

seabed, in-situ sampling of water or sediment cores, and maps derived from analyses of species distributions that may define biogeographic regions. To date, biogeographic boundaries have been more defined by expert opinions than analyses of species distribution data. This presentation reviews classifications in use regionally and globally (EUNIS, Australian, LME, MEOW, Longhurst's, IHO sea and oceans, Exclusive Economic Zones). A physical 'habitat' classification based on a Geographical Information System analysis of the best available globally integrated bathymetry will be reported here for the first time, and present and future options, including pelagic, benthic and hierarchical systems, for data management in OBIS and GEOSS are outlined.

15:45 - 16:00 LARGE-SCALE PATTERNS IN HARPACTICOID COPEPOD DIVERSITY AND DISTRIBUTION.

Garlitska Lesya, Ecology of Marginal Communities, Odessa Branch, Institute of Biology of Southern Seas, NASU, Ukraine.

Chertoprud Elena; Azovsky Andrey, Dept of Hydrobiology, Biological Faculty, Moscow State University, Moscow, Russia.

Kondar Daria, Coastal Ecology Laboratory, Shirshov Institute of Oceanology, RAS, Moscow, Russia.

Using an extensive collection of both original and published data from more than 200 sources, the data base of the marine benthic harpacticoid species is compiled. Up to date, the base includes (after removing the synonyms) more than 1720 species and covers the Arctic, North and Central Atlantic Oceans as well as the European enclosed seas. Analysis of the species composition similarity between 25 regions shows that five large groups could be distinguished: Polar (central Arctic basin, Laptev, East Siberian, Chukchi and Beaufort seas), Sub-arctic (North, Baltic, White, Barents and Kara seas, N-E and N-W Atlantics), Mediterranean, Ponto-Caspian (Black, Azov, Caspian and Aral seas) and Central W Atlantic (including Caribbean Sea and Gulf of Mexico). Central E Atlantic fauna is rather solitary and has a high degree of "endemism". Plankton, phytal and non-specific benthic species are the most widely distributed while interstitial and sand-dwelling forms usually have more restricted occurrence. The data on most the regions are still incomplete, and these results should be treated as rather preliminary. Thus, further cooperative efforts are necessary to obtain the more comprehensive dataset.

Polivalente room

Session 3.3 Fish and fisheries: genes to global market

Chairs : Reinhold Hanel; Mikko Heino.

15: 00 - 15:15 EFFECT OF RECENT CLIMATIC CHANGES ON ABUNDANCE OF SOLE, SOLEA SOLEA, IN THE KATTEGAT AND BELT SEA.

MacKenzie Brian; Else Nielsen, National Institute for Aquatic Resources, Technical University of Denmark, Denmark.

Sole populations are found in the Black Sea, Mediterranean Sea and as far north as Denmark. Commercial fisheries landings of sole in the Kattegat have increased 2-3 fold during 1952-2007. Here we use 4 research surveys to investigate whether abundances have increased and therefore are reflected in commercial landings data, or whether the increase is primarily due to changes in fishery-related factors (e. g., effort). The four surveys cover different time periods from 1957-present. Sole abundance has increased in research surveys, and much of the inter- and multi-annual variability in abundance was related to temperature fluctuations: warm years appear to lead to higher production and/or survival of young soles. The effect of temperature on sole in this area is consistent with expectations based on the geographic range of the species and also increases in abundance of several "southern" species (e. g., anchovy, *Engraulis encrasicolus*, and red mullet, *Mullus surmuletus*) seen in these waters during the past 10-15 years. Recent warm temperatures appear to be leading to a change in fish biodiversity in the Kattegat.

15:15 - 15:30 GENETIC VARIATION AT SNP LOCI ACROSS WILD POPULATIONS OF THE EUROPEAN SEA BASS.

Souche Erika; Hellemans Bart, Biology, Katholieke Universiteit Leuven- Laboratory of Animal Diversity and Systematics, Belgium.

Bargelloni Luca, Public Health, Comparative Pathology, and Veterinary Hygiene, University of Padova, Padova, Italy.

Guinand Bruno, Institut des Sciences de l'Evolution CNRS-Université de Montpellier 2, Montpellier, France.

Bonhomme François, Institut des Sciences de l'Evolution CNRS-Université de Montpellier 2, Montpellier, France.

Volckaert Filip, Biology, Katholieke Universiteit Leuven-Laboratory of Animal Diversity and Systematics, Leuven, Belgium.

The European sea bass (*Dicentrarchus labrax*) is an economically important marine species in Europe, living in the Atlantic Ocean and throughout the Mediterranean Sea. Atlantic and Mediterranean sea bass populations have been shown to be genetically diverse using microsatellite markers, generally located in non coding regions and supposedly neutral. Twenty-four natural populations from all over the Atlantic Ocean and the Mediterranean Sea have been screened for Single Nucleotide Polymorphisms (SNPs) both in coding and non coding regions. We want to understand how neutral and adaptive variation has shaped population variation. A total of 63 SNPs reasonably spread over the genome have been selected for genotyping. Among them 49 SNPs are located in annotated Expressed Sequence Tags, 23 being in amino acid sequences and 8 being non synonymous. The last 14 SNPs were developed from non coding genomic sequences (BAC end sequences) and are thus expected to be neutral. The results confirm the known neutral differences in genetic structure and point to a small number of SNP loci under selection.

15:30 -15:45 EXPLOITATION-DRIVEN EVOLUTION AND MARINE BIODIVERSITY.

Heino Mikko, Department of Biology, University of Bergen, Norway.

Dieckmann Ulf, Evolution and Ecology Program, International Institute for Applied Systems Analysis, Laxenburg, Austria.

Life-history diversity can be envisaged as spanning from "slow lane" life histories (implying late maturation, a long life span, slow growth to a potentially large body size, and a low potential rate of population increase) to "fast track" life histories (early maturation, a short life span, fast body growth to a moderate asymptotic size, and a high potential rate of population increase). Slow-lane life histories are viable only when mortality after recruitment is low. Consequently, modern fishing practices, which have greatly increased overall mortality levels in many marine fishes, are disadvantaging slow-lane life-history strategies and instead favour fast-track strategies, as evidenced by a worldwide range of well-documented changes in exploited fish communities. Similar changes, however, are also expected within species and populations: when heritable life-history variation exists, high and selective mortality usually favors the fast-track variants, causing the evolutionary truncation of natural life-history diversity. We present recent progress in documenting and understanding exploitation-driven evolution and its consequences, and discuss how management measures might be adapted to tackle this challenge.

15:45 - 16:00 LIVING ON THE EDGE - ISOLATED POPULATIONS OF A SMALL PELAGIC COLDWATER MARINE FISH SPECIES TRAPPED IN THE NORTHERN MEDITERRANEAN.

Hanel Reinhold, Debes Paul, Marine Ecology, Leibniz Institute of Marine Sciences, Germany.

Apart from the growing evidence of range shifts of marine fish species, extirpations and even extinctions are predicted but not yet observed consequences of actual climate change. Especially small pelagic fish species, generally characterised by large effective population sizes and a high potential for gene flow, quickly respond to changes in physical oceanographic conditions and have shown large population fluctuations and extirpations over glacial timescales. We present a range-wide phylogeographic survey of European Sprat (*Sprattus sprattus*) based on a 530 bp sequence of the mitochondrial control region that proves the existence of genetically isolated populations in northern Mediterranean basins. We conclude that these populations -characterized by a significantly reduced genetic diversity- remain isolated because of their inability to maintain gene flow under the present physical oceanographic conditions. Our results demonstrate the effect of glacially induced changes in physical oceanographic conditions on a cold adapted small pelagic fish species trapped in a geographically confined area at its southernmost distribution limit and for the first time identify distinct and highly vulnerable populations on the climate-change-induced edge of survival.

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