

Annex 1

Genepool outputs

Biodiversity Discussion and agreements

The talks presented on 14 May were briefly reviewed. An overview of the Yellow Sea Large Marine Ecosystem project was presented that included achievements so far including the National Data and Information reports on the 5 project components Biodiversity, Fisheries & Mariculture, Ecosystem, Pollution and Governance Analysis and their Regional Synthesis. These fed into the Transboundary Diagnostic Analysis which highlighted the major problems environmental problems in the Yellow Sea and the presented causes of those problems in a Causal Chain Analysis. At present the Strategic Action Plan (SAP) being developed, in which the Ecosystem Quality Objectives or Regional targets are identified. These targets include discharge levels and water quality goals for pollution; a Total Allowable Catch set at less than the Maximum Sustainable Yield for fisheries; Best Management Practice and Polyculture for Mariculture; No further land reclamation other than that already planned for Biodiversity; Diatom dominated phytoplankton community for Ecosystem. The next phase for the SAP is the identification of management action plans that will result in the achievement of the Ecosystem Quality Objectives.

Some ideas from Conservation Biology- Applied Ecology from a lecture by Dr Charles Krebs were used to highlight some of the problems facing the identification of regional targets in the Biodiversity Component.

- 1) How to protect biodiversity? Which aspect is more important species richness, species composition, vulnerable species, structural species or keystone species?
- 2) How do you protect genetic diversity (no. of distinct alleles) and genetic variance (homologous to heterozygosity)?
- 3) How do you select which habitat is important for biodiversity preservation?
- 4) How do you ensure adequate gene-flow between preserved habitats, especially for less mobile land based animals/mammals/insects?

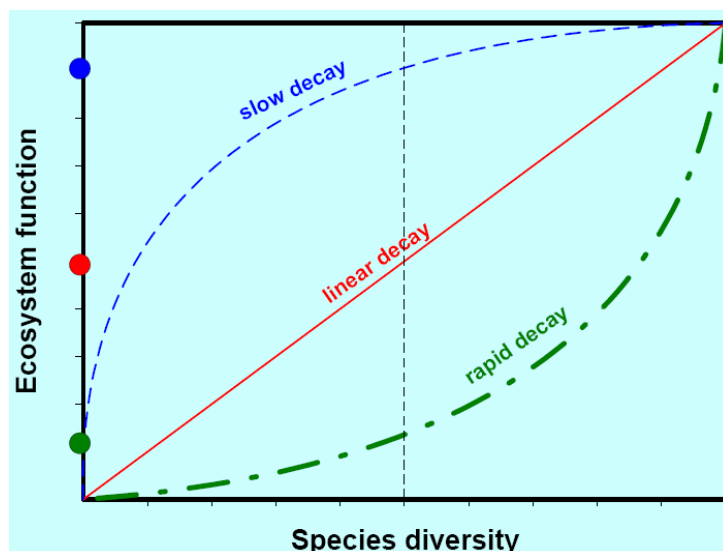


Figure 1: Theoretical decline in ecosystem function with species loss.

Reductions in biodiversity, both on a species level and genetic level result in a decline in ecosystem function, but what is the relationship? How much redundancy is built into the

system in terms of the number of species and amount of genetic diversity that can be lost without significant loss of ecosystem function? Figure 1 shows the possible relationships between the rate of decline in ecosystem function and the number of species removed. The non-linear rates of decay suggest some species may be more important in maintaining ecosystem function than others eg keystone or structural species. However most policy is made only considering a linear relationship between ecosystem function and species diversity, which may be an unreliable predictor.

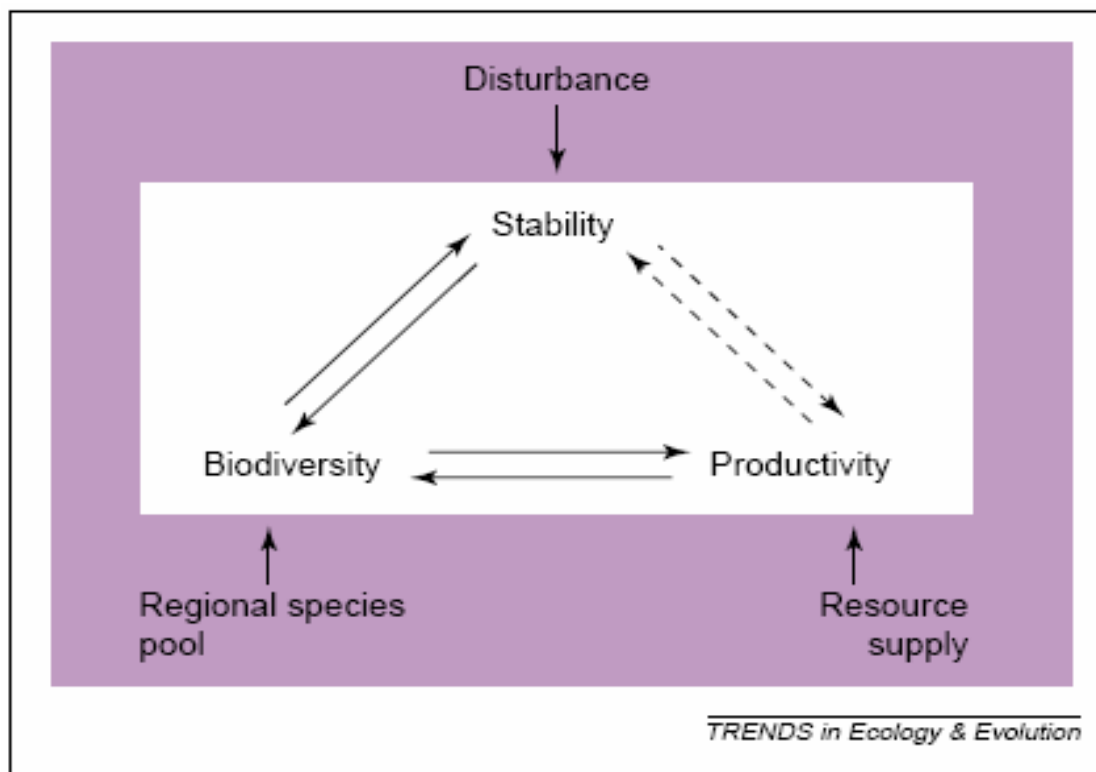


Figure 2: Relationship between biodiversity, stability and productivity hypothesised by Worm and Duffy (2003)

Communities with high levels of biodiversity in terms of composition and species richness frequently show greater stability (in terms of biomass) when exposed to environmental change or disturbance (Worm and Duffy 2003). Highly disturbed environments often show low species diversity, while stable environments show high diversity. These relationships are shown in Fig.2. Loss of biodiversity can also impact on productivity of a system, for example structural species such as mangroves or seagrass could have serious consequences for dependant organisms and a consequent loss in productivity (Worm and Duffy 2003). In contrast, other reports suggest that while generally biodiversity does increase stability, certain functional groups or the inclusion of particular species can have much more of an impact on stability than others (McCann 2000),

Food webs consist of interactions between many species, with an interaction defined as the relationship between predator and prey. But are strong interactors or keystone species more important? Models suggest that weak interactors dampen oscillations between predator and

prey and reduce extinction rates. Moreover analysis of food webs and experiments have shown variable, but frequently strong effects of weak interactors (Worm and Duffy 2003). Complexity within the system in terms of the number of energetic pathways in the food web is also related to stability (McCann 2000). These authors conclude that any loss of biodiversity could have serious consequences resulting in the reorganisation of the ecosystem through trophic cascades or a rapid shift to an undesirable stable state (McCann 2000, Worm and Duffy 2003). There are many examples of regime shifts in the marine system, such as that from fish to jellyfish dominated systems, and in the North Atlantic from cod to Atlantic herring (Bakun and Weeks 2006).

Another hypothesis suggests that simplified systems are more vulnerable to invasion from exotic species (McCann 2000).

Genetic diversity discussion

- 1) So why protect genetic diversity? One of the most important reasons is to preserve future evolutionary potential, which may be especially important given the impacts from both climate change and pollution. Genetic diversity also increased a species' resistance to disease. Moreover, it has been demonstrated that local ecotypes exist that are better adapted to local conditions and more productive in that specific environment, compared with the same species from outside the area (Joshi et al. 2001). Therefore loss of localised ecotypes would reduce the productivity of the system.
- 2) Are there any specific threats to genetic diversity? It was agreed that most threats come from aquaculture, specifically from selective breeding programs and the small initial number of brood stock used for breeding programs. Escapees from cultured species, such as the olive flounder and black rock fish and culture molluscs, may well have an impact on genetic diversity of wild stocks if there are enough escapees and sufficient interbreeding between the escapees and the wild stock. Restocking programs are another source of genetic degradation, due to the interbreeding of cultured individuals of low genetic diversity and the wild stock. Other threats come from the same sources that impact species diversity including; pollution, reclamation, introduction of exotic species/ecotypes and over-fishing/over-exploitation.
- 3) Are there any specific genetic diversity hotspots in the Yellow Sea? South west of Jeju Island and Hong Do in the SW of the Republic of Korea were suggestions, these are also known to be areas of high species richness.
- 4) In terms of preserving genetic diversity, are there any specific measures that need to be taken? Or will the management actions required to preserve species diversity also cover the needs of genetic diversity? There was general agreement amongst participants, that for the purpose of the YSLME project, the actions needed to preserve species diversity would also conserve genetic diversity and therefore could the both genetic and species diversity be considered the same. The only exceptions being, those raised in point 2.
- 5) Is there a method of observing the degradation in the Yellow Sea? Heterozygosity was suggested as a measure that could be used to observe declines in genetic diversity. (*Heterozygosity = The presence of different alleles (forms of a given gene)*)

at a particular gene locus. Heterozygosity provides a measure of the genetic variation, either in a population (the frequency of individuals heterozygous at a particular locus), or in an individual (the proportion of gene). However, at present there was not enough historical data for almost all of the species within the Yellow Sea. Moreover, it was agreed that although this method was very important, to obtain such data would be expensive and require long term monitoring. However, Dr Linsheng Song suggested that there maybe enough data to permit an examination of genetic decay in *Fenneropenaeus chinensis* stocks, as this species was subject to an extensive restocking campaign.

- 6) Lastly the need for a genetic database or germplasm bank specifically for the Yellow Sea was raised. In light of the large number of genetic databases that already existed in various institutions mentioned in the talks it was agreed that another data base was not needed. However, it was felt that although websites existed, such IUCN, that had links to a number of genetic databases, most of the local databases were not included in these lists.

Dr Linsheng Song agreed that he would be responsible for collecting the web addresses of all Chinese databases containing genetic information relevant to the Yellow Sea. For private databases and those not available to the public, only the contact details of the person in charge of the database would be provided.

Dr Tae-Jin Choi reported that he was already compiling a report for the Korean government that would include a list of databases and he would forward this list to YSLME project management office (PMO) by the end of June.

It was agreed that PMO would compile the complete list and make a webpage including all the links and contact details. This page would be distributed to other institutions for them to upload onto their websites

A germplasm bank already existed in China and one was in the planning stages in the R. of Korea.

References

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