Draft Genome Sequences of 27 *Salmonella enterica* Serovar Schwarzengrund Isolates from Clinical Sources

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**ABSTRACT** Twenty-seven *Salmonella enterica* serovar Schwarzengrund isolates from clinical sources were sequenced as part of a larger study to examine phenotypic and genotypic characteristics. The majority of the sequenced strains were isolated from human stool (n = 20) followed by urine (n = 3) and blood (n = 2). Four isolate sequences contained plasmids of known incompatibility groups.

*Salmonella enterica* serovar Schwarzengrund strains can cause salmonellosis in humans and infections in other animal species (1). The spread of multidrug-resistant *S.* Schwarzengrund from imported food products to humans has been reported (1). *S.* Schwarzengrund strains isolated from imported food products have been found to display a high level of resistance to fluoroquinolones (2). Furthermore, the production of extended-spectrum β-lactamase (ESBL), including carbapenemase (KPC-2), by *S.* Schwarzengrund has been found in different countries, which concerns observers (3–5). ESBL genes are often encoded on plasmids (3, 4, 6), which can facilitate their rapid transfer among Gram-negative pathogens, and this has created a major public health concern. Therefore, monitoring antimicrobial resistance (AMR) dynamics and characterization of mobile genetic elements, including plasmids of *S.* Schwarzengrund isolated from domestic and imported foods, food animals, and humans, is important. In the present study, whole-genome sequencing analyses of *S.* Schwarzengrund isolates from clinical sources will facilitate the study of AMR and resistance transmission.

Twenty-seven *S.* Schwarzengrund isolates from clinical sources were collected from the Minnesota Department of Health (Saint Paul, MN) and sequenced at the Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration (Jefferson, AR). Epidemiological information for these isolates is listed in Table 1.

Stool samples were plated on Hektoen enteric agar, salmonella-shigella agar, and enrichment broths (Becton, Dickinson and Company [BD], Franklin Lakes, NJ). The plate or broth was then incubated at 35°C for 18 to 24 h. Colonies that were suspiciously lactose negative and positive for H₂S were subsequently inoculated in motility-indole-lysine agar, triple sugar iron agar, and a urea agar plate (BD). Identification was confirmed using matrix-assisted laser desorption ionization–time of flight mass (MALDI-TOF) spectrometry. Likewise, blood and other clinical isolates were identified using standard microbiological procedures.

The total bacterial DNA was extracted with a DNeasy blood and tissue kit (Qiagen, Valencia, CA), and DNA sequencing libraries were constructed with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA). Samples were multiplexed with a unique combination of two indexes of the Nextera XT index kit. Whole-genome sequencing (WGS) reactions were carried out on an Illumina MiSeq instrument with a 2 × 300 paired-end format (7). Trimming and *de novo* assembly were performed with
CLC Genomics Workbench (v. 9, Qiagen, Germantown, MD). Genome sequences from individual samples were examined simultaneously with individual annotation tools, such as Rapid Annotation using Subsystem Technology (RAST) (8) and Pathosystems Resource Integration Center (PATRIC) (9), to cross-examine the sequence data. Subsequently, sequences were submitted to the NCBI using the WGS submission portal for final annotation with the Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (10) (Table 1). The number of contigs, assembly size, coding sequences (CDSs), and G+C contents of each sample included in Table 1 were annotated with PATRIC. Annotation performed with the PGAAP was used as the final annotation available in the NCBI. We applied default settings for the bioinformatic software tools used for sequence trimming, de novo assembly, and annotation of the sequences.

Among 27 S. Schwarzengrund clinical isolates, PlasmidFinder (11) analyses showed that four of the isolates contained plasmids of identified incompatibility (Inc) groups. MDH-8 contained the IncHI2 and IncHI2A plasmids, and MDH-18, MDH-20, and MDH-25 contained the IncI1 plasmid. ResFinder (12) analyses showed that MDH-8 contained the aph(6)-Id, strA, and tet(B) resistance genes; MDH-18 and MDH-20 contained the aph(3')-Ia and bladMV-2 genes; and MDH-25 contained the aac(3)-Vla, adaA1, and sul1 genes.

Data availability. This whole-genome shotgun project is deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1, and the SRA submission of raw data (FastQ format) is recorded under the accession number PRJNA312617.

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### Table 1: Whole-genome sequencing analyses of *Salmonella* Schwarzengrund isolates from clinical sources

| Strain no. | Source of isolate | Yr of isolation | No. of sequence reads | N_50 value (bp) | No. of contigs | Assembly size (bp) | No. of CDSs | G+C content (%) | GenBank accession no. |
|-----------|------------------|----------------|-----------------------|----------------|---------------|-------------------|-------------|-----------------|----------------------|
| MDH-1     | Blood            | 2003           | 4,813,548             | 255,417        | 61            | 4,771,771        | 4,845       | 52.2            | QZET00000000         |
| MDH-2     | Stool            | 2003           | 3,729,214             | 340,162        | 56            | 4,775,162        | 4,828       | 52.2            | QZES00000000         |
| MDH-3     | Stool            | 2004           | 3,706,472             | 112,364        | 100           | 4,684,005        | 4,717       | 52.1            | QZER00000000         |
| MDH-4     | Stool            | 2004           | 3,221,282             | 167,201        | 80            | 4,674,736        | 4,715       | 52.1            | QZEQ00000000         |
| MDH-5     | Stool            | 2004           | 4,754,358             | 149,628        | 118           | 4,715,784        | 4,767       | 52.0            | QZEQ00000000         |
| MDH-6     | Stool            | 2005           | 3,945,558             | 138,815        | 101           | 4,774,615        | 4,854       | 52.2            | QZEO00000000         |
| MDH-7     | Stool            | 2005           | 4,316,768             | 93,969         | 128           | 4,775,144        | 4,853       | 52.2            | QZEN00000000         |
| MDH-8     | Stool            | 2006           | 2,438,762             | 91,707         | 158           | 5,117,666        | 5,291       | 51.6            | QZEM00000000         |
| MDH-9     | Stool            | 2007           | 3,737,938             | 85,408         | 119           | 4,700,238        | 4,787       | 52.0            | QZEL00000000         |
| MDH-10    | Stool            | 2007           | 4,576,284             | 102,545        | 106           | 4,693,974        | 4,766       | 52.0            | QZEK00000000         |
| MDH-11    | Stool            | 2008           | 4,129,638             | 389,856        | 43            | 4,722,650        | 4,752       | 52.2            | QZFDO00000000        |
| MDH-12    | Stool            | 2009           | 4,399,374             | 230,080        | 54            | 4,706,223        | 4,745       | 52.1            | QZEF00000000        |
| MDH-13    | Stool            | 2010           | 4,764,064             | 310,035        | 49            | 4,739,724        | 4,806       | 52.1            | QZFF00000000        |
| MDH-14    | Blood            | 2011           | 3,208,474             | 312,411        | 51            | 4,767,578        | 4,829       | 52.2            | QZFG00000000        |
| MDH-15    | Stool            | 2011           | 2,124,138             | 177,815        | 85            | 4,766,481        | 4,829       | 52.2            | QZMP00000000        |
| MDH-16    | Stool            | 2012           | 1,892,712             | 153,861        | 64            | 4,800,611        | 4,894       | 52.0            | QZFH00000000        |
| MDH-17    | Stool            | 2012           | 1,532,044             | 123,253        | 100           | 4,802,467        | 4,863       | 52.0            | QZFI00000000        |
| MDH-18    | Gallbladder      | 2013           | 3,806,536             | 75,786         | 162           | 4,881,277        | 5,005       | 52.1            | QZFIJ00000000       |
| MDH-19    | Urine            | 2013           | 2,291,464             | 60,132         | 201           | 4,775,923        | 4,879       | 52.2            | QZFJK00000000       |
| MDH-20    | Subhepatic aspirate | 2013       | 2,936,934             | 69,988         | 168           | 4,888,146        | 5,028       | 52.1            | QZFL00000000       |
| MDH-21    | Stool            | 2014           | 2,343,572             | 57,255         | 195           | 4,688,259        | 4,773       | 52.1            | QZFM00000000       |
| MDH-22    | Stool            | 2014           | 2,023,560             | 59,303         | 176           | 4,687,016        | 4,762       | 52.1            | QZMQ00000000       |
| MDH-23    | Urine            | 2014           | 1,872,516             | 52,555         | 195           | 4,690,085        | 4,776       | 52.1            | QZFN00000000       |
| MDH-24    | Stool            | 2014           | 2,607,656             | 53,183         | 197           | 4,682,121        | 4,730       | 52.2            | QZMR00000000       |
| MDH-25    | Stool            | 2015           | 2,424,548             | 35,368         | 313           | 4,778,730        | 4,868       | 52.1            | QZFO00000000       |
| MDH-26    | Urine            | 2016           | 3,795,856             | 36,628         | 274           | 4,807,879        | 4,944       | 52.0            | QZFPO00000000       |
| MDH-27    | Stool            | 2016           | 2,566,758             | 54,067         | 225           | 4,807,042        | 4,891       | 52.0            | QZFPQ00000000       |
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