The present study reports the complete and annotated genome sequence of the human pathogen *Rickettsia slovaca* strain 13-B, which was isolated from a *Dermacentor* tick in Slovakia in 1968. The 1.27-Mb genome provides further insights into the acquisition of virulence related to genome reduction in *Rickettsia* species.

*Rickettsia* are arthropod-associated intracellular bacteria (7). *Rickettsia* genomes underwent a reductive evolution during their specialization to an intracellular lifestyle (1), but, paradoxically, a recent genome study of *Rickettsia africae* suggested that genome reduction is associated with higher virulence in rickettsiae (3). *Rickettsia slovaca* has been isolated from *Dermacentor* ticks (mainly *Dermacentor marginatus* and *Dermacentor reticulatus*) (6) and is the main agent of tick-borne lymphadenopathy (TIBOLA). TIBOLA is restricted to Europe, where it is the most frequent and is the main agent of tick-borne lymphadenopathy (TIBOLA).

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. slovaca* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens of *R. slovaca*.

The genome of *R. slovaca* was fully sequenced using the Illumina Sequencing System (Illumina, San Diego, CA). The genome sequencing of *R. conorii* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.

The genome sequencing of *R. slovaca* strain 13-B was performed as previously described (3). Briefly, sequencing to 10× coverage was performed by capillary sequencing using a 3730xl DNA analyzer (Applied Biosystems). Twenty-eight contigs were assembled into 8 scaffolds. Gaps were closed by PCR. The genome of *R. conorii* consists of one 1,275,802-bp circular chromosome (the G+C content is 32.5%, which is similar to the other *Rickettsia* genomes). The predicted total complement of 1,400 genes (1,641 ORFs) is in the range of genomes from other tick-borne pathogens.