

Lim S.H., Ilyasov R.A., Goto K., Noh G.R., Kim D.I., Takahashi J., Kwon H.W. Comparison of mitochondrial genome of two honeybee subspecies, *A. mellifera caucasica* and *A. mellifera carpathica*. Materials of the 33th Conference of the Apicultural Society of Korea. Gwangju, Korea. 13.04.2018. P. 40.

곤충산업(양잠, 양봉, 산업곤충) 발전을 위한 공동 학술대회



2018년 4월 12일(목) ~ 13일(금)

광주 김대중컨벤션센터

- 주관 : 국립농업과학원, 한국잠사학회, 한국양봉학회
- 후원 : 한국양봉협회, 한국양봉농협, 대한잠사회, 한국곤충산업협회

2018년 4월 13일 (금)

08:30~09:00	등 록
특별강연 <한국양봉학회 305호>	
09:00~09:25	프로폴리스 등 양봉산물 다양화 : 이용림(비엔케어)
09:25~09:50	Unique subspecies of Asian bees <i>Apis cerana</i> in Korean peninsula : Rustem Ilyasov(인천대)
09:50~10:00	휴식
일반학술발표 구두발표 <한국양봉학회 305호>	
10:00~10:15	Accurate identification of Israeli acute paralysis virus by multi detection points using ultra-rapid real-time PCR : A-Tai Truong(경기대)
10:15~10:30	Responses of the small hive beetle (<i>Aethina tumida</i>) to volatile chemicals reported from honey bee (<i>Apis mellifera</i>) and beehive-materials, and solvent extracts of fermented pollen dough : Aman Dekebo(안동대)
10:30~10:45	한국 벌꿀 시장의 소비자 인식 및 구매행태 분석 : 강동윤(서울대)
10:45~11:00	3 point PCR을 이용한 Black Queen Cell Virus의 특이적 검출법 : 김소민(경기대)
11:00~11:15	봉군의 환경을 대변하는 봉변; 꿀벌 주요 Virus성 병원체의 검출 : 김정민(경기대)
11:15~11:30	남부권역 유망 밀원수종 개화 특성 : 김영기(산림과학원)
11:30~12:00	시상 및 폐회식
박사학위 논문발표 <한국잠사학회 302호>	
09:00~09:30	Molecular phylogeny of Bombycoidea and Lasiocampoidea and familial relationships within Bombycoidea using complete mitochondrial genome sequences : 김민지(전남대)
일반학술발표 구두발표 <한국잠사학회 302호>	
09:30~09:45	실크 매트릭스에 의한 골재생 효과 관련 임상 시험 : 석현(충남대)
09:45~10:00	CRISPR/Cas 9 mediated genome editing of BmCactus in <i>Bombyx mori</i> cells : 박종우(농과원)
10:00~10:15	Identification of Flavonoids in Korean Mulberry Fruits : 권오철(농과원)

Comparison of mitochondrial genome of two honeybee subspecies, *A. mellifera caucasica* and *A. mellifera carpathica*

Soo Ho Lim^{1,2,*}, Rustem Ilyasov^{1,2,*}, Kenji Goto³, Gwang Rae Noh^{1,2},
Dong In Kim^{1,2}, Jun-ichi Takahashi⁴ and Hyung Wook Kwon^{1,2}

¹Division of Life Sciences, Major of Biological Sciences, Incheon National University

²Convergence Research Center for Insect Vectors, Incheon National University

³Department of Bioecology and Biological Education, Bashkir State Agrarian University

⁴Faculty of Life Sciences, Kyoto Sango University

(*These authors equally contributed to this work)

The complete mitochondrial DNA (mtDNA) sequence of honeybee subspecies *A. m. caucasica* and *A. m. carpathica* has been analyzed for the first time. Our results showed that length of *A. m. caucasica* and *A. m. carpathica* mtDNA sequences are 16,341 bp and 16,336 bp, respectively. Both sequences contained 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 AT-rich region. The overall composition of nucleotides in mtDNA in *A. m. caucasica* / *A. m. carpathica* is A (43.2/43.3%), C (9.5/9.6%), G (5.6/5.5%), and T (41.6/41.6%). Most of coding genes (CDS) (ND2, COX1, COX2, ATP8, ATP6, COX3, ND3, ND6, CYTB), and 14 tRNA genes are located on the heavy strand for both sequences. Four CDS genes (ND1, ND4, ND4L, ND5), 2 rRNA genes (12S rRNA, 16S rRNA), and 8 tRNA genes are located on the light strand for both sequences. A comparative analysis of whole mtDNA sequences of *A. m. caucasica* and *A. m. carpathica* has showed that *A. m. caucasica* belonged to the O lineage, in contrast to *A. m. carpathica* belonging to the C lineage. We suggested 34 SNPs, which allowed to differentiate subspecies *A. m. caucasica* and *A. m. carpathica*. These complete mtDNA sequence of honeybee subspecies *A. m. caucasica* and *A. m. carpathica* can be useful for further phylogenetic and population genetic studies in honeybees.

Comparison of mitochondrial genome of two honeybee subspecies, *A. mellifera caucasica* and *A. mellifera carpathica*

**Soo Ho Lim^{1,2,*}, Rustem Ilyasov^{1,2,*}, Kenji Goto³, Gwang Rae Noh^{1,2},
Dong In Kim^{1,2}, Jun-ichi Takahashi⁴ and Hyung Wook Kwon^{1,2}**

¹Division of Life Sciences, Major of Biological Sciences, Incheon National University

²Convergence Research Center for Insect Vectors, Incheon National University

³Department of Bioecology and Biological Education, Bashkir State Agrarian University

⁴Faculty of Life Sciences, Kyoto Sango University

(*These authors equally contributed to this work)

The complete mitochondrial DNA (mtDNA) sequence of honeybee subspecies *A. m. caucasica* and *A. m. carpathica* has been analyzed for the first time. Our results showed that length of *A. m. caucasica* and *A. m. carpathica* mtDNA sequences are 16,341 bp and 16,336 bp, respectively. Both sequences contained 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 AT-rich region. The overall composition of nucleotides in mtDNA in *A. m. caucasica* / *A. m. carpathica* is A (43.2/43.3%), C (9.5/9.6%), G (5.6/5.5%), and T (41.6/41.6%). Most of coding genes (CDS) (ND2, COX1, COX2, ATP8, ATP6, COX3, ND3, ND6, CYTB), and 14 tRNA genes are located on the heavy strand for both sequences. Four CDS genes (ND1, ND4, ND4L, ND5), 2 rRNA genes (12S rRNA, 16S rRNA), and 8 tRNA genes are located on the light strand for both sequences. A comparative analysis of whole mtDNA sequences of *A. m. caucasica* and *A. m. carpathica* has showed that *A. m. caucasica* belonged to the O lineage, in contrast to *A. m. carpathica* belonging to the C lineage. We suggested 34 SNPs, which allowed to differentiate subspecies *A. m. caucasica* and *A. m. carpathica*. These complete mtDNA sequence of honeybee subspecies *A. m. caucasica* and *A. m. carpathica* can be useful for further phylogenetic and population genetic studies in honeybees.