

## ECOLOGY OF *TIGRIOPUS FULVUS* FISCHER, 1860 (COPEPODA: HARPACTICOIDA): METAPOPULATIONS AND ENVIRONMENTAL FACTORS

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*Tigriopus fulvus* (Fischer, 1860) is a supralittoral harpacticoid copepod usually found in Mediterranean Sea splash-pools which has many biological applications (aquaculture, ecotoxicology, including genomics). Aim of the present paper is to contribute to the ecological knowledge of the *Tigriopus fulvus* populations of Genova Nervi studying the main environmental parameters in relation to the metapopulation structure and distribution. Beside its well-known resistance to short-term environmental fluctuations, less is known about climate change effects on this species, as already recorded and studied in *Tigriopus californicus*. A first analysis related to population and new environmental conditions has been done in order to understand the possible behavioural and physiological response to the climatic change.

## EVALUATION OF BIMANUAL PERCUSSION PERFORMANCE IN NORMAL SUBJECTS AS A METHODOLOGICAL APPROACH FOR INVESTIGATING THE PROFESSIONAL PATHOLOGY IN DRUMMERS

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Several studies showed that musculoskeletal disorders present a significant problem for musicians. In particular, for drummers can occur two types of drumming injuries: over-use injuries like inflammations due to continual impact, muscular contraction and gravitational force, and traumatic injuries due to a single accident. In this study we developed an original computer-aided method for evaluating bimanual percussion performances using two different types of drumstick grip (modern and traditional grips) in 72 non-professional subjects of both sexes aged from 13 to 56 years were studied. Statistical analysis of quantitative data in terms of temporal precision and intensity of these percussion performances (efficacy, efficiency) and of qualitative data in terms of perceived satisfaction was carried out. We consider that this method may be useful for investigating the professional pathology in drummers.

## FROM THE BALTIC SEA TO THE PADANA PLAIN. TRACES OF MEDIEVAL MIGRATIONS IN NORTHERN ITALY REVEALED BY UNIPARENTAL MARKERS AND DEEP-ROOTED PEDIGREES\*

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Social and cultural factors had a critical role in determining the genetic structure of Europe. Therefore, socially-stratified populations may help to focus on specific episodes of European demographic history. In this study we use uniparental markers to analyse the genetic structure of *Partecipanza* in San Giovanni in Persiceto (Northern Italy), a peculiar institution whose origins date back to the Middle Ages and whose members form the patrilineal descent of a group of founder families. From a maternal point of view (mtDNA), *Partecipanza* is genetically homogeneous with the rest of the population. However, we observed a significant differentiation for Y-chromosomes. In addition, by comparing 17 Y-STR profiles with deep-rooted paternal pedigrees, we estimated a Y-STR mutation rate equal to  $3.90 \times 10^{-3}$  mutations per STR per generation and an average generation duration time of 33.38 years. When we used these values for tentative dating, we estimated 1300-600 years ago for the origins of the *Partecipanza*. These results, together with a peculiar Y-chromosomal composition and historical evidence, suggest that Germanic populations (Lombards in particular) settled in the area during the migration period (400-800 AD, approximately) and may have had an important role in the foundation of this community.

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## THE REPOPULATION OF GIAGLIONE (TO), ITALY AFTER THE PLAGUE OF 1629-30: AN ANALYSIS WITH THE FREQUENCIES OF SURNAMES

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The epidemic plague between 1629-1631 caused a dramatic contraction in the size of north Italian populations. The effect has been similar to a genetic bottleneck that reduced genetic variability in populations. Because of random genetic drift some alleles may be lost, while others can be successful, originating a genetic pool very different from the previous. An estimation of the genetic change in the ancient populations can be obtained by a comparison between the structure of the surnames before the plague and after the bottleneck. In this paper we studied the population of Giaglione (Susa Valley), one of the first Italian communities who was affected by plague from summer 1629. Before the disaster the population was constituted by 1250 inhabitants; after the plague there was only 400 persons. The effects of the bottleneck were calculated using the distribution of burial's surnames, for the period between 1604-1644. The modality of repopulation were studied by the censuses of 1680, 1718 and 1799. After the plague has been observed a flow of migrants that have temporarily enriched the community of new surnames. These new alleles have not been successful and the repopulation of Giaglione occurred largely from the descendants of the survivors to the plague. Therefore, the surnames have remained the same, but with frequencies completely changed compared the beginning of the sixteenth century. The trend of surnames' structure has been studied using the relationship index of Chen & Cavalli-Sforza and the multidimensional scaling analysis.