



Brief Note

Detection and sequence analysis of the DNA repair gene *RAD51* in the Korean spider *Callobius koreanus* (Amaurobiidae)

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ABSTRACT. We identified a partial sequence (483 bp) of the *RAD51* gene from the Korean spider *Callobius koreanus*. Sequence variation was found at one position during alignment with the human *RAD51* gene sequence. This partial sequence included the region corresponding to exon 4 in the human *RAD51* gene, which encodes 39 amino acids. These results show that the *RAD51* gene is highly conserved between human and spiders.

Key words: *Callobius koreanus*; *RAD51*; Exon, DNA repair gene; Amaurobiidae

INTRODUCTION

The *RAD51* gene encodes the RAD51 protein, which is essential for repairing damaged DNA. In humans, the *RAD51* gene is located between base pairs 40,694,774 and 40,732,158 on the long (q) arm of chromosome 15, which corresponds to a length of 37,385 bp (NCBI's genome browser Map Viewer-*Homo sapiens* Annotation Release 107). The protein encoded by this gene is a member of the RAD51 protein family and is highly similar to bacterial *RecA* and *Saccharomyces cerevisiae* RAD51, which are involved in the homologous recombination and repair of DNA (Shinohara et al., 1992; Morais Jr et al., 1998). Characteristics of *RAD51* are relatively well-known in mammals, amphibians, and birds (Maeshima et al., 1995; Takata et al., 2002; Venkitaraman, 2002), but are poorly reported in invertebrates, especially spiders. In this study, we identified and analyzed a partial sequence of the *RAD51* gene from a Korean spider species, *Callobius koreanus*.

MATERIAL AND METHODS

Detailed methods used to obtain a partial sequence of the *RAD51* gene from *C. koreanus* are provided in [Table S1](#). The obtained *RAD51* gene sequence was compared with other homologous sequences deposited in GenBank using BLASTN2.2.31+ (Zhang et al., 2000). The amino acid sequence translated from the *RAD51* gene was compared with other homologous protein sequences in the PDB protein database (NCBI) using BLASTP 2.2.32+ (Altschul et al., 1997). To compare homology, sequences were aligned using the Clustal-W program found in Geneious Pro 5.5.9 (Biomatters, Auckland, New Zealand).

RESULTS AND DISCUSSION

We obtained a partial *RAD51* gene sequence of 483 bp (KT325925) from the Korean spider *C. koreanus*. Using a BLAST search in GenBank, the sequences with most homology to *C. koreanus* *RAD51* were found to be those belonging to the *H. sapiens* *RAD51* genes (NG_012120 and AY196785) with a query cover of 100% and identity of 99%. The aligned region spans positions 15,920 to 16,402 on the *Homo sapiens* *RAD51* gene (NG_012120) (Figure 1). The aligned sequences of the two genes differed at only one position (T->G at position 15,984). The *H. sapiens* *RAD51* gene contains 10 exons, which encode the 339 amino acid sequence of RAD51 recombinase (Park et al., 2008). Of these, exon 4 is located from position 16,017 to 16,134 within the aligned sequences and encodes 39 amino acids (Figure 1). In a BLAST search of the PDB protein database (NCBI), the sequence derived from 39 amino acids translated from 117 bp of the *C. koreanus* *RAD51* gene in the exon 4 region was found to be homologous to RAD 51 sequences reported in various vertebrates including primates, birds, and rodents. Although the results obtained in this study depend on the partial sequence of *C. koreanus* *RAD51*, they suggest that this sequence might be well conserved between human and spiders.

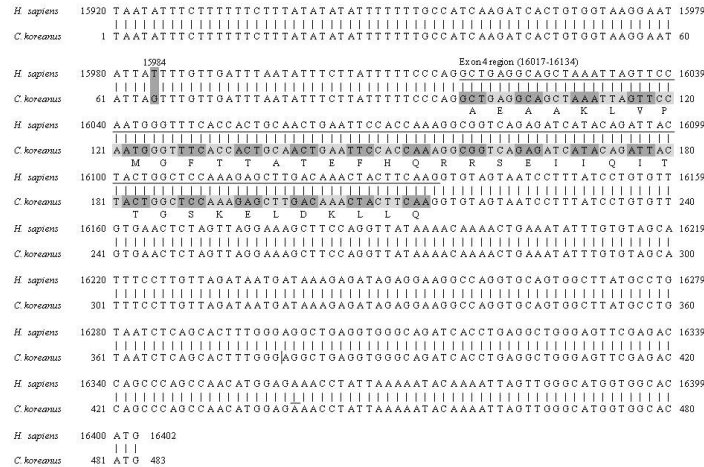


Figure 1. Sequence analysis of the *Callobius koreanus* RAD15 gene. The gene sequence was aligned from positions 15,920 to 16,402 on the *Homo sapiens* RAD51 gene sequence (NG_012120). All positions of the sequences are well conserved except for position 15,984. The exon 4 region of *H. sapiens*, which is located between positions 16,017 and 16,134, is underlined. One-letter amino acid symbols according to the IUPAC-IUB single-letter amino acid codes are denoted for each codon in the corresponding region of the *C. koreanus* RAD51 gene.

Conflicts of interest

The authors declare no conflict of interest.

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[Supplementary material](#)

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