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# Genetic Heterogeneity of *Borrelia burgdorferi* Sensu Lato in the Kemerovo region (West Siberia) of Russia Based on Restriction Fragment Length Polymorphism and Sequence Analysis.

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In West Siberia, landscape–geographic conditions proved to be favorable for the formation of large TBE foci with a high epidemiological potential, and the values of TBE and borreliosis morbidity annually recorded in all administrative units of this region are many times higher than the average indications for Russia as a whole. The climate is sharp continental. The summer t balances from +11 up to +36, the winter one from 0 up to minus 50. Mountain snow reaches 5m oh height, taiga snow goes up to 3 m. Statistically proved dependence of tick activity and frequency of unfavourable outcomes on climate isn't discovered.

In this study the genetic diversity of *B. burgdorferi* sensu lato in local tick populations from Kemerovo region of Russia was analyzed. Ticks were collected by blanket dragging from different forestry in region. One hundred twenty *Ixodes persulcatus* adult ticks were selected for analysis. DNA was prepared from ticks by alkali extraction and was used for nested PCR that targeted the *rrf* (5S)-*rrl* (23S) intergenic spacer of *B.burgdorferi* sensu lato. *B. burgdorferi* sensu lato DNA was detected in 26 of 108 adult ticks (24%). *B.burgdorferi* genotypes were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of 5S-23S intergenic spacer amplicons. On the basis of both the *Tru9I* and the *Dra*I restriction patterns, the 26 isolates were separated into two genospecies that had 4 different restriction patterns.*B. garinii* was found in 11 ticks, 14 ticks carried *B. afzelii*. Double infections with *B. afzelii* and *B. garinii* were found in one case.

To confirm the results of PCR-RFLP analysis and to assess the DNA relatedness within and between genospecies, the complete sequences of the *rrf-rrl* intergenic spacers from 9 positive DNA samples were determined. The DNA sequence analyses of *rrf-rrl* intergenic spacers confirmed our PCR-RFLP results. These sequences were then aligned against each other and the reference sequences downloaded from GenBank by using Clustal W. The 9 strains clustered into two separate lineages. One was more close to B. *afzelii* ticks from Czech Republic and the second one was close to *B.garinii* strains from Portugal.