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Genomic characterization of a human Salmonella Carrau isolate from Brazil carrying an IncM1 plasmid with six resistance genes

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Abstract

Purpose

Salmonella enterica serovar Carrau is a rare serovar recovered mostly from environmental, animal and food sources; human isolates have been reported in Brazil, but their genomic features and resistance determinants remain undocumented. Here we characterize a human *S. Carrau* isolate from Brazil.

Methods

Isolate Sal_821 – 22, from a fecal swab of a patient with sporadic gastroenteritis in 2022, was tested for antimicrobial susceptibility and sequenced (Illumina MiSeq). We performed multilocus sequence typing, resistome, virulome and plasmid characterization, and a phylogeny against 411 public *S. Carrau* genomes.

Results

The isolate belongs to a new sequence type (ST), ST14511, differing from ST226 only at *hisD*. It was resistant to ceftazidime, intermediate to cefoxitin, ciprofloxacin and nalidixic acid, and susceptible to imipenem and nitrofurantoin. An IncM1 plasmid reconstruction (~ 70 kb) carries *blaCTX-M-8*, *blaTEM-1*, *blaOXA-9*, *qnrE1*, *aadA1* and *aac(6')-Ib* in a cluster of attC sites lacking an integrase (CALIN); a mobilizable ColE plasmid carries *qnrB19*. The IncM1 sequence is nearly identical (99.990% average nucleotide identity) to that of the only other Brazilian human *S. Carrau* genome, GCA_053411395.1, although the chromosomes differ by 473 single-nucleotide polymorphisms; both align collinearly with a closed IncM1 plasmid of *Klebsiella pneumoniae*.

Conclusion

This is, to our knowledge, the first published genomic characterization of a human *S. Carrau* isolate from Brazil, but not the first human isolation or the first public human genome from Brazil. Almost identical IncM1 plasmids in chromosomally distinct hosts are compatible with horizontal dissemination, but route, direction and timing cannot be determined from these data.

1. Introduction

Salmonella enterica is among the main causes of foodborne illness worldwide, with an estimated 93.8 million cases and 155 000 deaths a year from non-typhoidal serovars [1, 2]. Whole-genome sequencing is now the reference method for serovar assignment, resistance prediction and outbreak tracing in *Salmonella* surveillance [3].

More than 2600 serovars are described under the Kauffmann-White-Le Minor scheme, and a small number account for most human cases, while rare serovars circulate in environmental and animal reservoirs and are seldom characterized at genomic level [4, 5].

Serovar Carrau (antigenic formula 6,14,[24]:y:1,7) was first described in 1944 from swine in Uruguay and has since been reported sporadically from animals, food and aquatic environments; human isolates are rare in the indexed literature. In Brazil, *S. Carrau* has been identified among human *Salmonella* isolates, including three cases in a serovar survey from Pará covering 1991 to 2008 [6], and [7] found it to be the most prevalent rare serovar in surface waters of the Northeast. Genomic data for human isolates remain scarce.

Non-typhoidal *Salmonella* producing extended-spectrum beta-lactamases, particularly CTX-M enzymes, has been spreading through large plasmids [8, 9]. In Brazil, *blaCTX-M-8* has been found in *Salmonella* from food, animals and clinical isolates [10, 11].

Here we present the first published genomic characterization of a human isolate of *Salmonella enterica* serovar Carrau from Brazil, recovered from a sporadic case of acute gastroenteritis in 2022, with attention to an IncM1 plasmid carrying six resistance genes and a separate mobilizable ColE-type plasmid carrying *qnrB19*.

2. Materials and methods

2.1 Isolate origin and clinical context

The strain Sal_821 – 22, isolated by the Ceará State Reference Laboratory (LACEN-CE), was recovered on Hektoen enteric agar from a fecal swab of a patient with sporadic acute gastroenteritis in 2022 and sent to the Laboratory of Enterobacteria, Oswaldo Cruz Institute (Fiocruz-RJ), the National Reference Laboratory for enteric pathogens. Serotyping followed the Kauffmann-White-Le Minor scheme and was confirmed in silico with SeqSero2. No treatment or outcome data were available.

2.2 Antimicrobial susceptibility testing

Antimicrobial susceptibility was assessed by disk diffusion (Kirby-Bauer) for ceftazidime, cefoxitin, nalidixic acid, ampicillin-sulbactam, gentamicin, streptomycin, trimethoprim-sulfamethoxazole, nitrofurantoin and imipenem, and by MIC for ciprofloxacin, with interpretation by CLSI breakpoints for Enterobacterales [12].

2.3 Whole-genome sequencing

DNA was extracted with the Qiagen DNeasy kit, libraries were prepared with Illumina DNA Prep and paired-end sequencing (2 x 250 bp) was performed on an Illumina MiSeq. Read quality was checked with FastQC v0.11.9 [13].

2.4 Genome assembly

De novo assembly used Unicycler v0.5.1 [14] in default mode, and assembly metrics were obtained with QUAST v5.2.0 [15] and completeness with BUSCO v6.0.0 (bacteria_odb12).

2.5 Molecular typing and genomic characterization

Sequence typing followed the Achtman seven-locus scheme hosted in EnteroBase [16]; the assembly was submitted to EnteroBase, which performed allele calling and sequence-type assignment, and hierarchical clustering levels (HierCC) were retrieved from the same record. Of the 429 records identified for *S. Carrau* in EnteroBase, every genome available for download was retrieved, with no filtering by assembly quality, together with the Brazilian environmental genomes of [7] from NCBI; both sets were accessed in September 2026. Records present in both repositories were identified through the EnteroBase Sample field and deduplicated, leaving 411 non-duplicated genomes for comparative analysis. Genome identifier, source, year and country of each genome are listed in Table S1.

Acquired resistance genes were screened in the 411 comparative genomes and in Sal_821 − 22 with ABRicate v1.0.1 and the ResFinder database [17]; ≥80% identity and coverage; the resistome of Sal_821 − 22 was also characterized with AMRFinderPlus v4.2.5 [18], whose database is more closely curated. Chromosomal mutations were screened with PointFinder in Sal_821 − 22 only, so the comparison across the 411 genomes covers acquired genes and not point mutations. Insertion sequences and metal or biocide resistance genes were screened with ISFinder and BacMet [19, 20]. Multidrug resistance refers throughout to the genotype, defined as acquired determinants for three or more antimicrobial classes, and is not a phenotypic classification. To place the two Brazilian isolates in a wider context, the AMR genotypes computed by NCBI Pathogen Detection for every *S. Carrau* isolate in that system were retrieved (240 isolates, eight countries, October 2014 to September 2026; accessed September 2026) and used only for the frequency of resistance determinants.

Plasmids were characterized with PlasmidFinder v2.1; Enterobacteriaceae database, 2025-03 release; ≥95% identity, ≥ 60% coverage; [21] and MOB-suite v3.1.4 [22]. In both Brazilian plasmids PlasmidFinder returned a single replicon, IncM1, at 99.46% identity over the full 739 bp of the template (U27345), and MOB-suite returned IncL/M, the former designation of the same incompatibility group [21]. No pMLST scheme exists for this group, so the plasmid was not subtyped; since neither plasmid was circularized, the element is referred to throughout as an IncM1 plasmid reconstruction. Contigs were annotated with Bakta v1.11.4 and visualized in PROKSEE.

Salmonella pathogenicity islands (SPIs) were screened with ABRicate v1.0.1 and the SPIFinder database [23]; virulence genes with VFDB [24] at ≥ 80% identity and coverage.

2.6 Phylogenetic analysis

A SNP-based maximum-likelihood phylogeny (N = 411; Table S1) was built by mapping assemblies against GCA_010570565.1 (BioSample SAMN15949847) with Minimap2 v2.28, Samtools and BCFtools [25, 26], masking recombination with Gubbins [27] and inferring the tree with IQ-TREE v2.2.0 under the best-fit model with 1000 ultrafast bootstrap (UFBoot) replicates [28, 29]; trees were visualized in iTOL v7

[30] and pairwise distances generated with snp-dists v0.8.2 [31]. No closed *S. Carrau* genome was available, so GCA_010570565.1 was chosen as reference for having the fewest contigs and the highest N50 among the *S. Carrau* assemblies in the dataset.

2.7 Pangenome analysis

Pangenome analysis used Bakta v1.11.4 [32] and Panaroo v1.5.0 [33] on the 89 genomes of the clade closest to Sal_821 – 22 (core ≥ 99%, soft-core ≥ 95%, shell ≥ 15%, cloud < 15%); UpSet plots were used for gene-content intersections.

2.8 Comparative plasmid analysis between Brazilian human isolates

To test whether the IncM1 plasmid of Sal_821 – 22 is shared with GCA_053411395.1, the only other Brazilian human *S. Carrau* genome, plasmid contigs of both were reconstructed with MOB-suite v3.1.4 and compared by BLASTN; sequence identity was calculated as the proportion of identical positions across gap-free aligned nucleotides and is reported with alignment length, coverage and mismatch counts. Average nucleotide identity was calculated with pyOrthoANI v0.7.0 [34]. Because neither plasmid was circularized, both were aligned against a closed reference to assess synteny: the closest match in PLSDB 2025 [35] was CP027699.1, a circular 71 749 bp plasmid of *Klebsiella pneumoniae* (GCF_003368025.1), retrieved at a Mash identity of 0.9993. Alignments were produced with NUCmer from MUMmer4 [36].

2.9 Integron detection

Integrons and clusters of attC sites lacking an integron-integrase (CALIN) were identified with IntegronFinder v2.0.6 (--local-max --func-annot) in Sal_821 – 22 and across the 411 genomes.

2.10 Prediction of bacterial defense systems

Anti-phage and anti-MGE defense systems were predicted with DefenseFinder v2 [37] in Sal_821 – 22 and across the 411 genomes; a system was counted as complete only when every mandatory profile was detected in the expected order and within the distance allowed by the model. Full outputs are given as supplementary material.

2.11 Use of AI-assisted tools

The authors used Gemini to assist in writing the R script used for pangenomic graph generation. The authors verified and validated all code and results and take full responsibility for the content.

2.12 Sequence data deposition

The genome assembly, including the plasmid pSal_821 – 22_qnrB19, was submitted to GenBank under BioProject PRJNA1543598 and BioSample SAMN64192748 (submission SUB16555388).

3. Results

3.1 Antimicrobial susceptibility profile

Isolate Sal_821 – 22 was resistant to ceftazidime and intermediate to cefoxitin, ciprofloxacin and nalidixic acid, and susceptible to ampicillin-sulbactam, gentamicin, streptomycin, trimethoprim-sulfamethoxazole, imipenem and nitrofurantoin; ciprofloxacin was tested by MIC and the remaining agents by disk diffusion. Resistance was recorded for a single antimicrobial category and the panel does not cover every category of the scheme of Magiorakos et al. [38], so no phenotypic multidrug-resistance classification is made. The isolate carries acquired determinants for three antimicrobial classes, β-lactams (*blaCTX-M-8*, *blaTEM-1*, *blaOXA-9*), aminoglycosides (*aac(6')-Ib*, *aadA1*) and quinolones (*qnrE1*, *qnrB19*), and is therefore described as having a multidrug resistance genotype. No carbapenemase gene was found, and PointFinder detected no resistance-associated mutation in the quinolone resistance-determining regions of gyrA, gyrB, parC or parE; the only change was parC p.T57S, a polymorphism widespread in *Salmonella enterica* with no known effect on its own [39].

3.2 Genomic characterization and sequence type

The assembly comprised 94 contigs with an N50 of 94 104 bp (QUAST) and 99.1% BUSCO completeness (bacteria_odb12), values typical of short-read *Salmonella* assemblies and sufficient for typing, resistome and virulome analyses, though fragmentation limits resolution of repetitive regions and plasmid junctions. EnteroBase assigned the isolate to ST14511, a new sequence type defined by a new *hisD* allele (2481). The full allele profile is *aroC* 84, *dnaN* 76, *hemD* 38, *hisD* 2481, *purE* 12, *sucA* 13 and *thrA* 4; ST226 has the same alleles at the other six loci and *hisD* 16, so ST14511 is a single-locus variant of ST226. Sal_821 – 22 is at present the only genome with this ST in EnteroBase and forms a singleton at the HC200 level (clusters defined by up to 200 core-genome MLST allele differences).

3.3 Antimicrobial resistance genes and plasmids

MOB-suite and AMRFinderPlus, with visualization in PROKSEE, identified two plasmids carrying antimicrobial resistance genes:

Plasmid pSal_821 – 22 (70 852 bp; Fig. 1a): a large IncM1 plasmid reconstruction carrying six resistance genes (*qnrE1, blaTEM-1, blaOXA-9, aadA1, aac(6')-Ib* and *blaCTX-M-8*) within an approximately 15 kb resistance region embedded in the IncM1 backbone.

Replicon sequences and multiple transfer genes and mobilization genes were detected on the same contigs, a structure consistent with IncM1 plasmids. Against the closed reference CP027699.1 the reconstruction covered 98.42% at 99.95% identity (NUCmer; see Comparative Analysis below).

Plasmid pSal_821 – 22_qnrB19 (2989 bp; Fig. 1b): a small mobilizable ColE-type plasmid, circularized by Unicycler, carrying the quinolone resistance gene *qnrB19* together with a ColE-type origin of replication, an RNAI regulatory element, an origin of transfer (oriT) and two putative mobilization CDS. It matched plasmid CP045448.1 of *Salmonella enterica* serovar Schwarzengrund at 100% identity across gap-free aligned positions and 100% coverage.

3.4 Comparative analysis of IncM1 plasmids from Brazilian human isolates

AMRFinderPlus on the plasmid reconstructed from GCA_053411395.1 (Brazil, 2025) found the same six resistance genes as pSal_821 − 22: *blaCTX-M-8*, *blaTEM-1*, *blaOXA-9*, *qnrE1*, *aac(6')-Ib* and *aadA1*, all at 100% identity and coverage except *aadA1* (98.48%/99.61%). The *qnrB19* gene, carried by Sal_821 − 22 on pSal_821 − 22_qnrB19, was absent from GCA_053411395.1.

Pairwise BLASTN between pSal_821 − 22 (70 852 bp) and the GCA_053411395.1 plasmid (71 852 bp) covered 99.63% and 98.31% of each sequence, with 7 differences over 70 588 gap-free aligned positions and 99.990% OrthoANI (Fig. 1a), while the chromosomes differ by 473 core-genome SNPs. To assess architecture rather than identity alone, both were aligned against CP027699.1, a closed 71 749 bp IncM1 plasmid of *Klebsiella pneumoniae* and the nearest match in PLSDB. The GCA_053411395.1 plasmid is a single contig covering the whole reference at 99.96% identity in two blocks meeting at the circular junction, so the sequences are collinear and differ by a rotation of the starting point. In Sal_821 − 22 the plasmid is distributed over three contigs (46 838, 21 636 and 2378 bp) tiling 98.42% of the reference in the same order at 99.95% identity; the largest contig aligns to both ends of the circular reference, which indicates that it spans the origin, and the reverse orientation of the 21 636 bp contig reflects assembly rather than inversion. Two reference segments of about 570 bp fall between contig boundaries and were not confirmed as deletions. No rearrangement, inversion or translocation was detected within the aligned regions; unresolved junctions limit exclusion of further structural differences, and whether transfer occurred between these two hosts or each lineage acquired a similar plasmid independently cannot be established from genomic data alone. GCA_053411395.1 came from a blood culture in São Paulo and was deposited in November 2025, with no accompanying publication. Across the 240 *S. Carrau* isolates with AMR calls in NCBI Pathogen Detection, only one carried the six-gene resistance profile, GCA_053411395.1 from Brazil (Table S4); the remaining isolates carried either the chromosomal determinants mdsA and mdsB alone, a single acquired determinant or a chromosomal resistance-associated mutation. Screening the 65 assemblies available for download, after removing records already in the EnteroBase set, found no further multi-gene profile. Because the collection is dominated by clinical isolates from the United States (179 of 240), these genotype-based frequencies should not be read as global estimates for the serovar.

3.5 Integron analysis

IntegronFinder identified a CALIN element in contig NODE_37 (46 838 bp), assigned by MOB-suite to pSal_821 − 22 and with ~ 45.8x coverage, about 2.4x the chromosomal mean, which is circumstantial evidence for plasmid location. The element spans four cassette positions in the *attC*_4 model, three of which carry resistance genes; no *intI* gene was detected, consistent with the classification as CALIN (Fig. 2).

3.6 *Salmonella* pathogenicity islands (SPIs)

All 11 SPIs, SPI-5 included, were detected with the default ABRicate settings (Fig. 3). The principal SPI-5 effector gene, *sopB/sigD*, was also recovered by VFDB at ≥ 80% identity and coverage.

3.7 Virulence factors and pangenome

VFDB (≥ 80% identity and coverage; Table S1a) identified 149 virulence genes, including all screened structural and effector genes of T3SS-1 and T3SS-2, the Fim and Csg fimbrial operons, and a cdtB allele closely related to that of *S.* Typhi.

For the pangenome we used the 89 genomes of the clade closest to Sal_821 − 22 in the global tree (Fig. 4, right panel).

The pangenome of the 89-genome clade comprised 8673 gene clusters, of which 3774 were core; Sal_821 − 22 contained 4415 clusters (Figure S1).

Thirteen genes were unique to Sal_821 − 22, most of them phage-related, plus one DNA methyltransferase (Table S2).

Functional annotation of the 92 genes shared only by Sal_821 − 22 and GCA_053411395.1 returned mobilization and transfer proteins and the resistance cassette (Fig. 5).

3.8 Comparative genomic context across 411 *S.* Carrau genomes

DefenseFinder identified seven complete defense systems in Sal_821 − 22 (Table S3); such systems were common across the 411 genomes (94.2%), and both IncM1-bearing isolates sat above the population median, so these counts are descriptive only. IS26 occurred in both IncM1-bearing isolates but is chromosomal in each, and the plasmid carries a truncated IS10R relic at the same position in both; neither is associated with the resistance cassette, which lies within the CALIN region of the backbone. BacMet found no metal resistance gene restricted to these isolates. Integron-associated elements occurred in 5 of the 411 genomes (1.2%), and AMR-carrying CALIN elements only in the two IncM1-bearing isolates, which share the same four cassette positions between two *attC* sites.

4. Discussion

We present the first published genomic characterization of a human isolate of *Salmonella enterica* serovar Carrau from Brazil, not the first human isolation of this serovar in the country. Human *S. Carrau* had already been recorded in Brazil in a serovar survey published in 2010 [6], which reported no whole-genome data and no analysis of resistance plasmids, and [7] later found the serovar to be the most prevalent rare serovar in surface waters of the Northeast. Our contribution is genomic resolution, not priority for the first human occurrence.

The contrast between environmental prevalence and the scarcity of human cases is more likely due to surveillance effort than to an intrinsic barrier: rare serovars are under-sequenced, and detection depends on where laboratories look.

4.1 Sequence type ST14511 and its relationship to ST226

Of the 429 EnteroBase records, 392 *S. Carrau* records (91.4%; accessed September 2026) are assigned to ST226, including GCA_053411395.1 and the genomes closest to Sal_821 – 22 in the phylogeny. Sal_821 – 22 differs from ST226 at a single locus, *hisD*, and for that reason received a new designation, ST14511. One allele out of seven does not make a new lineage: the SNP phylogeny places the isolate inside a well-supported clade, 196 SNPs from its nearest neighbour, and its singleton status at HC200 says only that no genome within 200 allele differences has been deposited so far. Whether the *hisD* allele arose in Brazil or was imported cannot be told from one genome.

4.2 Resistance genotype and phenotype

Among the determinants carried by the IncM1 plasmid reconstruction, *blaCTX-M-8* is frequently reported in Brazilian Enterobacterales [8, 40] and sits here in a mobile cassette, a context compatible with acquisition from *Escherichia coli* or another Enterobacterales host. The combination of *qnrE1* and *qnrB19* is unusual; both are associated with reduced fluoroquinolone susceptibility and may contribute to the intermediate phenotype observed, although the contribution of each was not assessed and chromosomal mechanisms cannot be excluded [41, 42]. All genotype-phenotype statements here are associations: no conjugation, transformation or knockout experiment was performed, and no treatment or outcome data were available for the patient.

No carbapenemase gene was detected and the isolate was susceptible to imipenem and nitrofurantoin. The cephalosporin phenotype is accounted for by *blaCTX-M-8* and the reduced quinolone susceptibility by the qnr genes, whereas the intermediate result for cefoxitin, a cephamycin poorly hydrolysed by CTX-M enzymes, is not explained by the resistome and remains without an identified genetic basis in this genome.

4.3 Virulence-associated gene content

The T3SS-1 and T3SS-2 genes detected here encode systems associated in other serovars with enterocyte invasion and intracellular survival; the csg operon is associated with biofilm formation; and a cdtB allele closely related to that of *S.* Typhi was detected. All of these are genomic markers: the analysis records gene presence and says nothing about expression, invasion, cytotoxicity or disease severity in this isolate.

4.4 Interpretation of the pangenome analysis

The core genome of Sal_821 – 22 shows no reduction relative to the other genomes of the clade, so the isolate shares the gene repertoire of its clade. In the IncM1 backbone, cassettes flanked by *attC* sites with no *intI* gene are consistent with a remnant of a class 1 integron, but the mechanism and timing of

acquisition remain untested hypotheses. The comparative analyses across the 411 genomes are exploratory and generate hypotheses rather than explanations for the confinement of IncM1-associated resistance to two isolates.

The 92 genes shared only by Sal_821 – 22 and GCA_053411395.1 are mostly the IncM1 plasmid itself: the resistance cassette, the transfer module and the backbone. With two isolates, the data are consistent with, but do not prove, circulation of the whole plasmid rather than of its resistance genes alone. In Brazil, *blaCTX-M-8* has been described on IncI1/pST113 plasmids of *Escherichia coli* from cattle [6], a different backbone from the IncM1 plasmid found here. Sal_821 – 22 came from gastroenteritis and GCA_053411395.1 from blood, so the same cassette has been found in an intestinal and an invasive infection.

4.5 Phylogeny

In the core-genome SNP phylogeny (Fig. 4), Sal_821 – 22 fell within a well-supported clade of 89 genomes (UFBoot 100%), apart from the main cluster; in the global tree 55% of internal nodes had UFBoot ≥ 95%. Within its clade, Sal_821 – 22 paired with SAL_BE5158AA_AS (196 SNPs; human, United States, 2021), and this pair was sister to SAL_PE6508AA_AS (440 SNPs) plus GCA_053411395.1 (473 SNPs), all at UFBoot 100%. Pairwise distances among these four genomes ranged from 196 to 488 SNPs (Table 1); the two Brazilian isolates differ by 473 SNPs, close to the clade median of 444, and no pair falls within the range usually associated with recent transmission in *Salmonella*. The three closest isolates are human, but the dataset is weighted toward human clinical isolates (288/411; 70%), so this should not be read as a human-adapted sublineage.

Table 1
Pairwise core-genome SNP distances between Sal_821 – 22, the other Brazilian human isolate (GCA_053411395.1) and the two genomes closest to Sal_821 – 22 in the phylogeny.

Genome	Country	Year	Source	(1)	(2)	(3)	(4)
(1) Sal_821 – 22	Brazil	2022	Human	0	196	440	473
(2) SAL_BE5158AA_AS	USA	2021	Human	196	0	471	488
(3) SAL_PE6508AA_AS	USA	2025	Human	440	471	0	372
(4) GCA_053411395.1	Brazil	2025	Human	473	488	372	0

4.6 Study limitations

The main limitations are these. (i) The study rests on a single case, so no population-level inference is possible. (ii) Neither exposure data nor the age and sex of the patient were available. (iii) Only short-read sequencing was performed, so plasmid structures may be incomplete at contig junctions and structural differences between the two IncM1 plasmids cannot be resolved without long-read sequencing. (iv) Although the nodes placing Sal_821 – 22 and GCA_053411395.1 received UFBoot 100%, about 45% of

internal nodes in the global tree and 28% in the clade had UFBoot below 95%, so finer relationships should be read with caution.

5. Conclusion

Isolate Sal_821 – 22, from a sporadic case of gastroenteritis in 2022, belongs to ST14511, a single-locus variant of ST226, and carries a multidrug resistance genotype: *blaCTX-M-8*, an ESBL determinant frequently reported in Brazilian Enterobacterales, plus *qnrE1* on the IncM1 plasmid reconstruction and *qnrB19* on a mobilizable ColE-type plasmid.

Sal_821 – 22 belongs to a well-supported sublineage whose closest members are human isolates from the United States, with no separate Brazilian clade. GCA_053411395.1 forms a distinct sublineage within the same clade (473 SNPs) while carrying an almost identical resistance cassette, so the two Brazilian human isolates belong to distinct chromosomal lineages carrying highly similar IncM1 plasmids.

S. Carrau should be considered for inclusion in *Salmonella* genomic surveillance in Brazil, with attention to the blaCTX-M-8-carrying IncM1 plasmid across human, animal, food and environmental isolates. These findings rest on one case and two sequenced human isolates and do not allow epidemiological conclusions.

Abbreviations

CALIN, cluster of attC sites lacking an integron-integrase; HierCC, hierarchical clustering of core-genome MLST; MLST, multilocus sequence typing; SNP, single-nucleotide polymorphism; SPI, *Salmonella* pathogenicity island; ST, sequence type; UFBoot, ultrafast bootstrap.

Declarations

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Competing interests

The authors have no relevant financial or non-financial interests to disclose.

Ethics approval

Ethical approval was not required. Isolate Sal_821-22 was sent to the national reference laboratory for enteric pathogens as part of routine surveillance, and the only patient information used in this study is the source and year of isolation.

Data availability

The genome assembly, including the plasmid pSal_821-22_qnrB19, was submitted to GenBank under BioProject PRJNA1543598 and BioSample SAMN64192748 (submission SUB16555388). The 411 comparative *S. Carrau* genomes, with their metadata, are listed in Table S1.

Author contributions

André Felipe das Mercês Santos - conceptualization, methodology, formal analysis, software, writing – original draft; Mariane Verinaud Soares - formal analysis, writing – review and editing, conceptualization, investigation; Pedro Panzenhagen - writing – review and editing, methodology, software; Maria Eduarda Moreira da Costa Miranda - investigation; Joyce Figueira Pereira de Souza - investigation; Laura Fabiana Vieira do Amparo - investigation; Maria Luiza Paula Pereira - investigation; Karene Ferreira Cavalcante – resources; Angela Maria Veras Stolp – resources; Thais Magalhães de Freitas – resources; Patrícia Carvalho Sequeira - project administration. All authors reviewed and approved the final version of the manuscript.

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