



WHAT ARE THE ECOLOGICAL DESIGN CRITERIA FOR MPA NETWORKS?

These eight criteria can help identify the ecological considerations that lie at the heart of designing MPA networks:

Representativeness. MPA networks should represent the range of marine and coastal biological diversity (from genes to ecosystems) and the associated physical environment within the given area.

Replication. All habitats in each region should be replicated within the network and distributed spatially throughout the network.

Viability. MPA networks should incorporate self-sustaining, geographically dispersed component sites of sufficient extent to ensure population persistence through natural cycles of variation. These sites should be independent (as far as possible) of activities in surrounding areas.

Precautionary design. Network designers should base their decisions on the best information currently available, rather than delaying the process to await more and better information. Where information is limited, designers should adopt a precautionary approach.

Permanence. Network design must provide long-term protection to effectively conserve diversity and replenish resources.

Maximum connectivity. MPA network design should seek to maximize and enhance the linkages among individual MPAs, groups of MPAs within a given ecoregion, or networks in the same and/or different regions.

Resilience. MPA networks must be designed to maintain ecosystems' natural states and to absorb shocks, particularly in the face of large-scale and long-term changes (such as climate change).

Size and shape. Individual MPA units within the network must be of sufficient size to minimize adverse impacts from activities outside the protected area (avoiding what is called the "edge effect").

The scale of benefits derived from individual MPAs will depend on their location, design, size, and relationship to other forms of management. MPA networks magnify the benefits of individual sites and protect the large-scale processes that maintain healthy populations, such as connectivity, gene flow and genetic variation.

