Draft Genome Sequence of *Nesterenkonia* sp. Strain F, Isolated From Aran-Bidgol Salt Lake in Iran

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The draft genome of the aerobic, Gram-positive, halophilic chemooorganotroph *Nesterenkonia* sp. strain F consists of a 2,812,133-bp chromosome. This study is the first to report the shotgun-sequenced draft genome of a member of the genus *Nesterenkonia*.

*Nesterenkonia* is an aerobic, Gram-positive, chemooorganotrophic, catalase-positive, mesophilic, and halophilic genus of the family Micrococcaceae (6). *Nesterenkonia* sp. strain F was isolated from Aran-Bidgol Lake, a hypersaline lake in Iran, and characterized as producing the halophilic and organic solvent-tolerant α-amylases (5). Despite its high potential for producing the various natural compounds and specialized mechanisms for adaptation to extreme conditions, there is a little information about the genetic and genome features of the *Nesterenkonia* genus.

Genome sequencing of *Nesterenkonia* sp. strain F was performed using 454 GS-FLX Titanium. We obtained a total of 201,320 random reads, covering a total of 44,347,672 bp. The approximate coverage of *Nesterenkonia* sp. strain F genome was 16-fold. The sequence reads were assembled into 138 contigs using Newbler Assembler software, v. 2.3. Then, the RAST annotation pipeline was used to annotate the DNA sequence (1).

The G+C content of the draft genome was 71.5%, similar to that previously reported by Stackebrandt et al. (6). The sum of the sizes of the 138 large contigs in *Nesterenkonia* sp. strain F is 2,812,133 bp. The draft genome contained 2,484 genes, with 1,794 nonhypothetical and 690 hypothetical protein coding sequences and 50 structural RNAs.

Analysis of annotated genome sequence of *Nesterenkonia* sp. strain F revealed the presence of genes involved in production of α-amylases, including maltodextrin glucosidase and alpha-glucosidase.

In addition, the genes encoding proteins involved in resistance to heavy metals and toxic compounds, including copper homeostasis, cobalt-zinc-cadmium resistance, arsenic resistance, and beta-lactamase, were identified. These results show the genetic potential of the *Nesterenkonia* sp. strain F to adapt to extreme lifestyles. Furthermore, *Nesterenkonia* sp. strain F comprises clustered regularly interspaced short palindromic repeats (CRISPR), which constitutes an adaptive mechanism against foreign genetic elements as an adaptive immune system (4). The CRISPR-associated helicase Cas3, the RecB family exonuclease Cas4b, and the CRISPR-associated protein Cas1 have been detected using the CRISPRFinder online program (3).

The *Nesterenkonia* sp. strain F also has glycolysis and gluconeogenesis systems, a pentose phosphate pathway, and a tricarboxylic acid cycle. It contains genes for response to osmotic and oxidative stresses, in addition to heat shock, cold shock, and detoxification systems.

Finally, we identified the genes involved in ammonia assimilation and nitrate and nitrite ammonification, which are very attractive for bioremediation studies (2).

**Nucleotide sequence accession number.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AFRW00000000. The version described in this paper is the first version, AFRW01000000. The genome project data are also available at GenBank under the Genome Project ID 68173.

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REFERENCES