Ilyasov R.A., Park J.H., Takahashi J., Lim S.H., Han G.Y., Song J.H., Kwon H.W. Unique subspecies of Asian bees Apis cerana in Korean peninsula. Materials of the 33th Conference of the Apicultural Society of Korea. Gwangju, Korea. 13.04.2018. P. 26.

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	등록
	특별강연 〈한국양복하히 205 ★〉
	특별강연 〈한국양봉학회 305호〉
09:00~09:25	프로폴리스 등 양봉산물 다양화 : 이용림(비엔케어)
09:25~09:50	Unique subspecies of Asian bees Apis cerana in Korean peninsula: Rustem Ilyasov(인천대)
09:50~10:00	휴식
	일반학술발표 구두발표 〈한국양봉학회 305호〉
Contra .	일반약굴말표 구누발표 〈한국양봉학회 305호〉
10:00~10:15	Accurate identification of Israelia and ISRA
	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 (Aething tumida) to volatile chaminal
	normoley bee (Apis mellifera) and beenive-materials, and solvent extracts of
10:30~10:45	fermented pollen dough : Aman Dekebo(안동대) 하구 범꾹 시작이 소비자 이시 미 그 매하다 보내 ㅋㅋㅋ
10:45~11:00	한국 벌꿀 시장의 소비자 인식 및 구매행태 분석 : 강동윤(서울대) 3 point PCR을 이용한 Black Queen Celly(mag) 투이지 지수비 지수하
11:00~11:15	3 point PCR을 이용한 Black Queen Cell Virus의 특이적 검출법 : 김소민(경기대) 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〉
	 좌장 김성곤(강통원주
09:00~09:30	Molecular phylogeny of Bombycoidea and Lasiocampoidea and familial relations within Bombycoidea using complete mitochondrial genome sequences: 김민지(전남대)
	일반학술발표 구두발표 〈한국잠사학회 302호〉
	I좌장I 김성곤(강릉원 ^주
and the second s	
09.30~09.45	신국 매트리스에 이하 공재생 효과 과려 인상 시험 : 석현(충남대)
09:30~09:45	실크 매트릭스에 의한 골재생 효과 관련 임상 시험 : 석현(충남대) CRISPR/Cas 9 mediated genome editing of BmCactus in <i>Bombys moricells</i> :
09:30~09:45 09:45~10:00	실크 매트릭스에 의한 골재생 효과 관련 임상 시험 : 석현(충남대) CRISPR/Cas 9 mediated genome editing of BmCactus in <i>Bombys moricells</i> : 박종우(농과원) Identification of Flavonoids in Korean Mulberry Fruits : 권오철(농과원)

Unique subspecies of Asian bees Apis cerana in Korean peninsula

Rustem Ilyasov^{1,2}, Jun Hyung Park³, Jun-ichi Takahashi⁴, Soo Ho Lim^{1,2} Gi Youn Han^{1,2}, Jong Hun Song^{1,2} 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 ³Bioinformatics company 3BIGS CO.LTD ⁴Faculty of Life Sciences, Kyoto Sango University

Apis cerana is sisterly related to a honeybee species Apis mellifera, which is highly important in agriculture in most Asian countries. The size of A. cerana population is decreasing every year due to Korean Sacbrood Virus (KSBV) and other diseases. It is believed that A. cerana populations are subdivided into several numbers of subspecies adapted to different climates, similar to Apis mellifera. Full mitochondrial genome of A. cerana from different countries and populations have been studied insufficiently. To date, full mitochondria DNA (mtDNA) sequence of A. cerana from Korean peninsula have not been researched. Here we sequenced and annotated the full mitochondrial genome of A.cerana from Jeollanam-d province of South Korea, which is most densely populated area of A. cerana. The mtDNA sequence consisted of 15,925 bp length, A + T content 84% and C + G content 16% and contains 22 tRNA genes, 13 protein-coding genes, 2 ribosomal RNA genes, AT-rich region, and 4 known non-coding intergenic loci (NC1-4). Comparative analysis A. cerana full mtDNA sequences showed that Korean A. cerana was more similar with Japanese and Chinese samples than Taiwanese species. Japanese and Korean samples wer subdivided in one common group located separately. Thus, based on analysis of full mtDN. sequences the samples of Korean A. cerana can be named as subspecies Apis ceran

Unique subspecies of Asian bees *Apis cerana* in Korean peninsula

<u>Rustem Ilyasov</u>^{1,2}, Jun Hyung Park³, Jun-ichi Takahashi⁴, Soo Ho Lim^{1,2}, Gi Youn Han^{1,2}, Jong Hun Song^{1,2} 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 ³Bioinformatics company 3BIGS CO.LTD ⁴Faculty of Life Sciences, Kyoto Sango University

Apis cerana is sisterly related to a honeybee species Apis mellifera, which is highly important in agriculture in most Asian countries. The size of A. cerana population is decreasing every year due to Korean Sacbrood Virus (KSBV) and other diseases. It is believed that A. cerana populations are subdivided into several numbers of subspecies adapted to different climates, similar to Apis mellifera. Full mitochondrial genome of A. cerana from different countries and populations have been studied insufficiently. To date, full mitochondrial DNA (mtDNA) sequence of A. cerana from Korean peninsula have not been researched. Here, we sequenced and annotated the full mitochondrial genome of A.cerana from Jeollanam-do province of South Korea, which is most densely populated area of A. cerana. The mtDNA sequence consisted of 15,925 bp length, A + T content 84% and C + G content 16% and contains 22 tRNA genes, 13 protein-coding genes, 2 ribosomal RNA genes, 1 AT-rich region, and 4 known non-coding intergenic loci (NC1-4). Comparative analysis of A. cerana full mtDNA sequences showed that Korean A. cerana was more similar with Japanese and Chinese samples than Taiwanese species. Japanese and Korean samples were subdivided in one common group located separately. Thus, based on analysis of full mtDNA sequences the samples of Korean A. cerana can be named as subspecies Apis cerana koreana.