First Case of Human Babesiosis in Korea: Detection and Characterization of a Novel Type of *Babesia* sp. (KO1) Similar to Ovine *Babesia*\(^\dagger\)

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We report on the first case of human babesiosis in Korea. The intraerythrocytic parasite (KO1) in the patient’s blood mainly appeared as paired pyriforms and ring forms; but Maltese cross forms were not seen, and the parasite showed morphological features consistent with those of the genus *Babesia* sensu stricto. The sequence of the 18S rRNA gene of KO1 was closely related to that of *Babesia* spp. isolated from sheep in China (similarity, 98%). The present study provides the first evidence of the presence of a hitherto unidentified, new type of *Babesia* parasite capable of infecting humans.

**CASE REPORT**

A 75-year-old female residing in Gurae, Jeon-nam Province, Korea, was hospitalized at the Ajou University Medical Center, Suwon, Korea, on 5 June 2005 with symptoms of severe anemia, an irregular high fever, rigor, muscle pain, vomiting, diarrhea, and jaundice. Her medical history included gastric cancer, diagnosed in 1998, for which she had received treatments including gastric resection and splenectomy. Because of those operations, she had received blood transfusions twice in 1999. Initially, her disease was diagnosed as malaria because the clinical symptoms and morphologies of the parasites found in her blood smear were quite similar to those of the malaria parasite and because tertian malaria has often been found often in Korea in recent years. She was treated with quinine, an antimalarial drug, but it was apparently ineffective. Therefore, the patient’s blood sample was transferred to the Division of Malaria and Parasitic Diseases, Korean Centers for Disease Control and Prevention, for systematic diagnosis on 20 June 2005.

On 22 June, her disease was diagnosed as babesiosis by microscopic examination and molecular biological methods. The patient was then treated with clindamycin on 23 June, which successfully reduced the parasitemia. The patient was discharged from the hospital on 1 July. When the second examination was done on 6 July, no parasite was detected by microscopic examination or PCR analysis.

Giemsa-stained blood smears from the patient revealed that intraerythrocytic parasites were most frequently observed as paired pyriforms and ring forms, but Maltese cross forms were not seen in most smears (Fig. 1). In general, the genus *Babesia*

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Information (NCBI) with the Basic Local Alignment Search Tool (http://www.ncbi.nlm.nih.gov/BLAST/) for similarity analysis. Interestingly, the result revealed that the sequence from the patient was virtually identical to that of a Babesia sp. isolated from a sheep in Hebei, China (GenBank accession number DQ159074). Thus, for a more accurate analysis we again amplified the full-sized sequence (~1.7 kb) encoding the 18S rRNA gene of the Babesia parasite from the patient with the primer set A (5’-ACCTGGTTGATCCTGCCAGT-3’) and B (5’-TGATCCTTCTGCAAGGGTCACCTAC-3’) described by Medlin et al. (9), cloned the PCR product, and sequenced it as described above. The sequence obtained was highly similar (98%) to that registered in GenBank under accession number DQ159074. Phylogenetic analysis was carried out with the MacVector software package (version 8.1.1; Genetics Computer Group, Inc., Madison, WI). A total of 1,684 bp of the 18S rRNA sequence obtained in this study and the 18S rRNA gene sequences available from NCBI’s database were aligned with the program ClustalW, followed by alignment with the phylogenetic analysis program available in the same package. The phylogenetic tree constructed by the neighbor-joining method is depicted in Fig. 2, which clearly demonstrates their close relationship. The Babesia sp. from the Korean patient formed a clade that included several Babesia spp. previously reported from sheep in Gansu, China (1), is also noteworthy. Whether or not the patient was infected with parasites naturally maintained in sheep in Korea, however, must await further epizootiologic investigations, because our preliminary surveys have yet to provide any evidence of the natural vertebrate hosts or the ticks involved in transmission. Until enough knowledge is accumulated to give certain specific nomenclature, we temporarily designate this parasite strain KO1.

We conducted further epidemiological surveys with blood samples from the residents in the patient’s village, Gurae, in southwestern South Korea. For this survey we were able to collect blood samples from 68 residents (30 males and 38 females; age range, 37 to 100 years), and we extracted DNA for parasite detection by PCR. PCR amplification was done with primers Bab5 and Bab8 for the first round of PCR and primers Bab6 and Bab7 for the second round of PCR. Three cases were confirmed to be positive (Fig. 3). Sequencing analysis of the three PCR products showed sequences identical to those detected in the patient (KO1) (data not shown). These results indicate that there may be some asymptomatic carriers in this village. We have also attempted to detect the Babesia parasite in 17 goats raised in the village, but unfortunately, no positive signal was detected.

Babesiosis, caused by infection with parasites of the genus Babesia, is one of the most ubiquitous infections in wild and domestic animals worldwide. The disease is transmitted by ixodid ticks to vertebrate hosts. Recently, it has increasingly gained attention as an emerging zoonosis in humans (4, 8). Two main species of Babesia parasites, namely, B. microti (so-called small Babesia) and B. divergens (large Babesia, or the genus Babesia sensu stricto) have been known to be involved in human infections in the United States and Europe, respectively (4, 6, 7). In addition, a newly emerging Babesia species, referred to as WA1 (13, 16) and CA1 (11), that causes human babesiosis has been reported and was recently identified as B.
duncani sp. nov. in the United States (3). In East Asia, cases of human babesiosis have been reported in Taiwan (15) and Japan (14). Both of these were caused by B. microti-like parasites, which often appear asymptomatically. Although field surveys of wild rodents and cattle have suggested the presence of Babesia parasites in Korea (2, 19), human babesiosis has not yet been reported. In this study we report the first case of human babesiosis in Korea, which was found to be a novel large Babesia parasite infecting a human and which was nearly fatal.

In conclusion, this is the first report of human babesiosis in Korea which was apparently caused by a hitherto unidentified, new type of Babesia sp. capable of infecting humans. The sequence of this new parasite is similar (98%) to that of Babesia spp. detected from sheep in China. Research collaboration will apparently be needed to further investigate the interrelationship between the parasites found in the Korean index case patient and those reported from sheep in China.

**Nucleotide sequence accession number.** The 18S rRNA gene sequence of strain KO1 can be found in the GenBank database under accession number DQ346955.

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**REFERENCES**


