica* LMG 7886\(^T\), *Serratia rubidea* LMG 5019\(^T\), *Serratia odorifera* LMG 7885\(^T\), *Serratia marcescens* subsp. *saukensis* CCM 7122\(^T\), *Serratia entomophila* LMG 8456\(^T\), *Serratia quinivorans* LMG 7887\(^T\), *Serratia grimesii* LMG 7883\(^T\) and *Serratia ficaria* LMG 7881\(^T\).

†Sequence similarities were calculated on the basis of sequence distances (either calculated as p-distances or with the K2P model).

The type strain is ATCC 29844\(^T\)=CCUG 14186\(^T\)=CCUG 37824\(^T\)=CIP 78.64\(^T\)=DSM 4576\(^T\)=IAM 1274\(^T\)=JCM 1242\(^T\)=LMG 7882\(^T\)=NBRC 102597\(^T\)=NCTC 12965\(^T\).

### References

Brady, C., Cleenwerck, I., Venter, S., Coutinho, T. & De Vos, P. (2013). Taxonomic evaluation of the genus Enterobacter based on multilocus sequence analysis (MLSA): proposal to reclassify *E. nimbipressuralis* and *E. amnigenus* into *Lelliottia* gen. nov. as *Lelliottia nimbipressuralis* comb. nov. and *Lelliottia amnigena* comb. nov., respectively, *E. gergoviae* and *E. pyrus* into *Pluralibacter* gen. nov. as *Pluralibacter gergoviae* comb. nov. and *Pluralibacter pyrus* comb. nov., respectively, *E. cowani*, *E. radicicinans*, *E. oryzae* and *E. arachidis* into *Kosakonia* gen. nov. as *Kosakonia cowani* comb. nov., *Kosakonia radicicinans* comb. nov., *Kosakonia oryzae* comb. nov. and *Kosakonia arachidis* comb. nov., respectively, and *E. turicensis*, *E. helveticus* and *E. pulvis* into *Cronobacter* as *Cronobacter zurichensis* nom. nov., *Cronobacter helveticus* comb. nov. and *Cronobacter pulvis* comb. nov., respectively, and emended description of the genera *Enterobacter* and *Cronobacter*. Syst Appl Microbiol 36, 309–319.


