## POLYMORPHISM OF COI GENE IN HONEY BEES FROM DIFFERENT REGIONS OF UKRAINE presentation

Aim. The rapidly evolving mitochondrial CoI gene is widely used in the molecular taxonomy of insects to identify closely related forms. Accordingly, to assess the distribution of subspecies/breeds of Apis mellifera in Ukraine, sequencing, and comparison of this gene was performed for bees from different geographical regions.

Methods. PCR amplification and sequencing of Col.

Results. Breed-specific mutations in the CoI gene have been identified for the Dark European, Carpathian, and Ukrainian Steppe honey bees, which are widely distributed in Ukraine. It was found that the current distribution of these breeds does not correspond to the traditional zoning.

Conclusions. The widespread practice of importing the genetic material of Apis mellifera from different regions of Ukraine leads to uncontrolled hybridization and represents a threat to the conservation of aboriginal breeds of honey bees.

Introduction Over the past decade, there has been growing concern about the global extinction of honey bees (Apis mellifera L.), which threatens catastrophic consequences not only for the planet's ecosystem but also for security and the global economy (Neumann and Carreck, 2010; Fedoriak et al., 2018). ). Intensive studies of the causes of mass death of bees have identified several factors that may adversely affect their lives, namely - the use of pesticides, reducing the number of flowering plants, the spread of diseases and parasites including (Epilobee et al., 2016; Trapp et al., 2017; Dalmon et al., 2019; Fedoriak et al., 2019). One such factor is also the import and breeding of bees of another geographical origin, which ensures the loss of aboriginal breeds (ecotypes) of honey bees, which are formulated for a long time under the influence of natural selection and the best present in natural conditions (Metlitska et al., 2015; Parejo et al., 2015; others, 2016). In particular, due to the significant diversity of natural conditions, three local breeds of A. mellifera should be distributed on the territory of Ukraine: Dark European, Carpathian, and Ukrainian steppe, which are known to belong to three subspecies of the honey bee: A. mellifera mellifera, Am. Carnica and A. m. macedonics (Ruttner, 1988a; Cherevatov et al., 2019). In recent years, the uncontrolled import of A. mellifera species from other regions and even abroad has become widespread in Ukraine (Grigorchuk et al., 2020). This leads to a violation of the natural distribution of subspecies/ecotypes, bees. The study of morphometric parameters shows that today in Western Ukraine, uncontrolled hybridization of purebred bees is almost absent (Cherevatov et al., 2014; Cherevatov et al., 2016). Morphological features in hybrid families vary greatly, significantly reducing the reliability and even making it impossible to determine the breed when using traditional morphometric analysis. Therefore, to create a reliable picture of the distribution of bee subspecies/breeds in Ukraine, it is necessary to conduct genetic certification using molecular brands of guidance (Metlitska et al., 2010; Meixner et al., 2013; Achou et al., 2015; Pentek-Zakar et al., 2015). The special use allows molecular methods to identify genetic material in most common Carpathian and Ukrainian steppe rocks (Ruttner, 1988a; Grigorkov, 2017). In terms of the quality of molecular brands, the guide in

taxonomic studies of insects makes extensive use of areas of mitochondrial DNA (mtDNA) (Franck et al., 2001; Martimianakis et al., 2011; Meixner et al., 2013; Pentek-Zakar et al., 2015). The peculiarity of mtDNA is that it is inherited only through the maternal line and the presence in its composition of genes that do not expand due to recombination. In particular, a comparative analysis of the whole genus of the first subunit of cytochrome oxidase (CoI) or certain parts of it (Rizwan et al., 2018) is often required to present the difference between elevated and A. mellifera rocks. Therefore, taking into account the identification of A. mellifera breeds, we deciphered (sequenced) and compared the nucleotide sequence of parts of the CoI gene in representatives of honey bees located in different regions of Ukraine.

## Presentation

https://docs.google.com/presentation/d/10KpbmVSqRsb1yQP\_CawX9MZRSrDwykTEslawQntWz5s/edit?usp=sharing

## My lab in Ukraine and me

https://www.youtube.com/watch?v=XBfEiLLNd2U&ab\_channel=StudentblogMoleculargeneticsU A

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