

be partly due to the expression of recessive mutations in the unguarded sex chromosomes of the heterogametic sex (X or Z chromosomes). According to the UXh, inbreeding is predicted to decrease the lifespan of the homogametic sex more than the heterogametic sex, as the expression of recessive deleterious mutations in the X (or Z) chromosome will only increase in the former. In this study, we tested this central prediction of UXh by exploring the effects of inbreeding on lifespan (across three different social environments) and fitness in male and female *Drosophila melanogaster*. We found that inbreeding resulted in a greater reduction of female than male lifespan. Crucially, this sex-specific lifespan effect was consistent across the social environments and was not counterbalanced by inbreeding effects on fitness, indicating that it was potentially maladaptative. Our results are consistent with the UXh and suggest that it might have a crucial contribution to sex-specific ageing; however, other processes such as sex-specific gene expression patterns and sexually antagonistic recessive genes could at least partly explain the results obtained here. Hence, we suggest that more attention should be paid to the potential role of sex chromosomes in the evolution of sex-specific lifespan.

Keywords: sex-specific ageing, unguarded x hypothesis, fitness

First record of *Terpios gelatinosus* (orifera: Demospongiae; Bowerbank, 1866) along the coasts of Mediterranean Sea in Turkey verified by DNA barcoding

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Hibernal activity tends to increase year by year, especially in steppe and forest openness microhabitats. The most preferred refuges are the sunny ones while comparing to shadows in each microhabitat. When foraging activity takes into account, major microhabitat preferences change due to seasonal ambient dynamics. For example, in the beginning of spring, they are very active in forest openness; whilst in the fall the steppes and meadows. Furthermore, the most suitable microhabitat for mating activity, which has only been recorded in spring, was the forest openness. As a result, it is clear that some irregular temperature values in the first months of the years, especially in 2018, may cause an “early spring effect” during its hibernal activity period. Additionally, microhabitat preferences change through the seasons due to ectothermic strategy.

Keywords: artificial refuges, seasonal activity, reptile

Phylogenetic and Phylogeographic resolution of the Ascidiaceans along the Turkish Levantine Coasts

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Tunicates are primitive chordate and unlike the other chordates they have whole body regeneration potential. They are used as a model organism for stem cell study in many laboratories. The ‘Stem Cell’ technology is one of the most innovative and essential application in biomedicine and thus, identification of the organism is the most basic step to able to use organisms in biotechnological studies.

Botryllus and Botrylloides are in the botryllid ascidiaceans genera most of which originated from Mediterranean Sea and these invasive colonial tunicates are globally distributed in almost all of the seas with 30 and 18-recorded species respectively. Due to low interspecific variation and high intraspecific diversity with respect to their colours, structural organization and zooid adaptation, identification of tunicates that only based

on morphologic features have some limitations. Molecular tools are necessary to get over these ambiguities and classify them into the right taxa. In the Levantine coasts, only two species of tunicates are recorded to date, which are *Botryllus schlosseri* and *Botrylloides leachii*. Nevertheless, our observation indicates the existence of at least 10 different botryllid ascidian morphs along the Mediterranean coasts of Turkey. In this study, we aim to determine the biodiversity of botryllid ascidians along the North-eastern Mediterranean Sea's 8 different stations between Hatay and Antalya regions and also North Cyprus using mitochondrial and nuclear DNA markers (COI, 28S, 18S and H3). In addition, we targeted to monitor variation of transient sampling residing at the Kızkalesi, Hatay and Alanya region populations. So far about 100 colonies have been collected from Hatay, Antalya and Mersin regions. DNA isolation for all the regions has been completed. With a preliminary work high sequence quality has been obtained from three samples by using the four different primers. The next step of the project will be to complete all samples' PCR and sequencing steps to perform bioinformatics analysis for the elucidation of species/population compositions and interaction.

Keywords: Botryllid ascidians, Molecular Markers, Mediterranean

A geographical survey of mitochondrial DNA variation in greenfinch populations in Anatolia

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One of the fundamental goals of phylogeographical studies should be to achieve a wide-ranging geographical sampling of any investigated group. In this study, we conducted the mitochondrial DNA phylogeography for the greenfinch (*Chloris chloris*), including populations from Anatolia, in order to evaluate its genetic structure. At the same time, we tested published sub-species limits (Roselaar, 1994) within the species, which currently includes 3 recognized subspecies based on morphological characters. We based our study on haplotypes for the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) and subunit 3 (ND3). Most haplotypes were obtained from fresh tissues. We also discussed gene flow pattern through isolation-by-distance. Results were further discussed with the biogeographic history of Anatolia.

Keywords: Anatolia, birds, gene flow, phylogeography, population genetics, species limits, ND2, ND3.

Pilot genetic assessment of the eastern most populations of Carpathian endemic Montandon's newt *Lissotriton montandoni* within Bibrka- Stilsko Hill ridge (Lviv region, Ukraine)

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The smooth newt (*Lissotriton vulgaris*) is a widely distributed amphibian in the lowland East and Central Europe, while the closely related Montandon's newt (*L. montandoni*) is only found in the Carpathian Mountains. Despite the fact that these two species have distinct geographical ranges, there is a wide introgression of both nuclear and mitochondrial genes between them, to the extent that the entire mtDNA of *L. montandoni* has been completely replaced by the one of mtDNA haplotypes of *L. vulgaris*, at least among the populations samples until now (Babik et al. 2005). The previous sampling of *L. montandoni* mtDNA haplotypes did not include the area of Bibrka-Stilsko Hill ridge (Lviv region, Ukraine). The population of *L. montandoni* in this area is isolated from the main range of the species by the wide valley of river Dniester, and is surrounded by the populations of *L. vulgaris*. The extent of the mtDNA introgression from *L. vulgaris* to *L. montandoni* has not been studied in