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Programma e Riassunti

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*Il Congresso è dedicato alla memoria del
Prof. Augusto Vigna Taglianti*

Programma

Venerdì 22 novembre 2019

11:00	INDIRIZZI DI SALUTO Annibale Mottana , Presidente Accademia dei XL Valerio Sbordonì , Presidente SIB
11:15	UN RICORDO DI AUGUSTO VIGNA TAGLIANTI Marco A. Bologna , Università Roma Tre
11:30	EVALUATING CORRELATION BETWEEN AREA, ENVIRONMENTAL HETEROGENEITY, AND SPECIES RICHNESS USING TERRESTRIAL ISOPODS (ONISCIDEA) FROM THE PONTINIAN ARCHIPELAGO (WEST MEDITERRANEAN) Gentile G. , Argano R., Taiti S.
11:45	ELEVATIONAL PATTERNS OF GENERIC DIVERSITY IN THE TENEBRIONID BEETLES (COLEOPTERA TENEBRIONIDAE) OF LATIUM (CENTRAL ITALY) Fattorini S., Mantoni C. , Di Biase L., Pace L., Biondi M.
12:00	FILOGEOGRAFIA MOLECOLARE E MODELLI DI DISTRIBUZIONE DELLE SPECIE (Simposio) Coordinatori: Paolo Gratton (MaxPlank Institute Lipsia), Silvio Marta (Università Milano Statale)
12:15	BIOGEOGRAPHIC HISTORY OF THE GENUS <i>HYCLEUS</i> INFERRED BY MOLECULAR DATA Riccieri A. , Mancini E., Salvi D., Bologna M.A
12:30	COMPARATIVE PHYLOGEOGRAPHY OF TWO MEDITERRANEAN CAVE CRICKETS' GENERA: <i>DOLICHOPODA</i> SPP. AND <i>TROGLOPHILUS</i> SPP. (ORTHOPTERA, RHAPHIDOPHORIDAE) Allegrucci G. , Sbordonì V.
12:45	MOLECULAR PHYLOGENY AND BIOGEOGRAPHY OF ITALIAN FRESHWATER AMPHIPODS: A TRIBUTE TO THE WORK OF SANDRO RUFFO AND AUGUSTO VIGNA TAGLIANTI Stoch F. , Flot J.F.
13:00	<i>Pranzo</i>
14:00	WHAT DO PHYLOGENETIC DATA TELL US ABOUT THE AMPHI-ADRIATIC DISTRIBUTIONS IN PLANTS? Frajman B. , Schönswetter P.
14:30	ECOLOGICAL GENETICS AND ADAPTATION IN EUROPEAN YEW (<i>TAXUS BACCATA</i> L.) AND ITALIAN STONE PINE (<i>PINUS PINEA</i> L.) Vendramin. G.G.
15:00	SURVIVING GLACIATION AT THE EDGES OF EMPIRE Casazza G. , Conti E., Grassi F., Guerrina M., Theodoridis S., Zecca G., Minuto L.
15:30	<i>Pausa caffè</i>

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- 16:00** PHYLOGEOGRAPHY OF THE WESTERN EURASIAN *STYRAX OFFICINALIS* L. (STYRACACEAE)
Spada F., Parducci L., Nobile A., Ribeiro, M.M. , Suyama Y.
- 16:15** PHYLOGEOGRAPHY OF *TRICHOSIROCALUS HORRIDUS*: A WEEVIL ASSOCIATED TO HOST PLANTS BELONGING TO TRIBE CARDUEAE (ASTERACEAE)
Moschella F., Colonnelli E., De Biase A.
- 16:30** TOWARDS A DATABANK-BASED PHYLOGEOGRAPHIC SYNTHESIS
Gratton P., Mafessoni F., Marta S., Bocksberger G., Mundry R., Kühl H.
- 16:45** BEYOND REFUGIA: PALAEOENVIRONMENTAL LEGACIES ON CURRENT AMPHIBIAN PHYLOGEOGRAPHIC STRUCTURE
Marta S., Druella D., Gratton P., Ficetola G.F.
- 17:00** EVALUATING SPECIES DISTRIBUTION MODELS TEMPORAL PROJECTION THROUGH HISTORICAL HERBARIUM DATA
Dolci D., D'Antraccoli M., Roma-Marzio F., Peruzzi L.
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17:30 *Assemblea dei soci della SIB*

20:30 *Cena sociale all'Hostaria Gran Sasso*
via Como 10, Roma

Sabato 23 novembre 2019

9:15	CITIZEN SCIENCE, BANCHE DATI E BIOGEOGRAFIA (Simposio) Coordinatore: Stefano Martellos (Università Trieste)
9:30	IL NETWORK NAZIONALE DELLA BIODIVERSITÀ E I DATI PROVENIENTI DA FONTI DI CITIZEN SCIENCE Di Noi A., Di Stefano C.
10:00	“BIOGEOGRAFIA PARTECIPATA”: COME LA CITIZEN SCIENCE STA CAMBIANDO IL MODO DI FARE SCIENZA Sforzi A.
10:30	CHECKLIST DELLE SPECIE DELLA FAUNA TRICOTTEROLOGICA ITALIANA Lodovici O., Valle M.
10:45	RIFLESSIONI SULL’ARANEOFAUNA ITALIANA Pantini P., Isaia M.
11:00	ON THE EDGE BETWEEN THE MEDITERRANEAN AND EUROSIBERIAN REGIONS: A NEW PHYTOGEOGRAPHICAL SUBDIVISION OF TUSCANY Carta A., D'Antraccoli M., Peruzzi L.
11:15	<i>Pausa caffè</i>
11:30	WIKIPLANTBASE #ITALIA, A CITIZEN SCIENCE PROJECT TO BOOST ONLINE PLANT OCCURRENCE RECORDS IN ITALY Bedini G., Peruzzi L.
11:45	WIKIPLANTBASE #LIGURIA: LA CITIZEN SCIENCE COME VOLANO PER LA FLORISTICA LIGURE Dagnino D., Longo D., Peccenini S., Barberis G.
12:00	IL MONITORAGGIO DELLA BIODIVERSITÀ NELLA RETE NATURA 2000 ATTRAVERSO IL VOLONTARIATO EUROPEO: PRIMI RISULTATI DEL PROGETTO LIFE ESC360 Campanaro A., Petriccione B.
12:15	STAMBECCO (<i>CAPRA IBEX</i>) SULLE ALPI OROBIE: ESPERIENZA DI CITIZEN SCIENCE NEL TRIENNIO 2017-2019 Pelliccioli L., Valoti P., Ghedina A., Cimberio P.
12:30	SCIENTIST BY CHANCE: NATURAL SCIENCE FORUMS AS PRECIOUS RESOURCE OF SUITABLE BIODIVERSITY DATA De Felici S., Mazzei P., Dinolfo T., Gioli F., Labriola C., Sbordon V., Cesaroni D.
12:45	ACTAPLANTARUM: DA FORUM DEDICATO ALLA FLORA SPONTANEA ITALIANA A BANCA DATI DI DISTRIBUZIONI FLORISTICHE NAZIONALI Longo D., Baglivo A., Cibei C., Dose G., Giordana F., Magni C., Nicoletta G., Salvai G., Servodio S., Tomasi D., Zepigi M.
13:00	<i>Chiusura del 41° Congresso SIB</i>

**Riassunti
delle
presentazioni**

EVALUATING CORRELATION BETWEEN AREA, ENVIRONMENTAL HETEROGENEITY, AND SPECIES RICHNESS USING TERRESTRIAL ISOPODS (ONISCIDEA) FROM THE PONTINIAN ARCHIPELAGO (WEST MEDITERRANEAN)

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Island biogeography, habitat diversity, taxocenosis structure, small island effect, path analysis

Area and environmental heterogeneity influence species richness in islands. Whether area or environmental heterogeneity is more relevant in determining species richness is a central issue in island biogeography. Several models have been proposed, addressing the issue, and they can be reconducted to three main concepts developed to explain the species-area relationship: 1) the area-per se concept (known also as the extinction-colonization equilibrium); 2) the random placement (passive sampling), and the 3) environmental heterogeneity (habitat diversity). In this work we explore correlation between area, environmental heterogeneity, and species richness by using faunistic data of Oniscidea inhabiting the Pontinian islands, a group of five small volcanic islands and several islets in the Tyrrhenian Sea, located about 60Km from the Italian mainland.

We found that the colonization of Pontinian archipelago might have taken place through random processes independent of geographic distance. Even in very small-size island systems, environmental heterogeneity and area are both good predictors of species richness even though environmental heterogeneity could prevalently influence the taxocenosis structure and, ultimately, affect the number of species of Oniscidea via direct effect and as a mediating factor of area.

ELEVATIONAL PATTERNS OF GENERIC DIVERSITY IN THE TENEBRIONID BEETLES (COLEOPTERA TENEBRIONIDAE) OF LATIUM (CENTRAL ITALY)

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altitudinal gradient; diversity; tenebrionid; beetles

Elevational variations in biodiversity are among the most investigated patterns in biogeography. The concept of generic diversity expresses the 'diversification' of species into genera as the probability that two species belong to different genera. Since niche overlap is assumed to be higher in congeneric species, competition should increase generic diversity. On the other hand, generic diversity might be low in highly selective environments, where only species with similar adaptations can survive. We used the distribution of 84 species and subspecies of tenebrionid beetles in Latium (Central Italy) to investigate how generic diversity varies with elevation from sea level to 2,400 m altitude. We found that, in general, generic diversity decreases with elevation. This suggests that most genera are progressively eliminated by increasingly unfavorable conditions, with the remaining species belonging to the few genera that include the best adapted species. However, while geophilous tenebrionids conform to this general pattern, xylophilous species tend to maintain high values of generic diversity across the gradient. These results suggest that geophilous species are more sensitive to variation in environmental factors and the advantages of close relationship (similar adaptations to harsh conditions) are greater than the drawbacks (competition). This is consistent with the fact that geophilous tenebrionids are mostly generalist detritivores and hence competition for food is expected to be low. By contrast, xylophilous species might be less directly exposed to harsh conditions, but more subject to competition to find appropriate microhabitats and food (hence higher generic diversity). Interestingly, above 1000 m, which marks the transition from the sclerophyll evergreen vegetation and heliophilic broadleaves to the sciaphilous broadleaves, all genera of xylophilous tenebrionids are represented by only one species, which suggests a combination of strong competition and harsh conditions. Further studies at finer scales are however needed to support these interpretations.

Simposio

*Filogeografia molecolare e
modelli di distribuzione delle specie*

Coordinatori: Paolo Gratton (MaxPlank Institute Lipsia)
Silvio Marta (Università Milano Statale)

BIOGEOGRAPHIC HISTORY OF THE GENUS *HYCLEUS* INFERRED BY MOLECULAR DATA

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hyperdiversity; BioGeoBEARS; Meloidae.

The genus *Hycleus* is the largest genus of the family of Meloidae with more than 500 species widely distributed in the Old World. In particular in the Palaearctic region occur almost 50 species, the Saharo Sindian Transitional region and the Oriental region comprises around 40 species each, whereas the highest number of species (~380) occurs in the Afrotropical region. The evolutionary history of *Hycleus* as well as the biogeographic processes related to its diversification have never been studied. Our work, based on a robust time-calibrated phylogenetic tree built on a matrix of five genes (one mitochondrial and four nuclear) and 125 species, provide a biogeographic hypothesis that allow explaining the current diversity and the observed distribution patterns of this genus. Biogeographic analyses were carried out with the R package BioGeoBEARS, that allow to select the best biogeographic model for our data to be used to infer a plausible biogeographic scenario for *Hycleus*. Our results suggested an Early Miocene origin (~20 Mya) of the genus *Hycleus* in the African continent. Subsequently (~14 Mya), a lineage diverged and spread in the Saharo-Sindian Transitional Region, whereas another lineage with Afrotropical origin spread ~9 Mya ago in the Palaearctic Region. From the latter Palaearctic lineage, in the Late Miocene (~6 Mya) a second Saharo-Sindian group branched off. The Oriental species of *Hycleus*, instead, originated ~5 Mya ago following a dispersal event through the Arabian Peninsula from the Afrotropical Region.

COMPARATIVE PHYLOGEOGRAPHY OF TWO MEDITERRANEAN CAVE CRICKETS' GENERA: *DOLICHOPODA* SPP. AND *TROGLOPHILUS* SPP. (ORTHOPTERA, RHAPHIDOPHORIDAE)

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cave crickets; Mediterranean region; phylogeography; molecular clock; Rhaphidophoridae.

A prediction in phylogeographic studies is that patterns of lineage diversity and timing will be similar within the same landscape under the assumption that these lineages have responded to past environmental changes in comparable ways. Most of the known *Troglophilus* and *Dolichopoda* species were included in this study. Both of them belong to the family Rhaphidophoridae Walker, 1869 and show wide, disjunct geographic distribution across the temperate areas of the Boreal and Austral hemispheres. They include species mostly confined to caves and other moist environments. Most species of the genus *Dolichopoda* are strictly dependent upon caves. However, especially in the northern part of the range, several populations inhabit cave-like habitat such as rock crevices and ravines and individuals are often observed outside in moist or mesic woods. The *Troglophilus* species are less dependent on caves; humid forests and any type of shelter that could protect them from dryness during the summer season and from low temperatures during the winter season represent potential habitats for these species. *Dolichopoda* ranges from the Caucasus to the eastern Pyrenees including some of the large Mediterranean continental islands (i.e., Sardinia and Corsica). The genus range overlaps with that of *Troglophilus* in its eastern portion only; *Dolichopoda* is more uniformly distributed along the Italian Peninsula, while *Troglophilus* does not extend its range past the eastern Alps.

Three mitochondrial genes (12S, 16S, COI) and two nuclear ones (18S and 28S) in both *Dolichopoda* and *Troglophilus* species were partially sequenced. Genetic diversity indicated a phylogeographic pattern, as resulted from Mantel Test, in both genera. Genetic distances distribution showed deeper divergences between *Troglophilus* species than *Dolichopoda* ones, while haplotype diversity was higher in *Dolichopoda*. Phylogenetic trees for each genus were reconstructed using Bayesian inferences. A relaxed molecular clock was used to test alternative biogeographical hypotheses. Results showed that a double colonization of the Hellenic Peninsula, following separate continental and trans-Aegean routes during the Messinian stage, best accounts for the present distribution of *Dolichopoda* species, while the radiation of *Troglophilus* species likely started from the Aegean and proceeded eastward to Anatolia and westward to the Balkan region, probably due to the formation of the Aegean Trench. These diverse patterns suggest that combinations of intrinsic (taxon ecology) and extrinsic (extinction and dispersal) factors can result in apparently different biogeographic outcomes.

MOLECULAR PHYLOGENY AND BIOGEOGRAPHY OF ITALIAN FRESHWATER AMPHIPODS: A TRIBUTE TO THE WORK OF SANDRO RUFFO AND AUGUSTO VIGNA TAGLIANTI

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crustaceans; barcoding; freshwaters; groundwaters.

Italian freshwater amphipod fauna includes at least 11 families and over a hundred species. Three genera – the epigeal *Homoeogammarus* and *Gammarus*, and the predominantly subterranean *Niphargus* – make up for over 60% of all Italian species. Morphospecies analysis carried out during the last century, largely due to 50 years of studies conducted by Sandro Ruffo, suggested that over 60% of all Italian species are endemic (sometimes known from a single site). Only two surface alien species were known. Unfortunately, species delineation remained quite uncertain in most genera, mainly due to convergent evolution and, especially for groundwater species, to paedomorphic heterochronic events, making the traditional morphotaxonomic approach quite unsatisfactory. To address this problem, morphology was combined with molecular techniques. Samples of freshwater amphipods were collected in over 1,300 sites in Italy and neighboring areas, including topotypes of nearly all species and their junior synonyms, and independent nuclear and mitochondrial markers were amplified and sequenced. Traditional species groups based on morphology turned out to be paraphyletic, and cryptic species richness was high both in surface than in groundwaters.

The biogeographical patterns delineated with the help of molecular analyses are quite complex. The most intriguing components of the Italian fauna are the paleo-Thyrrhenian clades (originating from the fragmentation of the Corso-Sardinian and other microplates) and especially the trans-Adriatic clades (some of them reaching the Thyrrhenian coast as well as Sardinia). These last clades were already pointed out in their pioneering papers by Sandro Ruffo and Augusto Vigna Taglianti in the sixties of last century, and molecular analyses confirmed their hypotheses based on traditional taxonomy. These clades form the core of the paleo-endemics which shaped the Italian fauna, together with some older relics (*Metacrangonyctidae*, *Salentinellidae*, *Metaingolfiellidae*, *Pseudoniphargidae*) probably deriving from the fragmentation of the Tethys Sea. More recent invaders of Balkanic origin are found in the Pre-Alpine areas (mainly *Gammaridae* and *Niphargidae*), while affinities with southern France and regions north of the Alps are very limited. An outstanding species richness was unexpectedly found in surface amphipods inhabiting Sicily, revealing new paleogeographic affinities of the island. Finally, the small part of the Dinaric Karst included in north-eastern Italy presents a few merodinaric elements that add further complexity to this biogeographic puzzle.

WHAT DO PHYLOGENETIC DATA TELL US ABOUT THE AMPHI-ADRIATIC DISTRIBUTIONS IN PLANTS?

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phylogeography; pleistocene; apennine peninsula; balkan peninsula.

The Mediterranean Basin is one of the richest areas in the world in terms of animal and plant diversity and considered one of the 25 Global Biodiversity Hotspots. In Europe, very species-rich areas in the Mediterranean are the Apennine and the Balkan Peninsula, where several thousand plant species have been recorded. The higher plant richness of the Balkan Peninsula is attributable to its climatic and topographic complexity, its geographic position on the crossroads among different floristic regions and relative topological stability through longer geological history. On the other hand, the Apennine Peninsula is the geologically youngest of the three Southern European peninsulas and after its emergence vast areas opened for immigration and diversification of biota. Several plant and animal species nowadays exhibit amphi-Adriatic disjunct distributions spanning both peninsulas. Such distribution patterns have traditionally mostly been explained by land connections between both peninsulas during the Messinian salinity crisis (Miocene/Pliocene), but recent studies employing molecular dating pointed to more recent, i.e. Pleistocene, dispersals from the Balkans to Italy in several plant species and indicated that migrations in earlier times resulted in amphi-Adriatic distributed species groups rather than single species. Interestingly, most of the inferred migrations were from the Balkans to the Apennine Peninsula, whereas the opposite direction seems to be rare. Besides presenting several recent studies based on the DNA sequence and amplified fragment length polymorphism (AFLP) data, an outlook in exploring this interesting biogeographical pattern using next generation sequencing and testing different demographic models will be given.

**ECOLOGICAL GENETICS AND ADAPTATION IN EUROPEAN YEW
(*TAXUS BACCATA* L.) AND ITALIAN STONE PINE (*PINUS PINEA* L.)**

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adaptation; candidate genes; climate changes; phylogeography; forest trees.

Studies on how forest tree species adapt to major environmental drivers have acquired great relevance in the last years, fostered by increasing societal demands to produce sound forest management and conservation plans in a context of climate change. Some species, such as the European yew (*Taxus baccata*), due to their fragmented (albeit large) distribution and typically low effective population sizes may be more severely affected by climate change than other forest trees. Here we provide an overview of our research on population genetics and adaptation in this iconic conifer. We first describe the multi-layered population genetic structure revealed by microsatellites at different spatial scales, from within-stand to rangewide. Second, we present our work on molecular adaptation to climate based on 1,210 candidate genes (25,726 SNPs) obtained from an exome capture experiment covering a continentality gradient in Europe. First results based on new-generation outlier detection and environmental association approaches identified a methionine synthase, involved in responses to stress, as a target of selection in this species. Similarly, we surveyed the patterns of nucleotide diversity and molecular adaptation across hundreds of loci in a circum-Mediterranean conifer (*Pinus pinea* L.) that represents one of the most extreme cases of genetic pauperization across widespread outbreeding taxa. We found very little genetic variation in both hypervariable non-coding (nuSSRs) and gene-coding loci, which translated into genetic diversity estimates one order magnitude lower than those previously reported for pines. Such values were consistent with a strong population decline that began some ~0.8Ma. Hypotheses on how stone pine, a species depleted of genetic variation, has been able to survive, thrive, and successfully compete with closely-related taxa that occupy a similar ecological niche, such as maritime pine, are formulated and discussed.

SURVIVING GLACIATION AT THE EDGES OF EMPIRE

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late quaternary glaciations; phylogeography; species distribution models; endemisms.

Three main hypotheses may explain the distribution of alpine and arctic endemic plants: i) endemics with preference for more temperate climatic conditions had narrower distributions during glacial maxima and, when the glaciers retreated, moderately expanded their distributional range; ii) cold-adapted endemics had larger distributions during glacial maxima and, when the temperatures raised, contracted their distributional range; and iii) in areas less affected by the Late Quaternary glaciations, the distribution of endemics results by local buffering from extreme environmental effects. The hypothesis of post-glacial expansion has been supported by studies on several endemic species in the Eastern Alps, while the other two hypotheses have rarely been supported for endemic species and never in the European Alps. This is likely due to the massive ice-sheet in large part of European Alps, which eliminated suitable habitats and restricted the possibility of glacial expansion and/or in situ survival for many mountain plants during the glacial period. Recent studies on several plants (i.e. *Primula allionii*, *Silene cordifolia*, *Viola argenteria* and *Berardia subacaulis*) endemic to the South-Western Alps (SW Alps) combined the results of species distribution models and genetic analysis to reconstruct potential contractions and expansions of species through the Late Quaternary. In these species both populations and genotypes extinction was minimal during the Last Glacial Maximum, and they largely survived in situ without range contraction, resulting in complex phylogeographical pattern. In general, the phylogeographical patterns detected in SW Alps differ from the pattern usually observed in the Alps, where endemic species primarily retreated into refugia during cold periods and expanded during warm periods. In fact, in most of the Alps, the massive ice covers prevented also cold-adapted endemics to reach or to survive in most of the potentially suitable areas. On the contrary, in the SW Alps, the ice cover was less extended than in the rest of the Alps and this may have not prevented species to persist or to expand in most of the climatically suitable areas even at high altitude during the glaciations. Taken together, our findings support to the idea that in area less affected by glaciations, the genetic pattern of endemic species may not result only from the effect last glacial period but from cumulative effect of Tertiary paleoenvironmental changes and also by more recent changes.

PHYLOGEOGRAPHY OF THE WESTERN EURASIAN *STYRAX OFFICINALIS* L. (STYRACACEAE)

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relictuality; disjunctions; biogeography; molecular differentiation; phylogeny.

Styrax officinalis is an Eurasian species with highly fragmented distribution in S.E. Mediterranean regions with core range in the Aegeo-Anatolian districts, reaching SW Italy and the Near East. Populations in peninsular Italy have long been considered by local scholars a human import from classic times, due to its very restricted local range close to Rome, the overall scanty and isolated populations and an uncritical treatment of historical sources about an alleged local use of its exudate in the past. Nevertheless the floral framework of its associates in the Italian stands is rich in species belonging to the eastern geo-element of the European flora, alternatively suggesting native status of the species. Closest relative is *S. redivivus* in SW/N America, adding intriguing issues about intercontinental disjunctions during the evolutionary history of *S. officinalis* s.l. We performed population genetic analysis using genome-wide sequencing markers in order to reconstruct patterns of geographical differentiation and demographic history (time of differentiation, migration routes) of the species, on samples selected from the whole total range of *S. officinalis* in the Mediterranean regions, from Lebanon to Provence, Results from the genetic analyses support generalized relictuality all over the W European range of the species and of the Italian populations specifically, rather than human import.

PHYLOGEOGRAPHY OF *TRICHOSIROCALUS HORRIDUS*: A WEEVIL ASSOCIATED TO HOST PLANTS BELONGING TO TRIBE CARDUEAE (ASTERACEAE)

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Trichosirocalus horridus; mtDNA; nuDNA; Pleistocene.

The phylogeographic studies aim to clarify the patterns and processes underlying the geographical distribution of genetic lineages, in particular one or more closely related species. Frequent gene flow generally reduces the level of differentiation between populations, while other factors and processes, current or past, such as geographical barriers and local adaptations, can lead to subdivisions of the population. Palaeoclimatic events and climatic oscillations have long been studied by evolutionary biologists, in particular the role played by glacial and interglacial phases in the diversification of many plants and animals.

The genus *Trichosirocalus* includes 16 species with Palaearctic distribution and associated mainly with Plantaginaceae and Asteraceae. In particular, *Trichosirocalus horridus* shows a distribution from the Iberian peninsula to the Caucasus and an association with plant species belonging to the genera *Carduus*, *Cirsium* and occasionally *Onopordum* (Asteraceae, Cardueae). Because these thistles are invasive in North America, Australia and New Zealand, *T. horridus* has been used as a biological control agent with the introduction of larvae in these countries. Samples of adult specimens were collected during sampling campaigns carried out in 9 different countries (France, Georgia, Germany, Greece, Iberian Peninsula, Italy, Romania, Slovakia, Turkey). We investigated, for the first time, the phylogeography of *Trichosirocalus horridus* by examining 621 base pairs of the gene encoding the subunit I of cytochrome c oxidase (*cox1*) for 215 individuals and 722 bp of the nuclear gene encoding the elongation factor alpha subunit (*Ef1α*) for 305 sequences. The analysis of the genetic divergence between the geographic groups was performed by MEGAX v10.1. Bayesian analyzes were performed using the BEAST v1.8.4 version by selecting the best nucleotide substitution models using jModelTest. The evaluation of the intra and interpopulational genetic structure was performed by building a network of haplotypes, using TCS v1.21, and an analysis of molecular variance (AMOVA) through ARLEQUIN v3.5.2.2. Spatial diffusion processes have been estimated by Bayesian phylogeographic reconstructions (BP). Historical demographic changes were deduced for each group based on mtDNA data through mismatch analysis and Extended Bayesian Skyline Plot analysis (EBSP). Our data show that the structure of genetic variation is consistent with the geographical distribution of populations, suggesting an eastern origin of this species. The model found is probably related to the demographic histories of the populations analyzed and most likely influenced by the climatic fluctuations of the Quaternary. Furthermore, the Italian populations surveyed appear to be grouped into two contingents, one exclusive to Italy and another showing relations with other European populations.

TOWARDS A DATABANK-BASED PHYLOGEOGRAPHIC SYNTHESIS

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comparative phylogeography; data banks; spatial modeling.

Comparative analysis of geographic patterns of intraspecific genetic diversity may reveal past range dynamics and community-level processes at continental and global scales.

Large-scale analyses of DNA data stored in public databanks have the potential to boost our understanding of the global distribution of biodiversity.

We 1) surveyed the global availability of georeferenced DNA sequences and evaluated their potential for a highly-automated analysis of intraspecific patterns of genetic diversity: 2) developed a pipeline based on spatial modelling of allele frequencies to generate spatially continuous maps of phylogeographically-informative summary statistics (nucleotide diversity, genetic uniqueness and slope of genetic change) from relatively sparse data; 3) applied our pipeline to BOLD and GenBank data sets for European butterflies and African mammals: 4) show that, depending on the abundance and quality of data, our methodology may provide an objective and consistent way to map global patterns of genetic diversity: 5) discuss current challenges for an effective application of DNA sequence databases in biogeography.

BEYOND REFUGIA: PALAEOENVIRONMENTAL LEGACIES ON CURRENT AMPHIBIAN PHYLOGEOGRAPHIC STRUCTURE

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refugia; environmental stability; nucleotide diversity; quadratic entropy(QE)-based index.

During the Pleistocene, species experienced range contractions, shifts or expansions due to repeated climatic oscillations, with these environmental changes leaving deep signatures on the genetic structure of single species. Traditionally, a discrete approach has been applied to the study of phylogeographic patterns, with the identification of a few glacial refugia for temperate species. Some authors have later expanded the refugial concept by pointing out the existence of both multiple and cryptic northern refugia, as well as the species' individualistic responses to these changes. All of these developments allowed highlighting the extreme complexity of past demographic histories, but still have the shortcoming of being spatially and / or ecologically discrete (i.e., one or a few refugia / ecologically similar taxa at a time). Under the assumption that the lesser the change through time is, the more continuously suitable an area has been, we propose stability (measured as rates of environmental and climatic change) as an ecologically and spatially "agnostic" approach to deal with the diversity in refugial positioning and species ecology. We used mtDNA data from 20 Amphibian taxa endemic to Italy and/or Corsica (382 populations, 2601 individuals and 573 haplotypes) to model the demographic responses to Late Quaternary climate-change velocity as well as to ecosystem stability, topographic complexity and human footprint. Both nucleotide diversity (π) and mean per-population originality (QE-based index) were evaluated as proxies of past phylogeographic histories. This allowed focusing on alternative outcomes of demographic persistence during adverse conditions, namely the maintenance of i) higher intraspecific diversity or ii) genetically divergent populations, respectively. Our analyses highlighted that diversity and originality can show different responses to environmental and climatic stability, while returning no response to contemporary human footprint. Nucleotide diversity frequently peaked outside stable areas as a likely consequence of secondary contacts between divergent lineages, whereas originality showed a significant association with stability, thus supporting the "agnostic" approach to environmental variation we propose.

EVALUATING SPECIES DISTRIBUTION MODELS TEMPORAL PROJECTION THROUGH HISTORICAL HERBARIUM DATA

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climate change; distribution; BIOMOD; SDM; vascular plants.

The ranges of species are typically changing over space and time. However, global changes (e.g., climate and land-use changes) are leading to shifts in species ranges at larger extents and overshooting periods than would otherwise occur. Measuring and predicting species range shifts in response to anthropogenic global changes is crucial for planning effective conservation strategies. To this aim, species distribution models (SDMs) have become a fundamental tool in ecology, biogeography, biodiversity conservation, and natural resource management, due to their ability to predict distributions across landscapes and to forecast future species distributions. In particular, predicting the response to climate change has become an extremely active field of research, albeit the effectiveness of SDMs when projected to the future is hardly assessed, due to the absence of 'future' experimental data. To assess the reliability of SDMs forecasts, we have planned an analysis based on the comparison between models built with historical distribution and climate data, then projected to 'the future' (= the present day), and models built with current distribution and climate data. We used nine Italian endemic plant species as case study, and for each of them we calculated ensemble models using Biomod 2. Models built with historical herbarium data (1910-1930) and historical climatic maps, then projected to current climate, represent the theoretical 'future' distribution for each species. Models realized with current biological data (1980-present) and current climatic maps represent the current potential distribution for each case study. Based on the comparison of the 'future' projection to the current potential distribution, and also using current actual distribution as a further independent testing method, we found an overestimation of the projection function for four taxa (*Aubrieta columnnae* Guss. subsp. *columnnae* - Brassicaceae, *Galium magellense* Ten. - Rubiaceae, *Saxifraga porophylla* Bertol. subsp. *porophylla* - Saxifragaceae, and *Sedum magellense* Ten. subsp. *magellense* - Crassulaceae), but an underestimation for the remaining five (*Adenostyles australis* (Ten.) Iamonico & Pignatti - Asteraceae, *Crocus biflorus* Mill. and *C. imperati* Ten. - Iridaceae, *Gypsophila arrostoi* Guss. subsp. *arrostoi* - Caryophyllaceae, *Helleborus viridis* L. subsp. *bocconei* (Ten.) Peruzzi - Ranunculaceae). Interestingly, these differences seem correlated to the ecological features of each taxon. In particular, the four species prone to overestimation are stenoeccious, showing a limited habitat tolerance range. On the contrary, the five species prone to underestimation are euryecious, showing wider habitat tolerance range. Our findings suggest that SDM projection under future climatic scenarios could be affected by systematic errors, seemingly depending on the autoecology of the species under study.

Simposio

Citizen Science, banche dati e biogeografia

Coordinatore: Stefano Martellos (Università Trieste)

IL NETWORK NAZIONALE DELLA BIODIVERSITA' E I DATI PROVENIENTI DA FONTI DI CITIZEN SCIENCE

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biodiversità, citizen science.

In adempimento alle vigenti normative nazionali ed internazionali, il Ministero dell' Ambiente e della Tutela del Territorio e del Mare (MATTM) ha promosso il progetto "Sistema Ambiente", che ha tra le sue finalità il supporto alla definizione delle strategie nazionali per l'uso sostenibile delle risorse ambientali e l'erogazione di servizi alla Pubblica Amministrazione, alle imprese e ai cittadini.

Nell'ambito del progetto Sistema Ambiente, il MATTM si è dotato di una infrastruttura capace di fornire e gestire in modo capillare informazioni geografiche sulla Biodiversità su tutto il territorio nazionale, denominata Network Nazionale della Biodiversità (NNB). L'infrastruttura è organizzata in maniera da consentire la condivisione di dati ed informazioni di rilievo sul tema della biodiversità senza che ne avvenga il trasferimento fisico, facendo sì che i dati restino nella disponibilità degli Enti che li producono e ne detengono i diritti legali.

Per garantire l'implementazione del Network Nazionale della Biodiversità, quale strumento a supporto della "Strategia Nazionale sulla Biodiversità", il MATTM ha stipulato con ISPRA una convenzione finalizzata alla gestione evolutiva.

La piattaforma ad oggi gestisce circa 9.000.000 di record di osservazioni di specie presenti sul territorio nazionale provenienti da 60 banche dati fornite da diversi Enti/provider facenti parte del Network.

Una quota significativa di questi dati proviene da osservazioni raccolte mediante processi partecipati di "Citizen Science", caratterizzati da 3 diversi livelli di validazione e verifica:

- iNaturalist: dati provenienti da cittadini non necessariamente esperti della materia, validati e verificati dalla stessa comunità;
- CSMON LIFE: dati provenienti da cittadini non necessariamente esperti della materia ma validati e verificati da esperti;
- EPE – EURING Protocol Engine: dati provenienti da cittadini formati sulla materia e validati e verificati da ISPRA.

Al fine di sfruttare appieno le potenzialità dei processi partecipativi tipici della "Citizen Science", ISPRA ha avviato un'ulteriore fase di sviluppo della piattaforma NNB, che prevede la realizzazione di APP scaricabili gratuitamente su dispositivi mobili.

Un primo prototipo di smartapp è già in via di definizione e consentirà presto il coinvolgimento di cittadini (esperti e non) in numerose campagne di raccolta dati. I record confluiranno direttamente sulla piattaforma NNB e contribuiranno a costruire il "sistema informativo" necessario alla conoscenza e alla conservazione della biodiversità (segnalazione della presenza di specie animali o vegetali non indigene, individuazione e monitoraggio di specie rare o minacciate, ecc.).

“BIOGEOGRAFIA PARTECIPATA”: COME LA CITIZEN SCIENCE STA CAMBIANDO IL MODO DI FARE SCIENZA

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citizen science; biodiversità; corologia; innovazione.

La coscienza popolare verso l'ambiente è in crescita, così come sta aumentando la disponibilità a forme di collaborazione trasversale. Le nuove tecnologie hanno aperto orizzonti impensabili solo pochi anni fa. L'ampia e rapida diffusione dei telefoni di nuova generazione, ad esempio, consente oggi di connettersi ad internet virtualmente in ogni luogo, registrare le coordinate geografiche di un punto (GPS), scattare una foto, gestire applicativi specifici. Da questi elementi ha tratto ulteriore slancio la Citizen Science, il coinvolgimento attivo dei cittadini nella ricerca scientifica. Le tipologie di persone coinvolte nei progetti sono varie: studenti, semplici appassionati, scienziati dilettanti non inseriti in strutture accademiche, come università ed enti di ricerca. Ma l'aspetto forse più rivoluzionario della Citizen Science è il cambiamento di paradigma, che porta la ricerca scientifica da materia ad appannaggio di soli esperti a motivo di inclusione e compartecipazione nella acquisizione delle conoscenze a vantaggio di tutti. Sono moltissimi e in continua crescita gli esempi di applicazioni della CS nei diversi ambiti scientifici, anche nel nostro paese. Tra questi la biogeografia è certamente uno dei settori in grado di trarre maggior vantaggio da attività di citizen science. La comunicazione verterà su alcuni esempi di progetti sviluppati ad oggi con queste finalità, fornendo inoltre una panoramica delle potenzialità e dei possibili sviluppi della citizen science nel nostro paese.

CHECKLIST DELLE SPECIE DELLA FAUNA TRICOTTEROLOGICA ITALIANA

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Trichoptera; checklist; Italy.

Viene presentata una nuova checklist della fauna italiana basata sull'analisi della letteratura prendendo in esame unicamente le segnalazioni di tricoteri adulti in quanto la determinazione delle larve non è sempre attendibile. Un'accurata ricerca bibliografica ha portato ad individuare 584 pubblicazioni relative alla tricoterofauna italiana che coprono un arco di tempo compreso tra il 1761 ed oggi.

La checklist verrà aggiornata annualmente e sarà scaricabile dal sito www.trichoptera.it

Per ogni taxon viene indicata la presenza in Italia continentale, Sicilia e Sardegna, inoltre vengono segnalate le specie a distribuzione ristretta (endemiche) indicando come endemiche italiane quelle che hanno l'intero areale compreso nel nostro Paese. Per tutte le specie e sottospecie endemiche viene riportata inoltre la località tipica e la distribuzione.

Una serie di note segnala: le specie rare, le specie citate nei decenni passati e mai più ritrovate, i taxa con problemi nomenclaturali o di riconoscimento ed altre eventuali criticità.

Attualmente la checklist comprende 20 famiglie e 94 generi 449 specie e 57 sottospecie. Dei taxa specifici e sottospecifici 134 sono endemici e 90 endemici italiani.

Per quanto riguarda l'ordine sistematico viene seguito quello proposto da Malicky nel 2005 ed i criteri nomenclaturali pubblicati all'interno del volume *Distribution Atlas of European Trichoptera* (Neu et al., 2019).

Un confronto con l'ultima checklist realizzata da Cianficconi (2002) evidenzia un notevole incremento dei taxa della tricoterofauna italiana rispetto ad una ventina di anni fa. Ciononostante riteniamo che le conoscenze sulla distribuzione di questo ordine di insetti nel nostro paese necessitino di ulteriori e più approfondite ricerche in particolare in vaste aree del territorio che risultano poco indagate.

Questo lavoro fa parte di un più ampio progetto che mira alla realizzazione di un catalogo dei tricoteri italiani che permetterà di avere informazioni puntuali sulla distribuzione delle specie nel nostro Paese.

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RIFLESSIONI SULL'ARANEOFAUNA ITALIANA

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data base; spiders; checklist; Italy.

Il nuovo catalogo sui ragni italiani, realizzato grazie all'analisi di oltre un migliaio di pubblicazioni, consente di fare alcune riflessioni sull'origine e lo stato di conoscenza dell'araneofauna italiana. Nel nostro paese sono presenti ad oggi 1670 tra specie e sottospecie raggruppate in 434 generi e 53 famiglie. Le informazioni sulla diversità dell'araneofauna italiana sono in costante crescita, come testimoniano le poco più di 400 specie note alla fine del XIX secolo diventate circa 1400 negli anni '90 fino ad arrivare alle oltre 1650 segnalate nel nuovo catalogo. Ciononostante molte nuove specie presenti nel nostro Paese sono ancora da descrivere e la conoscenza della distribuzione dei taxa noti è ancora lontana dall'essere nota in modo soddisfacente. Particolarmente accentuato risulta il gap tra le regioni settentrionali, maggiormente oggetto di studio e dunque meglio conosciute, e le regioni centro-meridionali la cui fauna è nota solo in modo frammentario. Per quanto riguarda le famiglie i Linyphiidae mostrano il maggior numero di specie (477) e di endemiti (114). Gnaphosidae (166) e Salticidae (144) seguono in termini di ricchezza specifica mentre Dysderidae (72) e Agelenidae (38) per numero di specie endemiche. Un'elevata percentuale delle specie note presentano un ristretto areale di distribuzione (344 pari al 21%) che rappresenta una peculiarità del popolamento araneico italiano. Di queste ben 216 sono conosciute esclusivamente del nostro Paese mentre l'areale delle restanti 128 specie comprende anche parte dei territori dei paesi confinanti. La distribuzione delle specie endemiche fa riferimento principalmente alle seguenti aree: le Alpi; gli Appennini; l'area tirrenica comprendente Corsica, Sardegna e le aree costiere dell'Italia occidentale e della Francia meridionale; la Sicilia. Il livello di conoscenza di questi taxa è molto eterogeneo e molti necessitano di ulteriori indagini non essendo mai stati segnalati dopo la descrizione (78), essendo noti solo della località tipica (53) o di uno dei due sessi (45).

È presente anche un piccolo contingente di 20 specie aliene riferibili a 9 famiglie.

**ON THE EDGE BETWEEN THE MEDITERRANEAN AND
EUROSIBERIAN REGIONS: A NEW PHYTOGEOGRAPHICAL
SUBDIVISION OF TUSCANY**

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beta diversity; biogeography; flora; hierarchical clustering; ordination.

Each species has a unique geographic distribution but many species share similar ranges. Similar ranges between two (or more) species may be due to shared evolutionary histories, physical barriers or ecological requirements that limit dispersion or survival. As a result, different regions of the globe host different sets of living organisms. This is the prerequisite for dividing the earth into distinct biogeographical units, which in the original conception also takes into account the ancestral (phylogenetic) relationships among taxa. Indeed, a biogeographical regionalization is a hierarchical system that classifies geographic areas according to their biota: the hierarchical relations among areas implicitly represent a shared evolutionary history. This way of representing the geographical distribution of taxa is very effective, because it represents a fundamental categorization for many basic and applied issues in ecology, evolution, and conservation.

Defining boundaries between biogeographical regions is not a straightforward task, especially in geographical areas where two or more biogeographical units of higher rank (kingdoms, regions) are in contact. From this point of view, Tuscany occupies an interesting geographical position, because it stands at the limit between the Mediterranean and Eurosiberian floristic regions. However, the exact location of the border is unclear, so that several authors have proposed conflicting phytogeographic subdivisions. Moreover, the lack of sufficiently detailed data on a large geographical scale has led to an extensive use of vegetation type maps to define biogeographical units.

In this work, for the first time a phytogeographic subdivision of Tuscany was obtained by combining the distribution data and the phylogenetic relationships of 2,973 taxa of vascular plants. Distribution data (164,683 georeferenced records) have been mapped in 5×5 km cells. The Simpson turnover index – which is not depending on species richness – was used to measure the dissimilarity among cell pairs and to quantify the change in the taxonomic (β_{sim}) and phylogenetic ($p\beta_{sim}$) composition among the flora of each cell. Then, a combination of hierarchical clustering and two-dimensional ordination was applied.

The results clearly demonstrate that the Eurosiberian region in Tuscany is restricted to the northern and high-altitude portions of the Apennines. Phylogenetic and taxonomic approaches adopted here are broadly congruent, albeit the first one ($p\beta_{sim}$) is more effective in terms of explained dissimilarity and in properly defining hierarchical relationships among clusters. This study represents an important update concerning the phytogeography of Tuscany. A more precise definition of smaller biogeographical units will be possible by superimposing the distribution of Tuscan endemic taxa to the obtained maps.

WIKIPLANTBASE #ITALIA, A CITIZEN SCIENCE PROJECT TO BOOST ONLINE PLANT OCCURRENCE RECORDS IN ITALY

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online databases; plant biodiversity; botany; biodiversity conservation.

Large databases of organism occurrence records are increasingly used in biodiversity studies in ecology, evolution, taxonomy, conservation, etc. About 1.3G animal, plant, and micro-organism occurrence records from all over the world are available in the GBIF (www.gbif.org), and have been used in almost 7,000 journal articles in the last six years. About 250M occurrence records in the GBIF are of land plants. The distribution of these records is strongly biased, as most are concentrated in Western Europe, Australia, USA, and Brazil. Italy (0.4M occurrences) stands out for the scarcity of records available to date, if compared to France (38M), Germany (25M), and Spain (15M). Data for other EU countries come mostly from institutional agencies as e.g., UMS PatriNat (France), Staatliche Naturwissenschaftliche Sammlungen Bayerns and Bundesamt für Naturschutz (Germany), Environmental Information Network of Andalusia and Banc de Dades de Catalunya (Spain). In Italy, most records are provided by the Department of Biology of the University of Pisa, through the federated projects Wikiplantbase. Launched in 2011 as an *online* version of a printed series of floristic contributions for Tuscany published since 2009, Wikiplantbase was quickly adapted to store, and expose all floristic records collected in Tuscany. Then it rapidly evolved, widening its aim to Sardinia, Liguria, and Sicily, under the supervision of regional coordinators. Presently, 166 registered users, both academic and non-academic, are collaborating to the project on a voluntary basis, collecting 300K occurrence records during the last 6 years.

In light of these encouraging results, a major upgrade was planned and implemented in 2019, aimed at enabling the platform to accept occurrence data from all across the country. It is expected that amount collaborators will increase steeply, thus boosting the amount of plant occurrence records available for Italy. The upgraded platform will go online by the end of the year as “Wikiplantbase #Italia” and will flank the extant regional projects #Toscana, #Sardegna, #Liguria, and #Sicilia. Wikiplantbase #Italia is designed to interact an exchange data with another Citizen Science project, namely Actaplantarum (www.actaplantarum.org), and with the Portal to the Flora of Italy (dryades.units.it/floritaly), in a comprehensive strategy to promote the knowledge, management, and conservation of plant diversity in Italy.

WIKIPLANTBASE #LIGURIA: LA CITIZEN SCIENCE COME VOLANO PER LA FLORISTICA LIGURE

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citizen science, erbario, floristica, Liguria

Nell'ambito del progetto Wikiplantbase, il database dedicato alla flora ligure contava, a fine 2018, 23 collaboratori e circa 40.000 record, essenzialmente relativi a dati bibliografici, letteratura grigia, dati d'erbario e osservazioni personali dei collaboratori, a volte anche corpose, ma comunque sporadiche. Mancando di un progetto organizzato per la sua crescita, il database ha mostrato nei primi anni alcune lacune: distribuzione dei dati non omogenea sul territorio, scarsità di dati recenti e georeferenziati, sovra-rappresentazione dei taxa più studiati o ritenuti più interessanti a discapito di quelli più comuni o trascurati dal mondo della ricerca. Tale situazione poneva limiti all'utilizzazione del database, in quanto incapace di fornire dati completi sulla distribuzione attuale della flora in Liguria. Mossa dall'intento di coinvolgere persone al di fuori del mondo accademico e di utilizzare il progetto Wikiplantbase come stimolo per la produzione di nuovi dati, non limitandosi a rendere più accessibili i dati preesistenti, la sezione Ligure della Società Botanica Italiana ha promosso nel 2019 l'iniziativa delle "Escursioni pro-Wikiplantbase": si tratta di eventi periodici (con frequenza mensile), aperti a tutti, mirati alla produzione di nuovi dati floristici per un veloce inserimento nel database. Le dodici aree da indagare sono state selezionate all'interno dei comuni liguri che presentavano nel 2018 i più bassi valori di record inseriti. L'attività di campo ha previsto la compilazione in gruppo di liste floristiche georeferenziate, posizionate lungo il percorso a una distanza di almeno 1 km l'una dall'altra o in occasione di evidenti cambiamenti delle condizioni ecologiche. Ogni escursione è abbinata a un'attività di laboratorio, in quanto tutte le specie non identificabili in campo sono state erborizzate per la successiva determinazione. L'iniziativa, attualmente in fase di completamento, ha riscosso notevoli risultati: i partecipanti, in maggioranza esterni al mondo accademico, sono stati complessivamente 23, per un totale di oltre 3.000 segnalazioni inserite e un arricchimento delle collezioni dell'Erbario di Genova di circa 300 campioni. I principali vantaggi sono l'esplorazione di aree storicamente poco battute dai floristi, la produzione di dati attuali e georeferenziati, e l'uguale rappresentatività dei taxa (anche grazie all'abbinamento con l'attività di laboratorio, che consente di produrre dati anche sui gruppi "critici" o comunque non identificabili con certezza in campo). Il coinvolgimento simultaneo di accademici e appassionati consente da un lato di produrre dati affidabili e dall'altro di aumentare il numero di osservatori che faranno crescere il database negli anni futuri, in quanto le escursioni assumono un valore altamente formativo per i partecipanti. In conclusione, l'esperienza di quest'anno suggerisce che le "Escursioni pro-Wikiplantbase" sono un utile strumento per una rivitalizzazione della floristica regionale, anche confermato dal rinvenimento, durante queste attività, di specie non note o non più confermate per la flora ligure.

IL MONITORAGGIO DELLA BIODIVERSITÀ NELLA RETE NATURA 2000 ATTRAVERSO IL VOLONTARIATO EUROPEO: PRIMI RISULTATI DEL PROGETTO LIFE ESC360

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ecosystems; protected species; Natura 2000; biodiversity; volunteers.

Il Progetto LIFE17 ESC/IT/001 “360 volunteers for monitoring forest biodiversity in the Italian Natura 2000 Network” è il primo progetto nazionale ed il più grande progetto europeo a coinvolgere giovani volontari del Corpo Europeo di Solidarietà per il monitoraggio di habitat e specie protetti all’interno della Rete Natura 2000. I volontari frequentano un corso di formazione intensivo e sono successivamente impiegati, con turni bimestrali, in attività di raccolta di dati sul campo per un totale di circa 10.800 giornate in 3 anni di progetto, nelle Riserve Statali gestite dall’Arma dei Carabinieri. Le aree indagate sono: i. Riserva di Bosco Fontana, uno degli ultimi relitti di foresta planiziale padana; ii. Riserve Casentinesi, un complesso di habitat forestali in ambiente montano dominati da faggio e abete bianco; iii. Riserve di Abruzzo e Molise, con foreste dominate dal faggio ed habitat di alta quota ad elevata naturalità.

Il progetto prevede il monitoraggio di specie di interesse dell’Unione Europea, fra le quali entità endemiche, caratterizzate da una distribuzione frammentata o minacciate, come *Osmoderma eremita* (Coleotteri), *Rana latastei* (Anfibi), *Vipera ursinii* (Rettili), *Gyps fulvus* (Uccelli), *Ursus arctos marsicanus* (Mammiferi) e *Iris marsica* (Iridacee). Inoltre, sono effettuati monitoraggi su habitat protetti di montagna, come ad esempio le praterie mesofile e xerofitiche di alta quota o gli arbusteti prostrati a ginepro nano, particolarmente suscettibili a variazioni nella loro composizione ed estensione come risultato del cambiamento climatico.

I dati raccolti nel primo anno di progetto (2019), e riferiti a 4 mesi di attività, hanno permesso di effettuare una valutazione sull’efficacia del volontariato nel campo del monitoraggio e di ottenere una notevole quantità di dati che andranno a accrescere le conoscenze sulla distribuzione e sullo stato di conservazione delle specie e degli habitat protetti dalle Direttive Habitat e Uccelli dell’U.E. Saranno presentati alcuni casi di studio.

STAMBECCO (*CAPRA IBEX*) SULLE ALPI OROBIE: ESPERIENZA DI CITIZEN SCIENCE NEL TRIENNIO 2017-2019

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Alpi Orobie; stambecco; citizen science; biodiversità.

Nel giugno 2017 si sono celebrati i 30 anni dalla prima operazione di reintroduzione dello stambecco delle Alpi (*Capra ibex*) sulle Alpi Orobie (45°40' - 46°10' N, 9°25' - 10°20' E).

A distanza di 10 anni (2008) dall'ultimo censimento ufficiale della specie è stato avviato dalla Sezione di Bergamo del Club Alpino Italiano (CAI), con il supporto del Comitato Scientifico Centrale CAI, il progetto 'Citizen science: Stambecco sulle Orobie e in Lombardia 2017-2019'.

Obiettivi del progetto sono stati da un lato stimolare gli escursionisti ad un'osservazione consapevole della biodiversità del territorio alpino, con particolare riferimento alla specie stambecco, dall'altro acquisire, attraverso le osservazioni degli escursionisti, dati sulla distribuzione spaziale, sex ratio, classe d'età ed aspetti sanitari della metapopolazione di stambecchi presenti sulle Alpi Orobie e in Lombardia.

A livello metodologico le osservazioni sono state raccolte, nel periodo 01 Giugno – 30 Novembre di ogni anno d'indagine, in modalità cartacea (mediante schede tecniche distribuite presso i rifugi alpini dell'area di studio), e modalità informatica attraverso l'invio di immagini georeferenziate (scattate con smartphone o macchine digitali) complete di dati sull'autore, data e orario dell'avvistamento tramite email, sito web dedicato, e pagine Facebook ed Instagram del progetto.

Complessivamente nel corso del triennio sono pervenute 612 segnalazioni fotografiche nel 2017, 803 nel 2018 e 613 nel 2019 (dato aggiornato al 09.10.2019), per un totale di oltre 2.000 immagini. Nei primi due anni di raccolta dati le osservazioni sono state effettuate da 473 autori (224 nel 2017, 249 nel 2018) con una prevalenza di uomini (76%) rispetto alle donne (24%).

Gli avvistamenti sono avvenuti principalmente in Val Seriana (48%) e in Val Brembana (46%). La pagina Facebook "StambeccoOrobie" è attualmente seguita da 2008 persone (41% donne – 59% uomini) con il range di età più significativo compreso tra i 25-54 anni. Il 10% dei followers risiede all'estero. Alla data attuale, la pagina Facebook ha generato 935.263 *impression*.

La georeferenziazione di tutte le segnalazioni ricevute è avvenuta su piattaforma ArcGis grazie al supporto della società Globo SRL. La mappa, accessibile dal geoportale della Sezione CAI di Bergamo permette di visualizzare con layer differenti le osservazioni del 2017 e 2018, i sentieri e i rifugi CAI oltre alle aree di espansione delle colonie lombarde identificate dallo studio "Progetto Stambecco 2020" (redatto da Istituto Oikos, Parco Naturale Adamello Brenta, Parco Nazionale dello Stelvio ed Università degli Studi di Sassari).

L'esperienza condotta nel corso del triennio ha permesso di contribuire a sensibilizzare i fruitori della montagna alla conoscenza della specie stambecco e ad un'osservazione consapevole della fauna selvatica nel rispetto del benessere animale.

I dati raccolti nel triennio di studio saranno oggetto di analisi per l'identificazione aggiornata delle aree di presenza dello stambecco in Lombardia e la definizione di una stima delle consistenze. La citizen science può quindi rappresentare uno strumento integrativo alle attività di monitoraggio e censimento esaustivo della specie.

SCIENTIST BY CHANCE: NATURAL SCIENCE FORUMS AS PRECIOUS RESOURCE OF SUITABLE BIODIVERSITY DATA

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butterflies; naturalist forum; biodiversity data.

As far as biodiversity is concerned, forums and social networks store a steadily increasing amount of data on flora, and fauna, collected especially by amateurs, with various degrees of expertise. Are these data potentially useful for the rapid growth of the biodiversity big data systems?

Forums and social networks dealing with natural sciences usually are not involved in any scientific project, not even those of Citizen Science, even if they can be an important, constantly updated and untapped resource of primary biodiversity data.

Thus, we addressed some questions about the "suitability for use" of primary biodiversity data from naturalists forums, specifically related to their taxonomic reliability, and geographical accuracy.

To test the suitability of these data we analyzed the threads from two of the most preeminent Italian naturalist forums, Natura Mediterraneo (FNM) and Forum Entomologi Italiani (FEI). These forums could be important repositories of data because discussions are managed by moderators, which are often skilled taxonomists.

The pilot dataset only concerned butterflies (Lepidoptera, Rhopalocera). A careful examination of threads, where amateurs posted their observations, allowed the development of an introductory dataset. Starting from textual sites descriptions and photos, we verified the correctness of the original validation, with the help of expert taxonomists, and the possibility to obtain accurate spatial and temporal data for each observation. For more than 4,000 observations the matching level between identifications in the forums and experts, and the degree of accuracy of spatial description were evaluated.

This exploratory study exposed the value of assembling biodiversity data from the web, particularly for taxa as butterflies, where validation by expert taxonomists via photographic image is affordable. However, it also revealed some limits and biases, which are typically associated with the lack of a sampling design. These analyses are also a starting point for converting naturalistic forums into efficient and appealing platforms of Citizen Science. The synergistic action of institutions, researchers and citizens scientists is expected to significantly improve the collection of data, and the achievement of additional elements to enhance knowledge and protection of biodiversity. In this context, a massive recovery of past data from forums through the automatic interpretation of forum threads should be carefully evaluated..

ACTAPLANTARUM: DA FORUM DEDICATO ALLA FLORA SPONTANEA ITALIANA A BANCA DATI DI DISTRIBUZIONI FLORISTICHE NAZIONALI

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citizen science; flora; databases.

Acta Plantarum (www.actaplantarum.org) nasce nel 2007 come progetto open source finalizzato allo studio della Flora spontanea d'Italia. La partecipazione al progetto è gratuita e avviene, previa registrazione, tramite l'invio dei propri contributi attraverso un Forum di discussione. Quest'ultimo, suddiviso per argomenti, rappresenta il cuore del sito insieme a IPFI (Index Plantarum Florae Italicae), database nomenclaturale completo delle specie della flora italiana, allineato con la nuova checklist della Flora italiana e successivi aggiornamenti. Nel corso degli anni, grazie soprattutto alla partecipazione di botanici dilettanti di tutte le regioni italiane, si è accumulata in Acta Plantarum una considerevole quantità di segnalazioni floristiche. Si tratta di un patrimonio ad oggi di oltre 93.000 record che coprono circa il 75% delle specie e il 64% dei taxa noti in Italia. Una nuova funzione consente ora il recupero delle segnalazioni floristiche contenute in Forum a partire dalla scheda IPFI contenente le informazioni della singola entità. L'informazione relativa alle segnalazioni verrà visualizzata sotto forma di una mappa distributiva suddivisa per regione e provincia. Per ogni singola provincia saranno quindi disponibili il numero totale delle segnalazioni e l'elenco delle segnalazioni stesse, complete delle informazioni di comune, data, autore e, ove disponibile, luogo preciso del ritrovamento.