CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
LA1	Conduct GPS telemetry studies of mountain lions utilizing core areas generally east of I-15 and SR 125 to determine extent and specific location of lion movement between core areas. Include collection and analysis of genetic material to determine gene flow among core areas and relatedness of individuals and population size.	Mountain Lion	Winston Vickers / UC Davis Wildlife Health Center	Western San Diego County west of the Cuyamaca Mountains, and extending from the US-Mexico border in the south to the area just north of Ramona	May 2012 – June 2014	Trail cameras, puma capture and GPS-collaring	Not really	Connectivity for pumas between certain San Diego County conserved lands is very limited, and mortality rates from roads are high...	Additional camera monitoring, acquisition of additional puma movement and genetic data, updated modeling of habitat and potential movement corridors (based on both habitat use data and genetic data) in the northern portion of the county.
LA1	Conduct initial surveys of habitat potentially occupied by badgers and assess the potential (both feasibility and cost) of conducting GPS telemetry studies to identify specific locations important to badger movement in habitats fragmented by roads. Include collection of genetic material to determine gene flow within and between occupied core areas.	American Badger	Cheryl Brehme / USGS	Western San Diego County (on or near Conserved Lands in MSPA)	2011, 2014	Sign surveys, canine scent detection of scat, genetic testing of scat, hair snags and cameras.	Too few to determine	Badgers are present but likely in low densities in areas of western San Diego County.	Identify areas within San Diego County with stable badger populations or recurring annual activity, characterize home range patterns within occupied habitat and document dispersal into adjacent conserved lands in the MSPA. Use these data to identify important movement corridors, foraging areas, primary threats, and causes of mortality.
LA1	Monitor large animal chokepoints identified by CBI (2002) and compare monitoring methodologies (cameras, tracks, etc.) as part of a long-term monitoring strategy for chokepoints.	Linkages	Carlton Rochester / USGS	San Diego MSCP	2011 through 2014	GIS, satellite imagery, land use data	Some yes, some no	Of the 16 linkages identified in the CMSP, eight are estimated to be functional, having a high likelihood to provide suitable habitat and movement routes to allow wildlife to effectively move back and forth between the conserved areas. Eight linkages were estimated as non-functional, having significant barriers to wildlife movement, so much so that it seems very unlikely that none but the most disturbance tolerant species will be able to move from one area to the next.	...monitoring critical points along the linkage should continue to help confirm or refute the linkage rating. Additional monitoring and wildlife use data will better inform species models and future management decisions.

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
LA2	Analyze existing genetic data from deer fecal analysis and utilize the data to evaluate core area connectivity for deer.	Deer	Andrew J. Bohonak & Anna Mitelberg / SDSU & ICR	Coastal San Diego County, particularly in the suburbs north of Miramar	2012 - 2013 and 2006-2007	Scat samples, DNA extraction and amplification of microsatellite markers	Yes & No	• Southern mule deer have less overall genetic diversity than subspecies elsewhere in the state. This is consistent with an effective population size that is less than 200 individuals for the region we studied (up to 500 km2), and perhaps less than 100. • Southern mule deer are relatively sedentary/territorial over many years. Offspring are often found very close to one or both parents. • Females in close proximity tend to be more closely related than males in close proximity. • There is statistical justification for dividing the area covered by this study into 2-9 management units. In the western part of our study area, where sampling was the most dense, populations generally correspond to existing reserves and canyons. • As in prior studies, the isolating effects of I-5 north of the I-5/805 merge are apparent, as well as the isolating effects of I-805 south of the merge.	• We recommend that existing levels of habitat connectivity in western San Diego County be maintained, in light of limited lifetime movement that appears to be typical of southern mule deer. • We recommend that additional non-genetic studies be conducted to quantify mule deer movement between SV and CC. • We recommend that additional genetic studies of mule deer be conducted on MCAS Miramar, to clarify its role in regional conservation of this species.
LA2	Analyze San Diego Tracking Team (SDTT) data collected subsequent to the data analyzed by Markovchick-Nicholls et al. (2008) to determine if SDTT data can be used to determine occupancy of habitat patches and infer connectivity for bobcats over time.	Multiple Species							

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
LA2	Obtain bobcat genetic material for core areas and utilize it to assess current connectivity for bobcats. Further evaluate multiple long-term monitoring strategies (e.g. genetic monitoring in a manner similar to that proposed by Vandergast et. al (2009) "Building better roads for wildlife: assessing the effects of roads on animal dispersal and genetic connectivity" or using camera traps as recommended by USGS for a preserve in Orange County or other or combination of methodologies).	Bobcat							
LA2	Utilize radio; telemetry to determine where bobcats frequently cross roads.	Bobcat	Megan Jennings & Rebecca Lewison / SDSU & Erin Boydsten & Lisa Lyren / USGS	San Diego MSCP Area - Los Penasquitos Canyon, Black Mountain, Boden Canyon, San Dieguito River lands, Ramona Grasslands, Boulder Oaks, Iron Mountain, Sycamore Canyon/Goodan Ranch, Rattlesnake Canyon, Mt. Woodson, Cleveland National Forest	2009-2012	Remote cameras, GPS telemetry, road kill collection, genetic analysis, habitat/connectivity modeling, occupancy modeling	Yes	• Overall, there is evidence of connectivity in the inland and coastal areas of the MSCP network that we sampled. • Genetic analysis showed some degree of genetic differentiation between coastal bobcats west of I-15 and inland animals to the east, but did not indicate subpopulation differentiation has occurred. This supports the assertion that the coastal and inland areas have some level of connectivity.	• Additional genetic data and analyses; • Region-wide analysis of genetic data; • Further occupancy analysis of remote camera data, including an analysis of the patterns of species co-occurrence in conserved cores, at pinch points, and in linkages; • Comparison of CBI connectivity assessment remote camera data from early 2000s to present day; • Additional roadkill collection and data mining to conduct hotspot analysis; • Ensemble analysis of connectivity using species distribution modeling and connectivity assessment programs such as Circuitscape, MaxEnt, Linkage Mapper, and ModEco; • Continue to map actual movement corridors between conserved cores using above data to improve monitoring and management • Testing and refinement of individual-based models developed from Orange County bobcat data (Tracey et al.) with San Diego bobcat data
LA2	Conduct review of roadrunner literature and identify potential connectivity monitoring considerations and costs.	Roadrunner							

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
SA1	Determine which small animal species are most sensitive to habitat fragmentation including fragmentation due to wildfire.	Multiple Species							
SA1	Determine (1) what type of genetic analysis (mitochondrial, micro satellite, single nucleotide polymorphisms (SNPs) would provide the meaningful data regarding connectivity and (2) which species have appropriate genetic markers already identified.	Multiple Species							
SA1	Using existing information and the new vegetation map (in prep), identify what portions of selected core areas and linkages are occupied by a suite of small animal species sensitive to habitat fragmentation and already have key genetics issues resolved.	Multiple Species							
SA1	Analyze genetic material previously collected (or evaluate existing analyzed data) to help inform decisions on appropriate approaches (sampling design, species, etc.) to genetic monitoring of connectivity for small animals.	Multiple Species							
SA1	Analyze post-fire monitoring data to identify small animal species that are slow to recolonize burned areas, identify potential re-colonization points and methodologies to evaluate potential re-colonization routes/mechanism.	Multiple Species							
SA1	Identify adaptive management actions that could improve inter- and intra-core area connectivity for the identified species.	Multiple Species							
SA1	Evaluate monitoring methods that are available, tested, feasible and cost-effective to determine which species will be selected for connectivity monitoring.	Multiple Species							

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
B1	Obtain and analyze cactus wren genetic samples from San Diego County.	Cactus Wren	Amy Vandergast & Barbara Kus / USGS	Southern California Range: (Ventura, Los Angeles, San Bernardino, Riverside, Orange and San Diego Counties)	2010-2011	Individual blood samples, DNA extraction and amplification of microsatellite markers	No	We detected 20 populations across the study area, a strong pattern of genetic isolation by distance, and pairwise FST values ranging from 0.033 to 0.182. Bayesian clustering methods detected 12 geographically-relevant genetic clusters. Genetic structure largely mirrors fragmentation patterns caused by urbanization, agriculture, and habitat conversion by wildfire, and many populations are in complete isolation.	• Does habitat restoration between aggregations = increased gene flow? • Translocations success rates adults vs. eggs • Does translocation = increased genetic diversity • Relationships between survival, fitness and genetic diversity
B1	Conduct banding studies to track dispersal of young cactus wrens to determine what habitats/corridors they utilize for dispersal and their dispersal distances.	Cactus Wren	Barbara Kus / USGS	Southern California Range: (Ventura, Los Angeles, San Bernardino, Riverside, Orange and San Diego Counties)						
B1	Obtain and analyze gnatcatcher genetic samples from San Diego County.	CA Gnatcatcher	Amy Vandergast & Barbara Kus / USGS	Southern California Range: (Ventura, Los Angeles, San Bernardino, Riverside, Orange and San Diego Counties)	2011-2012	Individual blood & feather samples, DNA extraction and amplification of microsatellite markers	Yes	We detected a single genetic cluster encompassing the study area using Bayesian clustering methods. Genetic differentiation among aggregations increased with increasing genetic distance indicating a stepping stone gene flow pattern among aggregations. We found no correlation between urban fragmentation and genetic differentiation among aggregations.	• Occupancy and abundance trends over time. • Future genetic monitoring every 5 generation or triggered by changes in occupancy or abundance
B1	Conduct banding studies to track dispersal of gnatcatchers to determine what habitats/corridors they utilize for dispersal and their dispersal distances.	CA Gnatcatcher	Barbara Kus / USGS	Southern California Range: (Ventura, Los Angeles, San Bernardino, Riverside, Orange and San Diego Counties)						

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
B2	Analyze collected least Bell's vireo genetic samples to determine current degree of connectivity and evaluate the need for further study of factors limiting connectivity.	Least Bell's Vireo							
B2	Evaluate the results of existing genetic analyses for southwestern willow flycatcher populations and assess the need for sampling for additional populations and evaluate the need for further study of factors limiting connectivity.	SW Willow Flycatcher							
NA	Not included in the CSP but was an existing project assessesing connectivity.	South-western Pond Turtle	Chris Brown & Robert Fisher / USGS	Coastal San Diego, Orange, Los Angeles and Riverside counties	2002-2013	Single nucleotide polymorphism / Visual encounter & trapping surveys	Yes within drainages, no across range	The SNP loci data had enough resolution to identify "natural" breaks in the species (where populations became genetically distinct from adjacent populations), so that management units for conservation could be developed. In assessing genetic bottlenecks, we determined that only the most remote and undisturbed sites appear to genetically retain high diversity and a full complement of haplotypes.	There are watersheds where we know little about turtle populations and/or their genetics which are regional gaps in knowledge that could help in making decisions for management and recovery of the species.
NA	Not included in the CSP but was an existing project assessesing connectivity.	Native bees (Hymen---optera: Anthophila)	Keng-Lou James Hung & Dr. David A. Holway / UCSD	Greater San Diego Region	2011-2012	Aerial netting, fluorescently painted bowl traps, visual plant surveys	No	In fragments of scrub habitat <40 ha in size (e.g. open space parks embedded in urban matrix), native bee species richness and genus richness were roughly 35% lower than those in large, intact patches of scrub habitat >400 ha in size (e.g. Mission Trails Regional Park), despite similar richness and density of blooming native plant species in the two types of habitats.	What is the rate of bee species recolonization to isolated fragments? How do different bee species move among discrete patches of urban habitat through non-green urban matrices? What constitutes a "corridor" from the point of view of native insect pollinators? What are the levels of pollinator diversity required for indefinite persistence of our native insect-pollinated flora?

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
NA	Not included in the CSP but was an existing project assessesing connectivity.	Small Vertebrates	Jeff A Tracey, Cheryl S. Brehme, Carlton Rochester, Denise Clark, and Robert N. Fisher / USGS	Large underpasses in coastal San Diego County that had no roads or water courses passing through them	2012-2014	Specialized infrared motion detection cameras in underpasses, BACI design to investigate the effectiveness of adding structures to underpasses to enhance small vertebrate use.	Can be with added structures in underpasses	The results of modeling gave evidence to support the short-term effectiveness of the added structure treatments on small vertebrate use and suggested that these rates changed on the specific side the treatment was applied rather than the entire underpass. The community composition appeared to differ within the underpasses in comparison to outside the underpasses. In particular, initial results indicate that small mammals, rabbits, bobcats, and roadrunners may tend to use underpasses less than the surrounding habitat, while reptiles (snakes and lizards), squirrels, medium sized mammals and deer use underpasses more than the surrounding habitat. Future modeling of these data will help us to better discern these effects.	...additional monitoring in 2017, five years after addition of structure, to reassess the effect of structure on the use of underpasses by small and large vertebrates.... additional field experiments, such as addition of ledges to underpasses and relocation experiments will provide further information to allow for informed and successful decision making for maximizing wildlife connectivity under roadways that would otherwise be barriers for movement or mortality sinks.

CSP Obj.	Actions to Achieve Objectives	Resource Assessed	Assessor / Affiliation	General Location	Time Series	Sampling Techn.	Connected?	Main Conclusions	Recommended Future Studies
NA	Not included in the CSP but was an existing project assessesing connectivity.	San Diego Fairy Shrimp	Andrew Bohonak & Marie Simovich / SDSU	Coastal San Diego County	Field collections primarily from 2002-2005; time series not explicitly analyzed	Genetic analysis of samples from pools across the species range	No	1. Genetic differentiation among vernal pools is statistically significant and relatively strong, even over relatively small distances. 2. … these mtDNA lineages are more divergent for microsatellite markers on average than one would expect. 3. Preliminary sampling of MCAS Miramar shows that the A4 complex is unusually divergent in terms of microsatellite markers, but not mtDNA. 4. In the microsatellite data set, Mira Mesa and Del Mar Mesa pools show somewhat higher divergence than one would expect. 5. …These two species can hybridize in the lab, consultants have previously speculated about hybrids in field populations, and we have published a paper demonstrating that hybrids are present in several disturbed pools in coastal San Diego County.	11. Movement of cysts among pools should be minimized, and especially outside of pool complexes....12. It follows that newly created pools should be stocked from a single pool complex as close as possible. Stocking single new pools from a single source pool (rather than a multi-pool mixture) is recommended unless logistical or endangered species impacts preclude this. 13. Beyond low levels of connectivity among pool complexes, there may be an even more significant amount of divergence between the pools of {Mira Mesa, Del Mar Mesa} and the remainder of the species range. Additional care should be taken to minimize homogenization of these sites with Miramar and populations south, with Ramona to the east, and with Pendleton to the distant north. 14. We have published a method for identifying hybrids from mature fairy shrimp females. We are attempting to develop a genetic hybrid index at this time. 15. Quantifying the extent of hybridization and its correlates is our current goal