

Introduction

- The aim of this study was an examination of 30 polyfloral honey samples collected directly from small Kosovo beekeepers (artisanal producers) to determine the presence of *Clostridium botulinum*.
- The Kosovo territory was divided into 30 equal surface units spanning the entire region of Kosovo.
- Samples were collected from July to September 2018 and dark stored at 8° C until further analysis.

Materials and methods

- The direct centrifugation method was used for culturing the *C. Botulinum* and to confirm the presence of *C. Botulinum*, cultured bacterial colonies were subjected to Gram's stain, catalase, and oxidase tests.
- From identified colonies, enrichment culture was prepared, DNA extracted and the amplification of the 16S rRNA gene with two sets of universal 16S rRNA bacterial primers was performed.
- After an electrophoresis step to detect specific bands of 1450 bp for 16S RNA, the PCR products were sequenced at MacroGen-Europe and phylogenetic relationships of 16S rRNA sequences were estimated using MEGA X software.



RESULTS

Table 1. Biochemical tests of isolated bacteria

Sample #	Gram's stain	Catalase	Oxidase
K18	+	-	-
K9	+	-	-
K11	+	-	-
K3B	+	-	-
K20S	+	-	-
K17P	+	-	-
K29	+	-	-
K22	+	-	-
K25	+	-	-
K4	+	-	-
K23	+	-	-
K5	+	+	-
K27	+	+	+
K30	+	+	+
K26	+	+	-
K16	+	+	+
K13	+	+	-
K19	+	+	-
K14B	+	+	-
K24	+	+	-
K28	+	+	-
K17S	+	+	-
K15	+	+	-
K14K	+	+	-

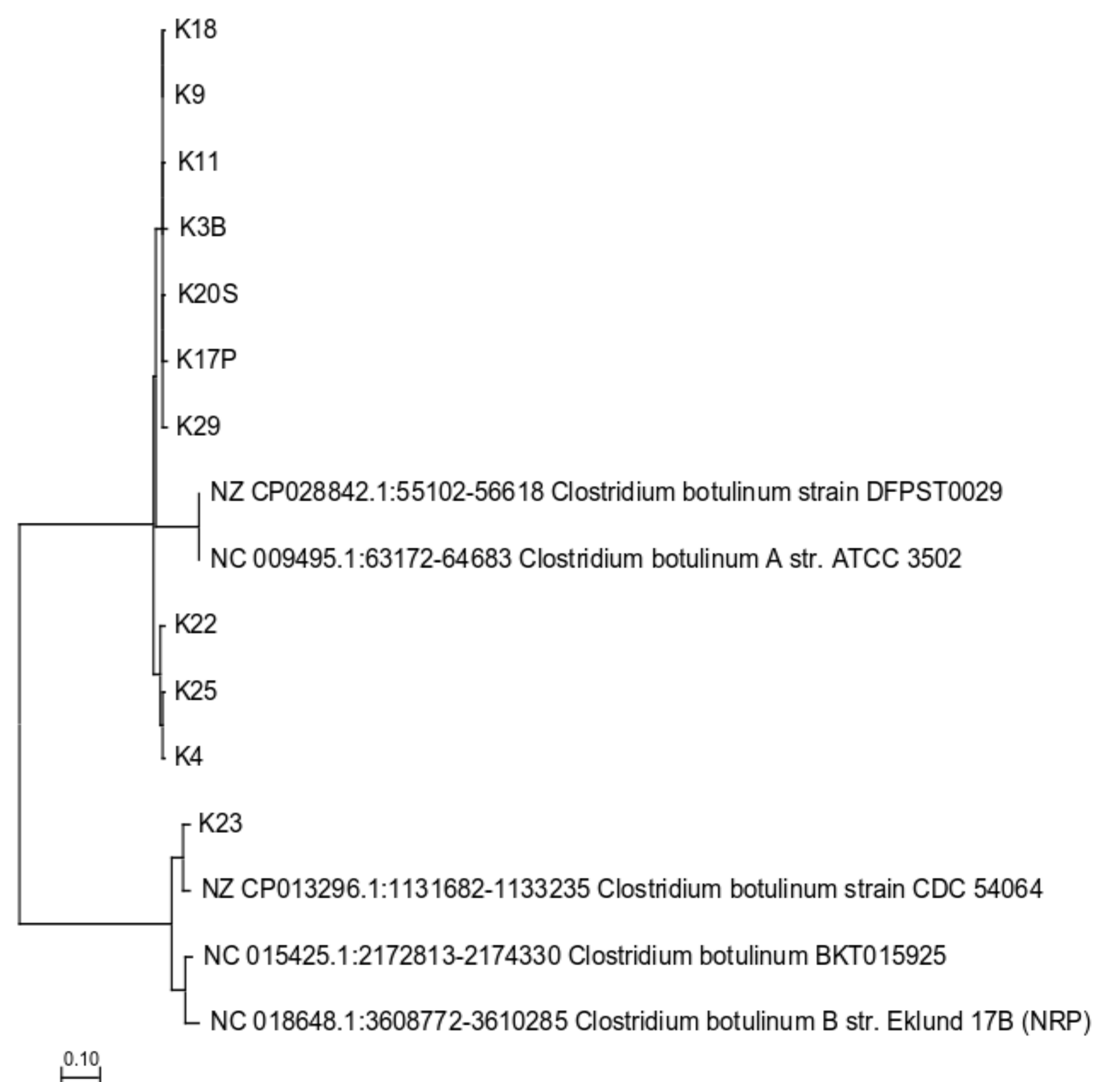


Figure 1. Phylogenetic tree of *Clostridium botulinum* with reference and representative genomes 16S rRNA sequence region. First number indicated the genomes accession numbers (NZ_CP013296.1), and second number showed the 16S rRNA sequence location (1131682-1133235) in the genomes (*C. botulinum* strain CDC 54064).

Conclusions

- ✓ In this first representative study on the occurrence of *C. botulinum* in honey collected in Kosovo, sequence analyzing results showed that isolates from 11 samples (K18, K9, K11, K3B, K20S, K17P, K29, K22, K25, K4, and K23) were similar to *C. botulinum* via nearly 96% identities.

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