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한국양봉학회 추계학술대회

프로그램 및 발표논문 초록

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Program and Abstracts

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•장소 : 논산시농업기술센터

•주관 : 한국양봉학회

•후원 : 논산시농업기술센터

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Dark forest honeybees *Apis mellifera mellifera* L. in the Ural and Volga region

Rustem Ilyasov, GwangRae Noh, DongIn Kim, SooHo Lim, JongHun Song
and HyungWook Kwon

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Dark forest bee *Apis mellifera mellifera* is an aboriginal subspecies for the Nordic countries and has an area extending up to 47° of North Latitude. Despite the fact that the dark forest bee became known for its highly developed protective behavior, it is most preferable for breeding in most parts of Northern and Central Russia. The gene pool of a dark forest bee is currently threatened because of mass hybridization with imported southern subspecies *A. m. carpathica* and *A. m. caucasica*. Based on molecular population genetics analysis of 9 microsatellite loci (*AP243*, *4A110*, *A24*, *A8*, *A43*, *A113*, *A88*, *AP049*, *A28*) in nuclear genome of honeybees *A. mellifera* and analysis a nucleotide sequences polymorphism of following loci: *ND2* mtDNA, *COI-COII* mtDNA, *VG* of nuclear DNA, we developed criteria for identification of native bee subspecies *A. m. mellifera*. Using method of cluster analysis, we constructed dendrograms and median networks, which allow differentiating of honeybee subspecies from different evolutionary lineages. We researched a level of introgressed genes from southern populations in the dark forest bee populations in the Ural and Volga region. Now we began a molecular genetic research in Korean *Apis cerana* populations in the Sensory Neurobiology and Biomodeling Laboratory (SNBL) of Incheon National University. Our aims is: comparing genomes *A. mellifera* and *A. cerana*; research of expression of immune-related genes in *A. cerana*; make a population genomics research of *A. mellifera* and *A. cerana*.