Island Life:
Coming to Grips with the Insular Nature of Southeast Alaska

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> *Island environments have been generally misunderstood, misinterpreted, and mismanaged ... Islands are not simply miniature continents and ... continental solutions do not simply need to be scaled down in order to be successful.*
> (Nunn, 2004:311, 319)

INTRODUCTION

Southeast Alaska (Figure 1) extends from Icy Bay southward to the international border at Dixon Entrance. Across this 800 km expanse, more than 2,000 islands of the Alexander Archipelago extend along the coastline. The adjoining mainland is narrow and bordered to the east by the Coast Mountains and towering Wrangell-St. Elias ranges. These mountains extend to over 5,400 m in elevation, are capped by alpine glaciers and extensive ice fields, and form a substantial barrier to the movement of organisms into the coastal region. Hence, two physiographic features, the precipitous coastal mountains and the highly fragmented Alexander Archipelago, overwhelming contribute to the current geographic structure of the biota of Southeast Alaska. The dominant influence of these two physiographic features on species composition suggests that a comprehensive view of the fauna and flora of the region will require a critical appraisal of the role of physiographic features in community assembly and species persistence in the region. Moreover, recognition of the peculiar processes associated with island life provides a powerful framework for management of the incomparable wildlife of the Tongass National Forest. It is now evident that the ever-changing geographical configuration and environmental change that characterizes this archipelago and nearby mainland are crucial to understanding processes occurring at both ecological and evolutionary time scales. A fundamental understanding of these processes, in turn, is critical for sound management under the concept of adaptive management (Walters, 1997).

Deeper History: Regional Colonization Following Deglaciation

The geologic history of the North Pacific Coast was dynamic and heavily influenced in the Quaternary by large-scale climatic change (Mann and Hamilton, 1995; Barrie et al., 2005). During the Late Pleistocene (Figure 2), most of Southeast Alaska was covered by the Cordilleran Ice Sheet (Mann and Hamilton, 1995; Carrara et al., 2003, 2007), hence glacial dynamics played a primary role in shaping biotic communities (Klein, 1965; Heaton et al., 1996; Conroy et al., 1999). Two species were ice adapted and no longer occur in Southeast Alaska (arctic fox, ringed seal; Heaton and Grady, 2003). Phylogeographic studies, combined with insight from fossils recovered from the extensive karst system on Prince of Wales Island and elsewhere in the region, however, also suggest that some species persisted near the region during glacial advances. About 12,000 years ago, ice retreated eastward into the coastal mountains exposing a clean slate that allowed most extant species to recolonize the deglaciated territory during the Holocene. Species colonized from distinct primary sources and at different times. Species distributions, community composition, and other fundamental attributes of this highly productive coastal region, therefore, have been dynamic due to extensive glacial cycling and associated sea level changes that characterize the last several thousand millennia.

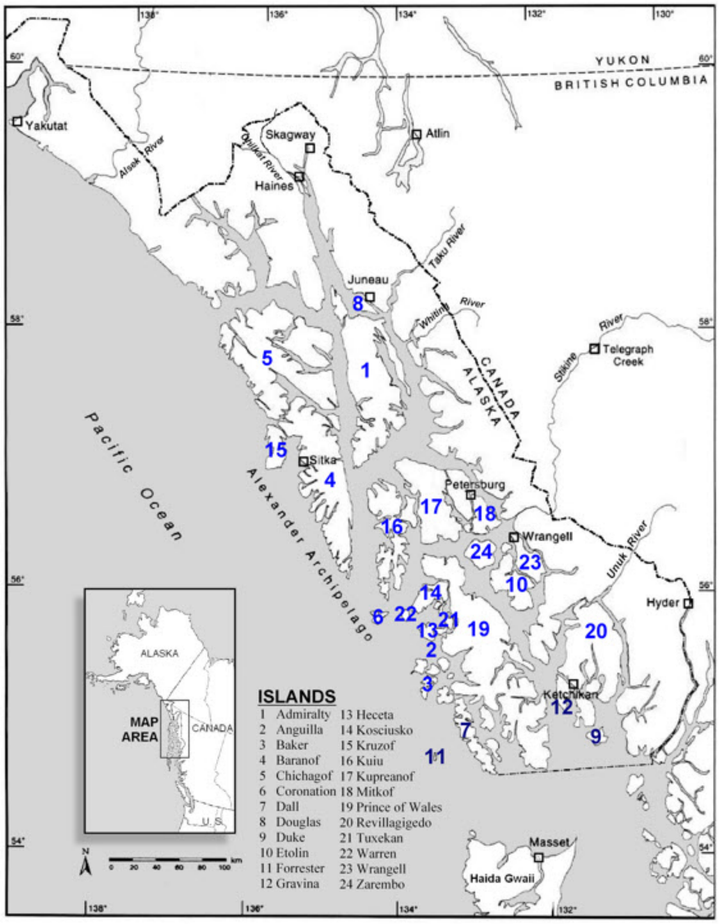


Figure 1. Map of Southeast Alaska with major islands identified (see Table 1).

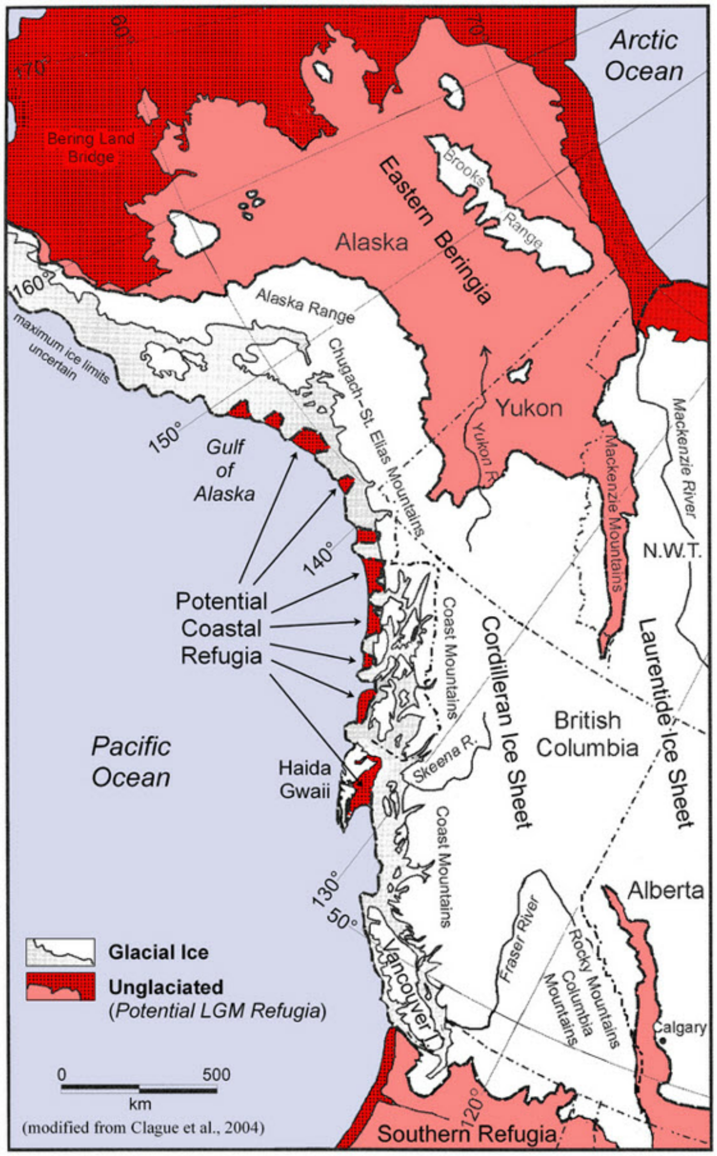
Because some of the oldest lineages occur on the more western islands of the archipelago, extant organisms may have first colonized this region of the coast along a tide water route or from refugia that persisted on the continental shelf. There are strong molecular genetic signals that suggest a suite of periglacial species may have persisted in coastal refugia during the Last Glacial Maximum. These early colonization events may have occurred in the early Holocene. Much later in the Holocene, corridors through the Coastal Mountains were opened from the interior and allowed species to colonize the coastal mainland and eventually the nearshore islands of the archipelago. This dynamic geologic history of glaciation (Figure 2), sea level change, and isostatic rebound shaped the distribution of mammals along the coast, and this backdrop is key to interpreting variation in distributions and rates and patterns in evolutionary change so far uncovered in the region (Cook et al., 2006; MacDonald and Cook, 2007).

Nelson (1887) recognized that this portion of the North Pacific coast (his "Sitkan District") was distinctive from the remainder of North America. Later, Swarth (1936) and Klein (1965) provided overviews of vertebrate diversity and concluded the region was isolated from the remainder of continental North America by the coastal mountains. That physiographic barrier, transected by relatively few west flowing large rivers, apparently played a large role in structuring diversity.

Patterns of Intraspecific Variation Provides Insight into Management Units

Molecular genetic investigations of a variety of mammals have identified common patterns of geographic differentiation that reflect common responses to large scale geologic events in Southeast Alaska (Cook et al., 2006). Some species originated from a single refugium and expanded into Southeast Alaska (e.g., Lessa et al., 2003; Frances, 2008). Single origin species (summarized in Cook et al., 2006) arrived from the northern Beringian Refugium (e.g., moose *Alces alces gigas*, wolverine *Gulo gulo*, northern red-backed vole *Myodes rutilus*, root vole *Microtus oeconomus*, arctic ground squirrel *Spermophilus parryii,* collared pika *Ochotona collaris,* brown lemming *Lemmus trimucronatus*); from a southern coastal refugium (e.g., cinereus shrew *Sorex cinereus*, northwestern deermouse *Peromyscus keeni*, wolf *Canis lupus,* Sitka black-tailed deer *Odocoileus hemionus sitkensis,* mountain goat *Oreamnos americanus,* Pacific marten *Martes caurina*); or from an eastern refugium located south of the Laurentide Ice Sheet (e.g., northern flying squirrel *Glaucomys sabrinus*, southern red-backed vole *Myodes gapperi,* meadow vole *Microtus pennsylvanicus*).

In contrast, several mammal species now found in Southeast Alaska are represented by more than one lineage. Multiple lineages indicate multiple colonization events from independent source populations or refugia. Substantial genetic divergence within several species (e.g., American marten *Martes americana*, dusky shrew *Sorex monticolus*, long-tailed vole *Microtus longicaudus*, black bear *Ursus americanus*) indicate that diversification was initiated in the mid-Pleistocene with differences persisting through repeated cycles of glacial advance and retreat. Most of these species are represented by lineages originating from a combination of southern coastal (termed Coastal) and southern continental (Continental) refugia (Cook et al., 2001, 2006).



(modified from Clague et al., 2004)

Figure 2. Map showing the extent of glaciation in Northwestern North America at the Last Glacial Maximum about 20,000 years ago. Lowered sea levels raise the possibility of the persistence of coastal refugia to the west of contemporary exposed land.

Overview of Island Biogeography

Island biogeography, essentially the study of the distribution and dynamics of insular species, provides a theoretical and operational foundation for the design of research and management plans for wildlife in Southeast Alaska. Over the past 150 years, studies of islands systems have played a large role in the formation of ecological and evolutionary theory (Darwin, 1859; Wallace, 1902; MacArthur and Wilson, 1967) including key insight into processes related to colonization, extinction, and speciation. Today, advances in technology combined with intensive studies of organisms on island systems worldwide are proving detailed and often novel views of the history and contemporary dynamics of species (Ricklefs and Bermingham, 2008;

Trewick and Cowie, 2008). To date, the vast Alexander Archipelago has played a limited role in the evolutionary, ecological, and conservation biology literature, although this system is one of the largest temperate archipelagos worldwide with 7 of the 15 largest US islands. The region could become a model system for testing fundamental hypotheses related to environmental change.

Continental (Land Bridge) Archipelago?

Wallace (1902) identified a fundamental dichotomy between islands based on their origin by proposing that archipelagos could be classified as either oceanic or continental (land bridge). Oceanic islands are formed over oceanic plates and have never been connected to continental landmasses. These islands typically are devoid of life at the outset by gradually accumulate species from distant mainland source populations. In contrast continental shelf (land bridge) islands have been directly connected to the mainland during the Pleistocene ice advances when sea level dropped as much as 130 m (Whittaker and Fernández-Palacios, 2007).

Because of their proximity to the mainland, land bridge islands are more heavily dominated by repeated colonization than are distant island archipelagoes, resulting in a relatively high diversity of lineages. Some groups also have diversified within the islands, providing an opportunity to study both intrinsic and extrinsic processes responsible for the build-up of diversity. Although technically considered land-bridge islands, the Alexander Archipelago differs in two primary ways that can only be understood within the context of the geologic history of the North Pacific Coast.

During the Last Glacial Maximum about 18,000 years ago, cordilleran ice over rode most of the region, essentially erasing terrestrial biota from most of the region. This cataclysmic event, which was likely repeated on multiple occasions through the Pleistocene may not have encompassed all of the available terrestrial areas as falling sea level exposed substantial sections of the continental shelf to the west. Following the retreat of the Cordilleran Ice sheet, the region was essentially presented a clean slate and the contemporary biota is derived from organism that colonized Southeast Alaska from elsewhere. This clean slate scenario suggests that subsequent assembly of species on the islands of the Alexander Archipelago more closely resembles dynamics on "oceanic" islands rather than land bridge islands (Whittaker and Fernández-Palacios, 2007).The sources for colonizers included multiple mainland locations, but also coastal refugia which were distinct from "mainland" sources.

Evolutionary Expectations of Island Life

Potential for Rapid Morphological Evolution

Millien (2006) showed that rates of morphological evolution are much higher for island mammal populations than for mainland populations and may be evident over time scales as short as a few decades. Cardini et al. (2007) further investigated Vancouver Island marmots (*Marmota vancouverensis*) and reported limited genetic differentiation from mainland populations of *M. caligata*, but substantial morphological differences. They concluded that the Vancouver Island marmot is a good morphospecies and essentially the other side of the coin of the many "cryptic" species that have been recently uncovered via molecular genetic studies (Bickford et al., 2007). Cardini et al. (2007) suggested rapid morphologic variation of this island population (Millien, 2006) and noted that insular populations may be distinctive due not only to temporally deep separation (allopatry), but also due to peculiarities that may arise rapidly from "island life" (e.g., dwarfism, gigantism, changes in fecundity, population density, behavior, increased survival, reduced aggressiveness, and so forth). This documented rapid morphological change on a North Pacific island drives home the point that each Tongass island population is potentially distinctive. Differences may arise not only from deeper temporal evolution, but also from changes that occur at ecological time scales. Similarly, dwarfism of the now extinct Dawson caribou of Haida Gwaii is hypothesized to have occurred within less than 1,500 years (Wigen, 2005).

Potential for Rapid Molecular Evolution

Lucid and Cook (2004) assessed levels of genetic variability across 23 island populations of the widespread northwestern deermouse. Populations of this ubiquitous species showed highest levels of variability on the mainland and larger islands while lowest variability was recorded on the smallest and most distant islands. Other island endemics show extremely low levels of variability (Prince of Wales Island flying squirrel and *caurina* marten). Hence, insular faunas show not only reduced species richness, but individual species also have a characteristic signature of lower genetic variability which may increase the probability of local extirpation (Frankham, 1995). Lower genetic variability decreases the ability of organisms to meet novel environmental challenges, but the relationship between genetic variability and the process of extinction is complex (Aguilar et al., 2004). The few mammals examined on the Alexander Archipelago to date exhibit this trend (e.g., Bidlack and Cook, 2002; Small et al., 2003; Cook et al., 2006; Dawson, 2008), but the generality of trend for other Alexander Archipelago organisms should be examined.

Endemism on the Prince of Wales Island Complex and Haida Gwaii

There are likely a number of parallels between the Alexander Archipelago and other glaciated nearshore archipelagos of mid-latitudes such as the nearby Haida Gwaii islands of British Columbia, the Japanese Archipelago, and the British Isles. Tongass managers should identify collaborative projects with ongoing research and management initiatives in other archipelagos to meet the challenges associated with managing insular biotas. Limited effort has been focused on threats to the endemic fauna of the North Pacific Coast (Cook et al., 2001), primarily because limited documentation has been available on the status of insular species (Cook and MacDonald, 2001). The few studies published on island organisms along the coast of nearby British Columbia (Nagorsen, 1994, 2004; Shank, 1999) have documented extinctions or high endangerment (e.g., Vancouver Island marmot, < 50 individuals; Bryant, 2002) of insular species (COSEWIC, 2005). In British Columbia, 88% of the endemics are restricted to islands and are listed as Threatened or Endangered (CACR, 2008). At least 40 of these taxa are forest dwelling, while others occur in small, relatively discrete habitat types within forests such as shady cliffs and talus slopes. Management plans in British

Columbia and Southeast Alaska (e.g., Tongass Land Management Plan Revision, 2007) still have not tuned in to the special attributes of island life (Paquet et al., 2004).

Temporal Scale of Endemism

The Coastal Refugium Hypothesis has gained momentum in the last decade following a series of studies (Rogers et al., 1991; Heaton et al., 1996; Byun et al., 1999) and two summary volumes focused on the natural history of Haida Gwaii (Scudder and Gessler, 1989; Fedje and Mathewes, 2005). For example, three distinctive lineages of ermine have been detected in Southeast Alaska (Figure 3). Two of these lineages occur widely outside of Southeast Alaska while the third lineage is restricted to a few North Pacific islands (Fleming and Cook, 2002). This island-restricted lineage represents a periglacial relict or paleoendemic that persisted in the region since before the LGM and it requires a significant reassessment of the temporal horizon over which elements of this fauna has diversified. The LGM apparently did not wipe the slate completely clean along the entire coast and the possibility of Pacific Coastal Refugia suggests the possibility of a suite of highly divergent taxa that may require special management status under the Endangered Species Act.

A review of endemic mammals for North America north of Mexico concluded that the North Pacific Coast supports high levels of endemism (Cook and MacDonald, 2001; Reimchen and Byun, 2005). Subsequent molecular phylogeographic studies largely supported this finding (Cook et al., 2006). Indeed, endemic lineages of northwestern deermouse, northern flying squirrel (Bidlack and Cook, 2002), spruce grouse (*Falcipennis canadensis isleibi*; Dickerman and Gustafson, 1996), chum salmon (*Oncorhynchus keta*; Kondzela et al., 1994), and subalpine fir (*Abies lasiocarpa*; Carrara et al., 2003) have also been identified on the Prince of Wales Island complex. Likely numerous other endemic organisms occur there that that have yet to be analyzed, but the baseline samples necessary to complete those analyses are lacking.

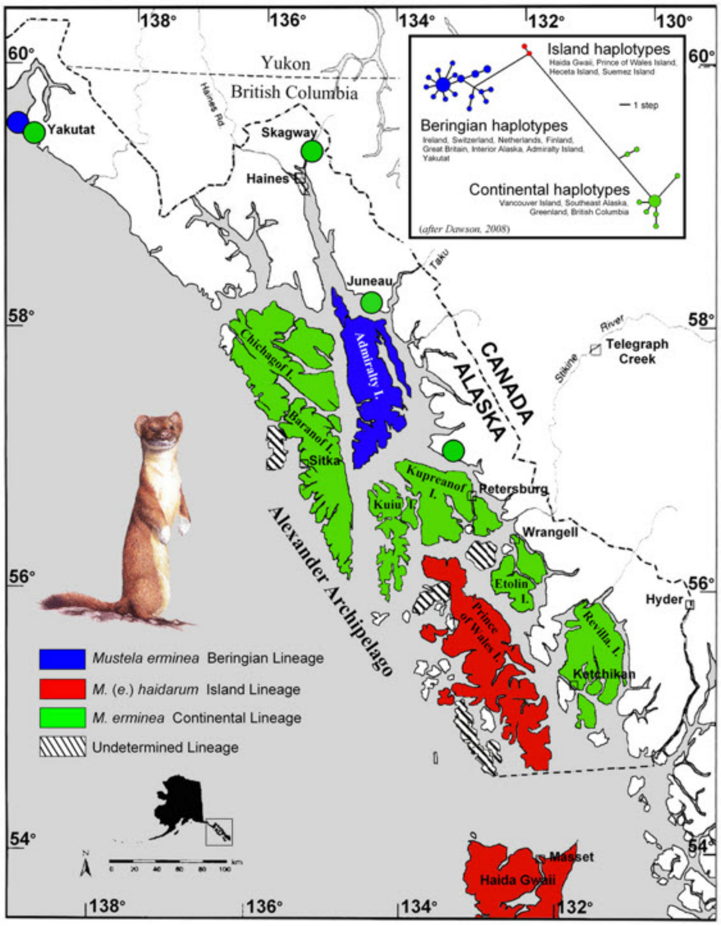


Figure 3. Map of the distribution of the three clades of ermine that occur in Southeast Alaska. The Beringian clade is widely distributed from Europe, through Asia and into far northwestern North America. The Continental clade is distributed elsewhere in North America with the exception of Haida Gwaii and the Prince of Wales Island complex where the third (Island) clade is endemic (Fleming and Cook, 2002; Dawson, 2008).

Island Communities

Consistent with classic island biogeography theory (MacArthur and Wilson, 1967), size and distance from the mainland have played a prominent role in shaping diversity across the Alexander Archipelago (Table 1). Larger islands (e.g., Revillagigedo) close to the mainland have higher species richness, while small distant islands (e.g., Forrester) have lower species richness (MacDonald and Cook, 1996). Nonetheless, when the factors of size, distance and greatest elevation for each of 20 islands is regressed against species richness, only island distance is significant (Figure 4). Conroy et al. (1999) used species lists for each island to explore factors responsible for community assembly of mammals across the archipelago and showed that mammalian communities on smaller islands were nested within communities on larger islands. Conroy et al. (1999) concluded that, across all species, colonization ability (not extinction probability) has been the most important determinant of current community composition on islands, a result that is consistent with the history of heavy glaciations. That study, however, was unable to consider endemism that has since been documented based on molecular analyses. Reanalysis based on the lineage richness (unpublished data) indicates that endemic lineages are not nested; those older forms instead appear to be structured by extinction processes (i.e., island size rather than island distance is important).

Despite the overall nested pattern found in the archipelago (Conroy et al., 1999), species assemblages vary spatially (i.e., from island to island) and temporally (Heaton and Grady, 2003). For example, cinereus shrews are found on Baranof and Chichagof islands, but not Admiralty and Prince of Wales islands (Figure 5a), while dusky shrews show the opposite pattern of occurrence. Both species are sympatric on the mainland, on nearshore islands (e.g., Revillagigedo, Wrangell) and on the peninsula like islands of Mitkof, Kupreanof, and Kuiu (Figure 5b). Historically, brown and black bears coexisted on Prince of Wales Island and Haida Gwaii, but in the last 10,000 years brown bears have ceased to occupy these islands (Heaton and Grady, 2003; Wigen, 2005). Now, black bears (and wolves) occupy islands south of Frederick Sound, while brown bears (and no wolves) occur on northern islands of the Alexander Archipelago. All three of these top predators are sympatric on the mainland. Patterns of exclusion also are seen in rodents of the genus *Microtus* (voles) (Figure 5c).

Table 1. List of 24 major islands in the Alexander Archipelago. Map number refers to location of island in Figure 1. For each island, species richness, island area, distance from mainland and highest elevation are reported. Species richness varies across major islands of the Alexander Archipelago with highest richness found on the larger, higher islands that are near the mainland (e.g., Revillagigedo Island). In contrast, endemic lineages are found on islands that are more distant from the mainland.

MAP NUMBER	Island	Area (ha)	Distance to Mainland (km)	Maximum Elevation (m)	Number of Native Species
1	Admiralty	431,309	5	1418	14
2	Anguilla	1,210	9	198	8
3	Baker	13,512	12.75	697	9
4	Baranof	424,016	6	1644	9
5	Chichagof	545,317	5	1192	9
6	Coronation	9,120	10.5	598	7
7	Dall	65,869	7.25	949	12
8	Douglas	20,274	1	1018	20
9	Duke	15,538	5	503	8
10	Etolin	88,995	2	1135	18
11	Forrester	1,013	33.75	409	3
12	Gravina	23,307	3	833	14
13	Heceta	18,916	8.75	761	11
14	Kosciusko	48,259	7.25	947	12
15	Kruzof	44,680	7	976	9
16	Kuiu	193,455	3	1080	19
17	Kupreanof	282,415	2	1091	20
18	Mitkof	54,753	1	1012	26
19	Prince of Wales	578,202	6.25	1219	16
20	Revillagigedo	302,659	2	1401	24
21	Tuxekan	8,523	6.5	320	11
22	Warren	5,067	10.5	710	8
23	Wrangell	56,948	1	991	26
24	Zarembo	47,263	5	777	13

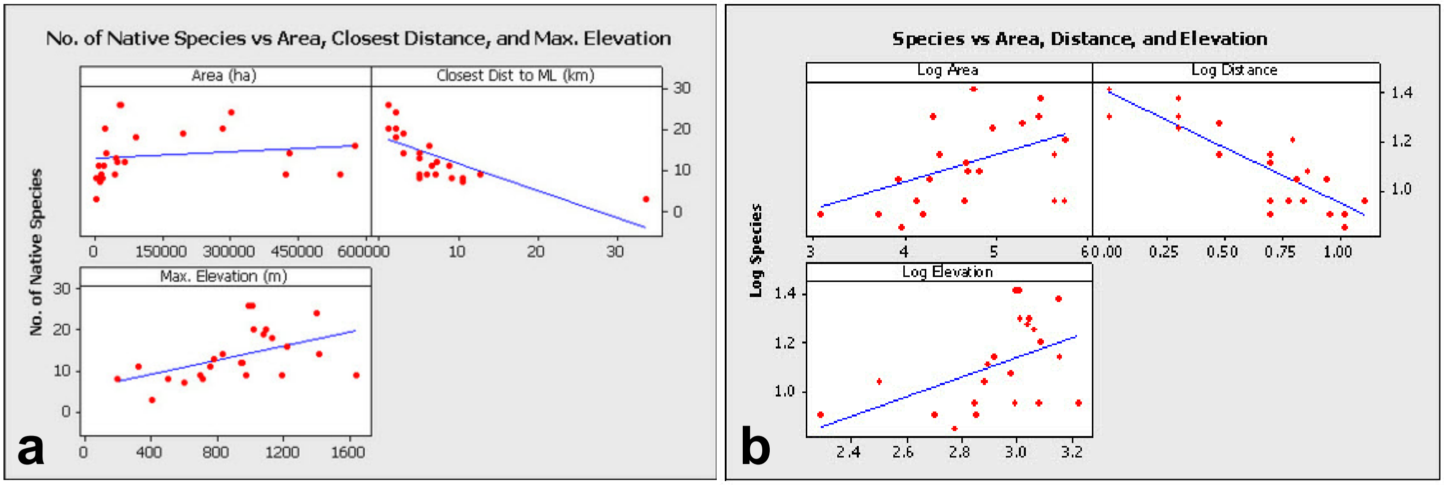


Figure 4. Plots of species richness by island area and by island elevation and by distance from mainland for the 24 islands reported in Table 1. a) Only island distance from the mainland is a significant ($p<0.05$) factor in explain differences in species richness. b) Island distance remains the only significant factor when the outlier (Forrester Island) is removed from the regression analyses.

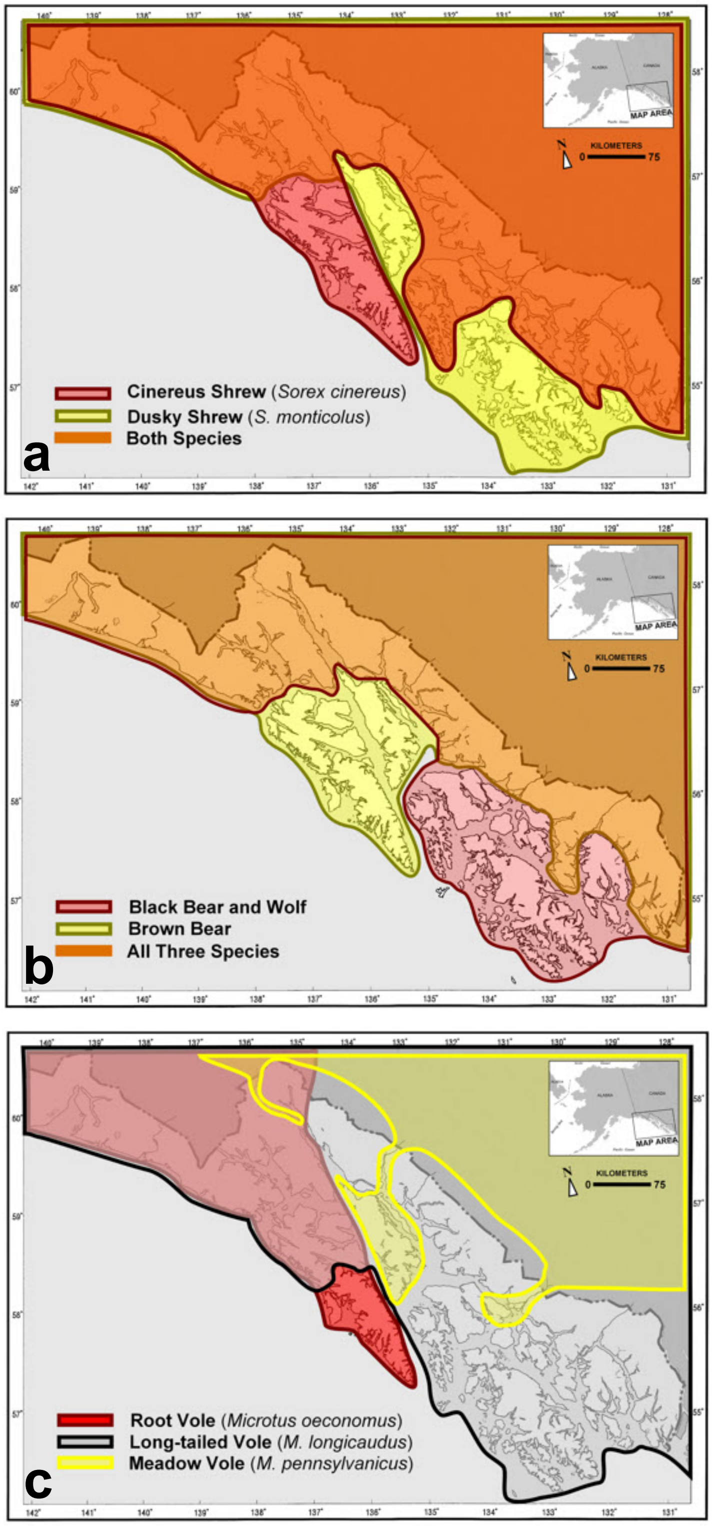


Figure 5. Series of three maps showing the general pattern of insular allopatry among ecologically equivalent a) shrews, b) large carnivores and c) microtine rodents.

Inter-island Connectivity

MacDonald and Cook (2007) suggested the possibility of identifying linkages among islands that may facilitate movement of organisms among islands. Those sites might be priorities for conservation because gene flow is a critical process with conservation benefits ranging from persistence of small populations to introducing traits necessary for adapting to fluctuating environments (Templeton et al., 2001; Manel et al., 2003). Those hypothesized connections fail to account for potentially crucial factors such as oceanic currents or similarity of habitat on either end of the crossing. Reconstruction of sea level fluctuations and the related influence of underwater topography on historic connections among islands should factor into our understanding of linkages. Sites that may facilitate connectivity among islands should be identified by establishing disturbance buffers and associated wildlife corridors for natural movement of organisms between islands. Proposed connections should be viewed as hypotheses that should be tested and are aimed at raising awareness to the complex interactions and metapopulation dynamics that may occur among islands. Molecular studies across a number of species have provided preliminary tests of linkages (Cook et al., 2006; MacDonald and Cook, 2007). The endemic Prince of Wales Island flying squirrel (*Glaucomys sabrinus griseifrons*), for example, has diverged from mainland squirrels (Demboski et al., 1998; Bidlack and Cook, 2001), but not from other populations of squirrels within the Prince of Wales Island complex (e.g., Prince of Wales, Heceta, Suemez, Dall; Bidlack and Cook, 2002). Such a pattern, also shared in northwestern deermice, ermine and potentially southern and northern dusky shrews (*Sorex monticolus*; Demboski and Cook, 2001), suggests high historic or contemporary levels of connectivity among these islands (Fleming and Cook, 2002; Lucid and Cook, 2004).

Islands within Islands

Temporal and spatial scale must be considered as management actions are initiated that further fragment habitats. In addition to the dynamic geologic history and natural fragmentation of the archipelago, industrial logging has recently produced a patchwork of habitats within many islands. Maintaining connectivity or corridors among patches to help mitigate important processes such as dispersal and gene flow should be a goal of management plans on the Tongass. Nevertheless, hypotheses of how landscape corridors will reduce the negative effects of fragmentation are largely untested (Damschen et al., 2006; Dixon et al., 2006) and predictions are especially uncertain in the face of climate change (Thomas et al., 2004). Highly vagile birds, carnivores and ungulates may disperse among islands more easily than flightless arthropods and small mammals. Preliminary molecular perspectives on mammals (Cook et al., 2006) indicate differential connectivity across taxonomic groups. With regard to assessing barriers throughout the archipelago, ubiquitous species are good candidates for identifying overall levels of connectivity, while less vagile species with more limited distributions or narrow habitat requirements may provide finer scale views of connectivity.

Faunal exchange among islands may be asymmetrical, with some islands acting as source populations while others act as sink populations. Kuiu Island has high black bear density (e.g., 1.5 bears/km^2) and a larger number of migrants per generation move from Kuiu to Kupreanof Island than vice-versa (Peacock, 2004; Peacock et al., 2007). Unequal rates of immigration and emigration illustrate the distinctive microevolutionary dynamics that populations in close proximity, but on different islands, may be experiencing. Peacock (2004) also recorded little exchange of black bears between Kuiu and Prince of Wales islands. With heavy harvest pressures on these two islands, these new perspectives on connectivity in black bears provide an important framework for designing sustainable harvests.

Conservation of Island Ecosystems

Logging, mining, human sprawl, tourism, hunting and trapping, and introductions of exotic and domesticated species present significant challenges to the maintenance of viable and well distributed wildlife populations. Each of these impacts may be magnified in insular endemics (Steadman, 2006; Whittaker and Palacios-Fernández, 2007). All are present, to varying degrees, in Southeast Alaska. Several islands have experienced significant impacts from one or more of these threats (e.g., central Prince of Wales, Long, Revillagigedo, Kuiu, Heceta) and the future will likely see a shift from one set of impacts to others. Logging drastically converted habitat on northern Chichagof and central Prince of Wales islands. Increased accessibility and habitat fragmentation resulting from the associated high density network of roads has severely impacted wildlife (Person et al., 1996). In most cases, these challenges have not been rigorously evaluated or monitored. Now added to this mix of potential threats, is anthropogenic climate warming which is predicted to substantially increase extinction risk for populations and species with limited ability to disperse (Thomas et al., 2004), such as many of those found on islands. Inability of insular species to respond (disperse) as conditions change raises the possibility that anthropogenic climate change could become a major cause of extirpation of species from islands in Southeast Alaska or even extinction for the insular endemic forms.

Inventory programs should be tied to laboratories that would be interested in investigations of selected species. An example is the recent series of papers on northwestern marten that established a molecular framework for understanding geographic variation in these economically important furbearers. This framework, if it had been available earlier, would have demonstrated the folly of the introduction of mainland marten (*Martes americana)* onto several islands in the Alexander Archipelago where the other species (*M. caurina*) may have been endemic. Active management of marten and marten habitat over the last 50 years has likely hastened the extirpation of Pacific marten (*M. caurina*) on several islands in the region, but the overall impact remains unknown (MacDonald and Cook, 1996, 2007). Koehler et al (2009; unpublished) uncovered significant phylogeographic structure in a nematode that is parasitic on marten across a number of locations in Southeast Alaska. Molecular genetic variation in these worms from marten on Chichagof correspond to two independent introductions of American marten (*M. americana*) from the Southeast mainland and Anchorage area as noted by historic records of introductions of this species. In addition, Koehler et al. (unpublished) found an endemic lineage of worm on Chichagof that is more closely allied with worms from Pacific marten on Admiralty Island and Haida Gwaii. This signal from the parasite is consistent with the recent extirpation of *M. caurina* on Chichagof Island, perhaps hastened by the introduction of *M. americana*.

Management recommendations and research needs

Preliminary investigations of mammals clearly indicate inadequacies in our current understanding of diversity and of the outdated taxonomic designations still in use for characterizing diversity and identifying forms unique to the region, i.e., are endemic there. These investigations also show that past logging efforts are strongly correlated with the occurrence of hot spots of endemism (Cook et al., 2006). In the future, a well-annotated set of natural history collections could provide the basis for assessing the status and distribution of Tongass endemics. Assessing biotic change begins with modern inventory studies that are conducted hand-in-hand with long-term monitoring programs in an effort to develop rigorous databases related to the status of Tongass wildlife and ecosystems. These data should be accessible via the internet and linked to other on-line databases, GIS applications, research programs, and management initiatives (Figure 6). A baseline for wildlife and their associated parasites, especially the pathogens that may impact wildlife (and human) health, is essential to evaluate emerging threats on federally managed lands. The relationship between climate change and emerging pathogens, for example, has recently been explored in high latitude ungulate populations (Kutz et al., 2005; Jenkins et al., 2006; Hoberg et al., 2008). Because these large mammals play a critical role in subsistence economies, efforts to monitor their health are essential to persistence of northern indigenous cultures. The list of potential studies is primarily limited by the availability of specimens and creativity of investigators.

What is needed now?

1. Interagency and Intergovernmental (USDA Forest Service, US Fish and Wildlife Service, Alaska Department of Fish & Game, Native Sovereign Nations, National Marine Fisheries, National Park Service, universities and natural history museums) agreements and working groups should focus on establishing a comprehensive management plan aimed at preserving the endemic biota and natural ecosystems of the Alexander Archipelago (Figure 7). Substantial physical and personnel infrastructure already exists in Southeast Alaska, but coordinated action on island issues is lacking. Because agencies are mandated to manage resources wisely, this infrastructure could be used to implement an island centered plan. Managers of archipelagos elsewhere are grappling with similar issues and have developed guiding principles for management of island systems (e.g., Golumbia, 2000; Sherley, 2000; McNeely et al., 2001; Wittenberg and Cock, 2001). An international conference focused on island management would be one productive outcome of such a working group.
2. Rigorous, integrated inventories of all islands over 500 hectares. There is a pressing need for specimen-based, all-taxa inventories of these islands. Work on nearby Haida Gwaii provides examples of taxonomic groups that could also be the focus or more intensive studies on the Tongass. Prior work opens productive opportunities to engage international collaborators and expand seminal studies along the North Pacific Coast on mosses (Schofield, 1989), flowering plants (Calder and Taylor, 1968), ground dwelling beetles (Kavanaugh, 1992; Clarke et al., 2007), song birds (Martin et al., 1995), and fish (Moodie and Reimchen, 1973; Reimchen, 1989, 1994). Spatially exten-

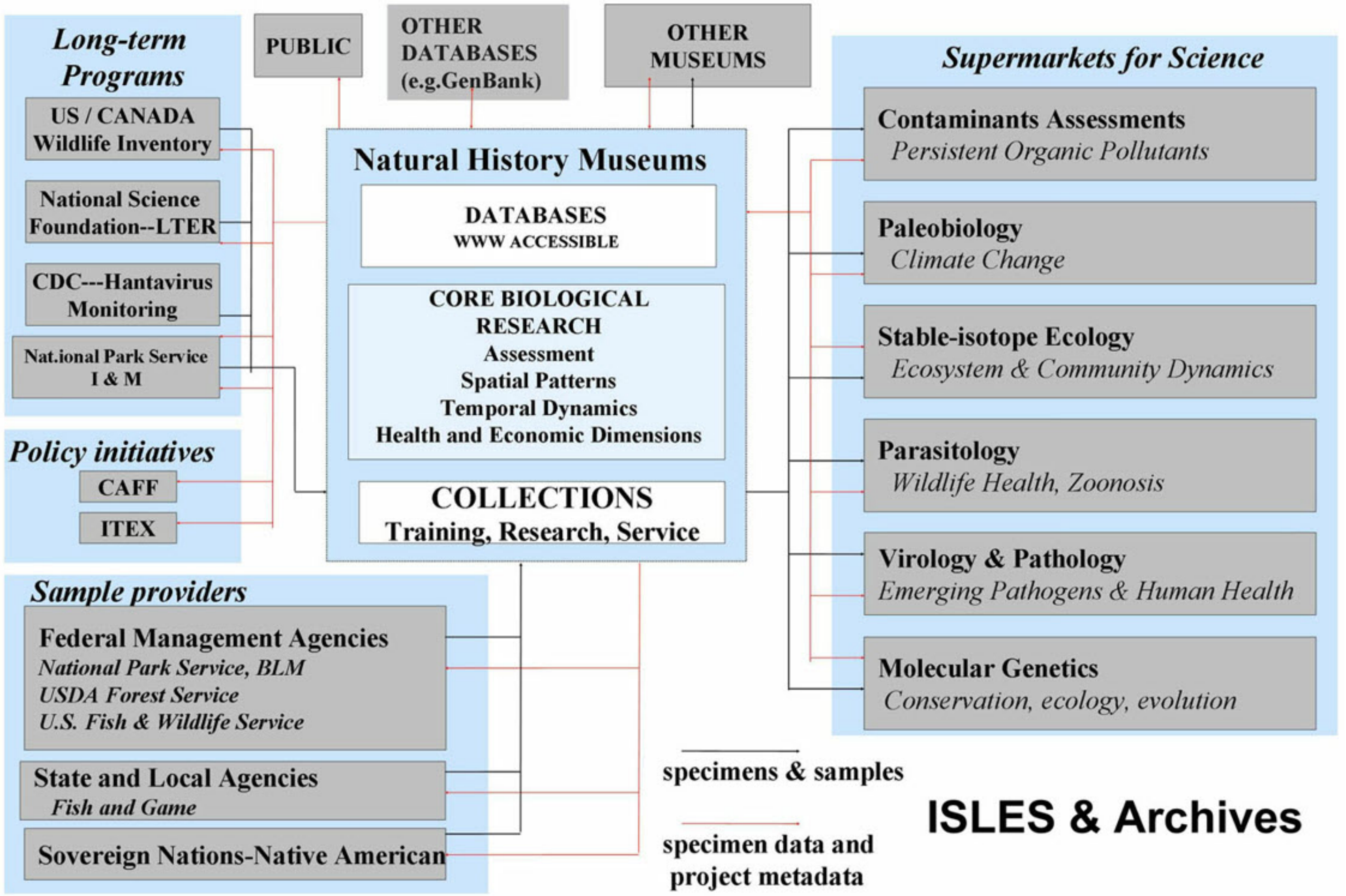


Figure 6. Schematic of a multiagency effort on the Tongass National Forest called Island Surveys to Locate Endemic Species (ISLES).

sive and site intensive archives of insular organisms on the Tongass are critical to stimulating investigations that will form the basis for careful management (Chapman, 2005). Sophisticated and varied technologies (e.g., stable isotopes, molecular genetics, biotoxins assays) have transformed wildlife management recently and can be employed through truly integrated investigations (Hoberg et al., 2003). Specimen archives are fundamental to the development of multidisciplinary views of diversity as all of these studies can be tied together through the voucher specimens.

3. Monitoring efforts should be designed to provide information necessary to assess environmental change. Elements of the environment to be monitored could include taxa that: are most susceptible to impacts (e.g., endemics), are introduced exotics, span multiple trophic levels, have complex lifecycles, or are key to human subsistence.

4. Actively seek and then build partnerships to investigate and monitor the region. Subsistence hunters, trappers, rural K-12 schools and academia are three examples of partnerships that could have powerful and lasting impact on resource management in Southeast Alaska.

5. Introduction of exotic species is a looming mega-issue for Tongass managers. Introductions must be thoroughly regulated as there are a growing number of exotics in the region (MacDonald and Cook, 2007). The best way to manage these pests is to deny their entry. If they become established, detect them quickly and eradicate them or manage them at acceptably low densities to prevent significant negative effects (Simberloff, 2002).

Given the complexity of issues facing resource managers along Alaska's southeastern coast and particularly on this vast archipelago, a diverse set of approaches is needed to effectively administer wildlife management plans and monitor potential threats to these native biotas. Several steps can be taken immediately that will lessen costs associated with impacts and facilitate swift responses to these perturbations in the future. Lack of available baseline materials has become the primary limitation to effective application of new technologies.

Acknowledgments

We first thank the large cast of stimulating colleagues who have participated in field, museum and/or laboratory work on Tongass wildlife since 1991. We also acknowledge the tireless efforts of personnel of the USDA Forest Service (Tongass Forest and Pacific Northwest Laboratory), Alaska Department of Fish and Game, US Fish and Wildlife Service and National Science Foundation (0415668) for providing logistics or funding our investigations along the North Pacific Coast. We thank Yadeeh Sawyer for technical assistance.

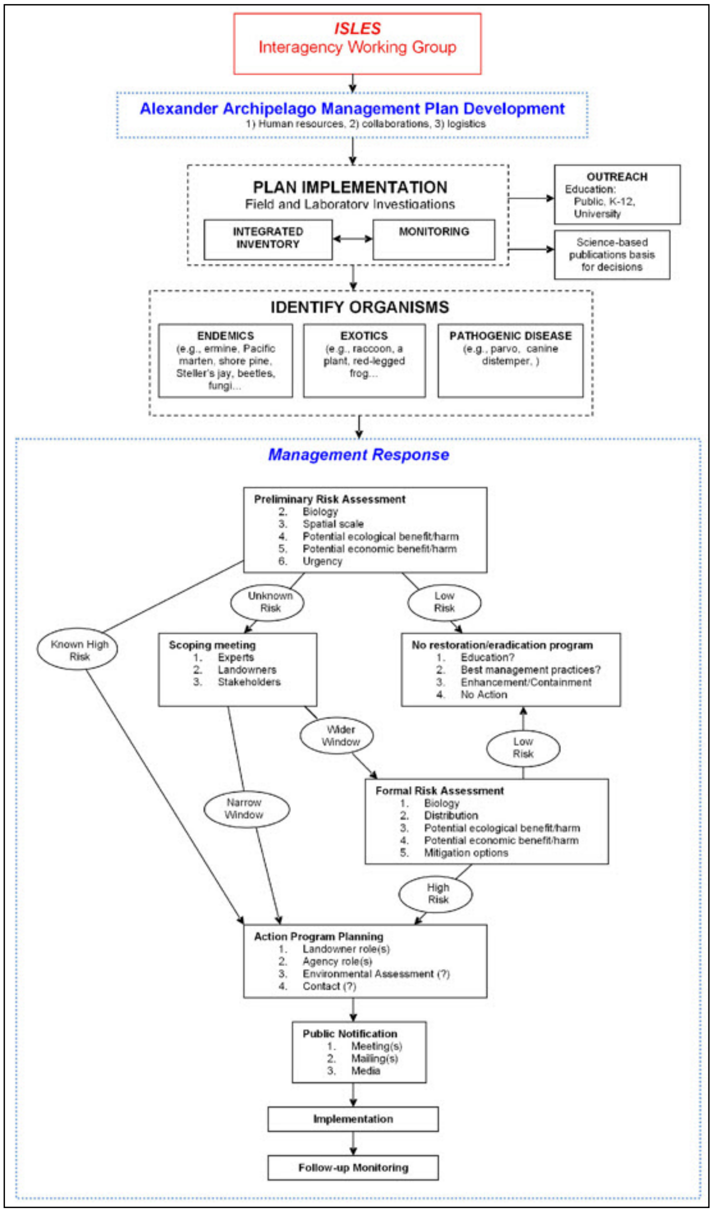


Figure 7. ISLES Management plan development and response.

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