Soft Bird’s-Beak
(Chloropyron molle ssp. *molle)*

5-Year Review:
Summary and Evaluation


Image credit: Mark Hayes, USFWS

U.S. Fish and Wildlife Service

San Francisco Bay-Delta Fish and Wildlife Office

Sacramento, CA

5-YEAR REVIEW
Soft Bird's-Beak / *Chloropyron molle* ssp. *molle*

GENERAL INFORMATION

Species: Soft Bird's-Beak (*Chloropyron molle* ssp. *molle*)

Date listed: November 20, 1997

FR citation(s): 62 FR 61916 61925

Classification: Endangered

BACKGROUND

Most recent status review:

U.S. Fish and Wildlife Service. 2009. *Cordylanthus mollis* ssp. *mollis* (Soft Bird's-Beak). Five-year review: summary and evaluation. Sacramento Fish and Wildlife Field Office. Sacramento, California. January 2009. 22 pp.

FR Notice citation announcing the species is under active review:

86 FR 27462 27464, Initiation of 5-Year Status Reviews of 76 Species in California and Nevada; request for information; May 20, 2021.

Critical habitat/4(d) rule/Experimental population designation/Similarity of appearance listing:

In the final listing rule for *Chloropyron molle* ssp. *molle* and *Cirsium hydrophilum* var. *hydrophilum*, we determined that the designation of critical habitat was not prudent because the designation would not be beneficial to the conservation of the two subspecies (U.S. Fish and Wildlife Service 1997). On November 17, 2003, the Center for Biological Diversity and others filed a lawsuit in the Northern District of California against the Secretary of the Interior, challenging the not prudent determination of critical habitat for the two subspecies (Center for Biological Diversity, *et al*. v. Gale Norton, Secretary of the Department of the Interior, *et al*., CV 03-5126-CW). On June 14, 2004, the U.S. District Court Judge signed an Order granting a stipulated settlement agreement between the two parties. The Service agreed to propose critical habitat for the two-plant subspecies on or before April 1, 2006, and finalize the designation on or before April 1, 2007. A proposed rule to designate critical habitat for the two-plant subspecies was published in the Federal Register on April 11, 2006 (71 FR 18456).

On April 12, 2007, the Service published a final rule in the Federal Register to designate critical habitat for *Cirsium hydrophilum* var. *hydrophilum* (Suisun thistle) and *C. molle* ssp. *molle* (72 FR 18517; U.S. Fish and Wildlife Service 2007). The designated sites were Fagan Slough Ecological Reserve; Hill Slough Wildlife Area; Point Pinole Regional Park; Rush Ranch/Grizzly

Island Wildlife Area; and Benicia State Recreation Area (BSRA) (U.S. Fish and Wildlife Service 2007).

Purpose of 5-year Reviews:

The U.S. Fish and Wildlife Service (Service) is required by section 4(c)(2) of the Endangered Species Act (Act) to conduct a status review of each listed species at least once every 5 years. The purpose of a 5-year review is to evaluate whether or not the species' status has changed since it was listed (or since the most recent 5-year review). Based on the 5-year review, we recommend whether the species should be removed from the list of endangered and threatened species, be changed in status from endangered to threatened, or be changed in status from threatened to endangered. Our original listing of a species as endangered or threatened is based on the existence of threats attributable to one or more of the five threat factors described in section 4(a)(1) of the Act, and we must consider these same five factors in any subsequent consideration of reclassification or delisting of a species. In the 5-year review, we consider the best available scientific and commercial data on the species and focus on new information available since the species was listed or last reviewed. If we recommend a change in listing status based on the results of the 5-year review, we must propose to do so through a separate rule-making process defined in the Act that includes public review and comment.

Methodology used to complete the review:

This review was prepared by staff of the San Francisco Bay-Delta Fish and Wildlife Office, U.S. Fish and Wildlife Service. Information was compiled from technical and data reports published by other federal agencies, published and unpublished Service reports, and Service documents related to *Chloropyron molle* ssp. *molle*. These documents were used to consider the current species status, historical and current threats relevant to species survival, a comparison of the current species status to previously determined species recovery criteria, and recommendations for future actions and research. Biologists who have been actively engaged in activities associated with *Chloropyron molle* ssp. *molle* were consulted for recommendations on recovery activities for the next five years.

REVIEW ANALYSIS

Application of the 1996 Distinct Population Segment (DPS) policy:

The Endangered Species Act defines "species" as including any subspecies of fish or wildlife or plants, and any distinct population segment (DPS) of any species of vertebrate wildlife. This definition of species under the Act limits listing as distinct population segments to species of vertebrate fish or wildlife. Because the species under review is a plant, the DPS policy is not applicable, and the application of the DPS policy to the species' listing is not addressed further in this review.

Updated Information and Current Species Status

Taxonomy:

At the time of listing, the genus *Cordylanthus* was placed in the Scrophulariaceae (figwort family), and the accepted taxonomic nomenclature for the species of interest in this review was

Cordylanthus mollis ssp. *mollis*. However, a molecular systematics study by Olmstead *et al.* (2001) provided evidence to move the hemiparasitic group Castillejiinae that includes *Cordylanthus,* to the Orobanchaceae (broomrape family) thereby placing the species into the genus *Chloropyron*. This revision has been reflected in the 2nd Edition of the Jepson Manual (2012), which also recognizes the previously published name *Chloropyron molle* (A. Gray) (1868) A. Heller (1907) subsp. *molle* for soft bird's-beak. The current recovery plan for *C. molle* ssp. *molle* has also recognized this revision (Service, 2013). Thus, this review uses the currently accepted name, *Chloropyron molle* ssp. *molle*.

Species Overview:

Chloropyron molle ssp. *molle* is a hemiparasitic annual herb in the Orobonchaceae (broomrape) family (Figure 1). The plant gets its common name, soft bird's-beak, from a pair of fused petals at the top of the corolla that resemble the shape of a bird's beak. Mature plants can range in height from 10 to 40 centimeters and display a typical branching pattern from the middle or above.

Stems and leaves are gray-green, with some purple-tinge, and are covered in fine, gland-bearing hairs, and soft, non-glandular hairs. The leaf glands exude salt crystals which result in a sparse to heavy covering on the leaves and stems. Leaf morphology is variable, where oblong leaves are either entire or pinnately lobed with three to seven lobes.

Flowers are tubular in shape, transitioning from pale cream to yellowish, and arranged in elongated spike-like inflorescences of three to 30 flowers. Each flower is partially covered by leafy, gray-green and purple-tinged, calyx-like, lobed bract. The corolla, which is almost entirely enclosed by the sheath-like calyx, displays yellowish-white or greenish-yellow lips, is wooly, and commonly bears purple pollinator guides. The flowers have four stamens; two stamens are functional and the other two are sterile. Flowers have been noted to develop as early as May but flowering typically peaks in July and concludes in August, although later flowering has occasionally also been observed.

Fruits are a capsule form and the number of seeds produced per fruits can vary widely (from approximately 8-79 seeds per fruit), with an estimated average number of seeds produced per plant being 495 (Ruygt, 1994). Seed maturation can occur as early as July. Seed of *C. molle* ssp. *molle* have a reticulated seed coat that traps air thereby allowing seeds to float in saline and fresh water for hours to days long periods. The details of how this contributes to seed dispersal are not currently well understood but a reasonable prediction is that it can enable water dispersal by tidal flows. Germination is reported to begin sometime in December and some early seedlings have been observed to overlap with the previous year's plants that were in a late-fruiting state (Ruygt, 1994). No new information on seed ecology or germination biology for this species exists at this time but increased understanding of these topics could be important to future restoration efforts.

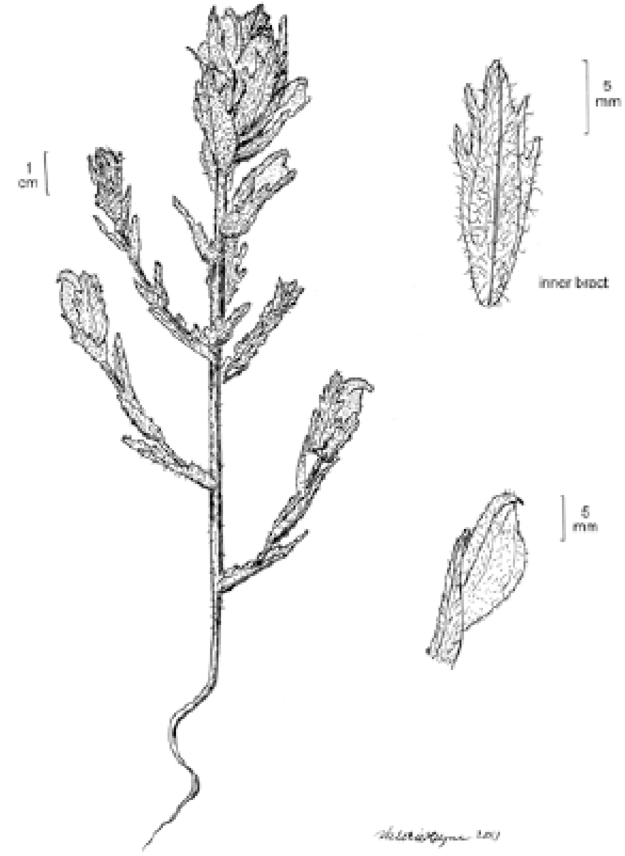


Figure 1. Illustration of *Chloropyron molle* ssp. *molle*. This figure is adapted from Figure II-3 of Service (2013). Illustration credit, Valerie Layne, USFWS.

Habitat, Distribution, and Abundance:

Chloropyron molle ssp. *molle* grows in the coastal salt marshes and brackish marshes in the mean higher high water (MHHW) tidal datum of San Pablo and Suisun Bays (Figure 2; Service, 2013). The historical western limit of *C. molle* ssp. *molle* ranged from marshes between the Petaluma River and San Rafael in the west, to the brackish tidal marshes at the mouth of the Sacramento River in the east. The subspecies is not thought to have inhabited the marshes of the San Francisco Bay. The species is typically found at sites that experience regular tidal inundation or sites that are consistently well-saturated within mixed halophytic plant communities (i.e., salt tolerant plants). It is most recently recorded to exist in 11 widely scattered populations across Napa-Sonoma, Point Pinole, Carquinez Straits, Suisun Marsh area, and northern Contra Costa County (Service, 2013; Goals Project, 2015). A recent range wide survey conducted by USGS in 2021 surveyed 25 marsh sites that included nine sites with historical records of species presence, plus two additional sites and sites that represented potentially suitable habitat (Figure 3; Thorne et al., 2023). This work confirmed species presence at all sites that were previously documented, but no new populations were found.

Chloropyron molle ssp. *molle* does not appear to be edaphically restricted as it has been recorded to occur on a range of soil types (e.g., peaty clay silt tidal marsh soils, mineral alluvial sediments along the margins of shallow salt pans at the upper marsh edge, and marsh soils that formed on top of artificial fill; Ryugt, 1994 and Service, 2013). Data was collected for several habitat characteristics across 73 transects and 346 plots, including soil porewater salinity, elevation, and plant community composition, as part of the range wide survey conducted by USGS in 2021 (Thorne et al., 2023). The results of that study suggest that the species is possibly most narrowly restricted by elevation (-0.10 - 0.29 meters relative to MHHW) and salinity (tolerance range of 6.51 - 74.00 parts per thousand; Thorne et al., 2023). This makes sense, as muted tidal flows have been previously identified as problematic for the survival of *C. molle* ssp. *molle;* and habitat, elevation, and salinity are intrinsically linked to tidal flow.

This species is hemiparasitic, which means that it is capable of photosynthesizing, but it drains water and nutrients from a host plant. Therefore, it must establish a relationship with a host plant early on in its development in order to survive and reproduce. It has been observed to associate with several plants, such as, *Sarcocornia pacifica* (pickleweed), *Distichlis spicata* (salt grass), *Jaumea carnosa* (fleshy jaumea), *Frankenia salina* (alkali heath), and *Troglochin maritima* (arrow-grass) (Stromberg and Villasenor, 1986). The recent USGS study provided updated observations of plant species with which *C. molle* ssp. *molle* occurs, including *D. spicata* and *S. pacifica* at 100% of sites; *J. carnosa* at 70% of sites; and *Cuscuta salina* at 53% of sites (Thorne et al., 2023). These plant associations are similar to what was reported previously by Grewell (2003). *Cuscuta salina* was previously reported to sometimes parasitize *C. molle* ssp. *molle*, however, it was also predicted to be beneficial because it can clear dense vegetation and create bare ground that might then be colonized by *C. molle* ssp. *molle* (Grewell, 2004). The hemiparasitic relationship is critical to the survival of *C. molle* ssp. *molle* but little is known about its specific plant-host parasite relationship(s) and no new information exists (Service 2013).

Chloropyron molle ssp. *molle* was also found at 93% of sites with an average of approximately 19% bare ground (Thorne et al., 2023). The presence of bare ground has been linked to increased establishment of a close relative, *Chloropyron maritimus* (see Service, 2013 for additional details). These findings suggest it could also be a relevant factor for establishment of *C. molle* ssp. *molle*, however, it has not yet been investigated.

Chloropyron molle ssp. *molle* might have few other specific habitat constraints as precise population locations can be highly variable between years (Service, 2013). The recent USGS survey compared abundance estimates recorded in 2021 to those recorded from the previous range wide survey (Ruygt, 1993). They found that abundance estimates at most sites in 2021 were similar to those recorded in 1993, except four populations (Hill Slough – North and East, MOTCO East, Fagan Marsh, and Joice Island) that have suffered moderate to large declines in estimated population size (Table 1; Thorne et al., 2023). Population locations and sizes of this species have been recorded to fluctuate between years, with some subpopulations going undetected some years, then re-emerging years later. Therefore, specific locations and estimates of population sizes on shorter timescales (i.e., year-to-year) might be less important to this species' survival than estimates of population sizes and locations of regularly inhabited sites over longer timescales, such as estimates calculated from multiple years of observations (Service, 2013). *Chloropyron molle* ssp. *molle* has experienced extensive habitat degradation, fragmentation and loss primarily due to alteration of marsh lands for development that have resulted in muted tidal action.

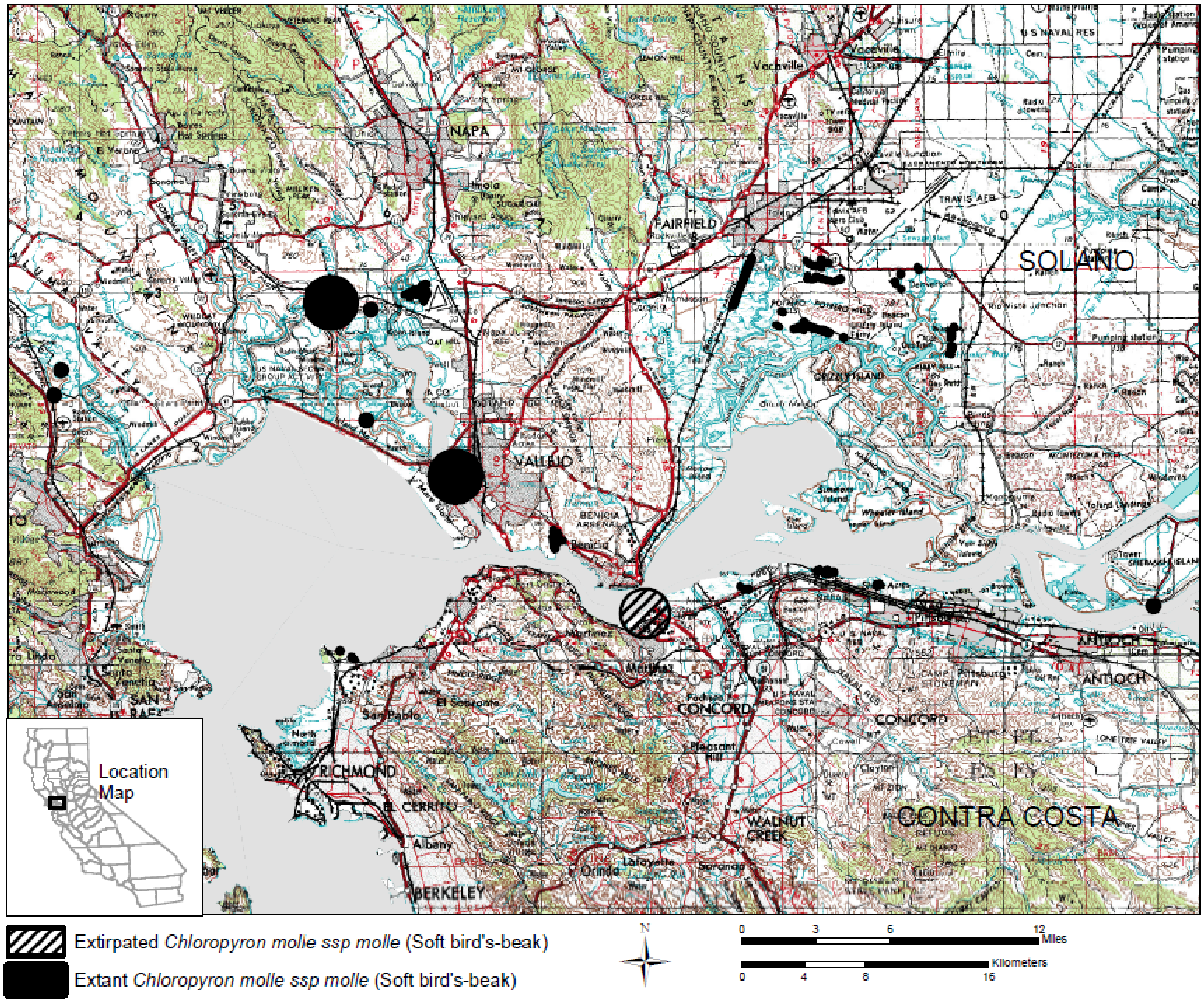


Figure 2. Mapped distribution of *Chloropyron molle* ssp. *molle*. This figure is adapted from Figure II-4 of Service (2013). Extirpated sites indicated by hatched marks. Extant sites indicated by solid marks.

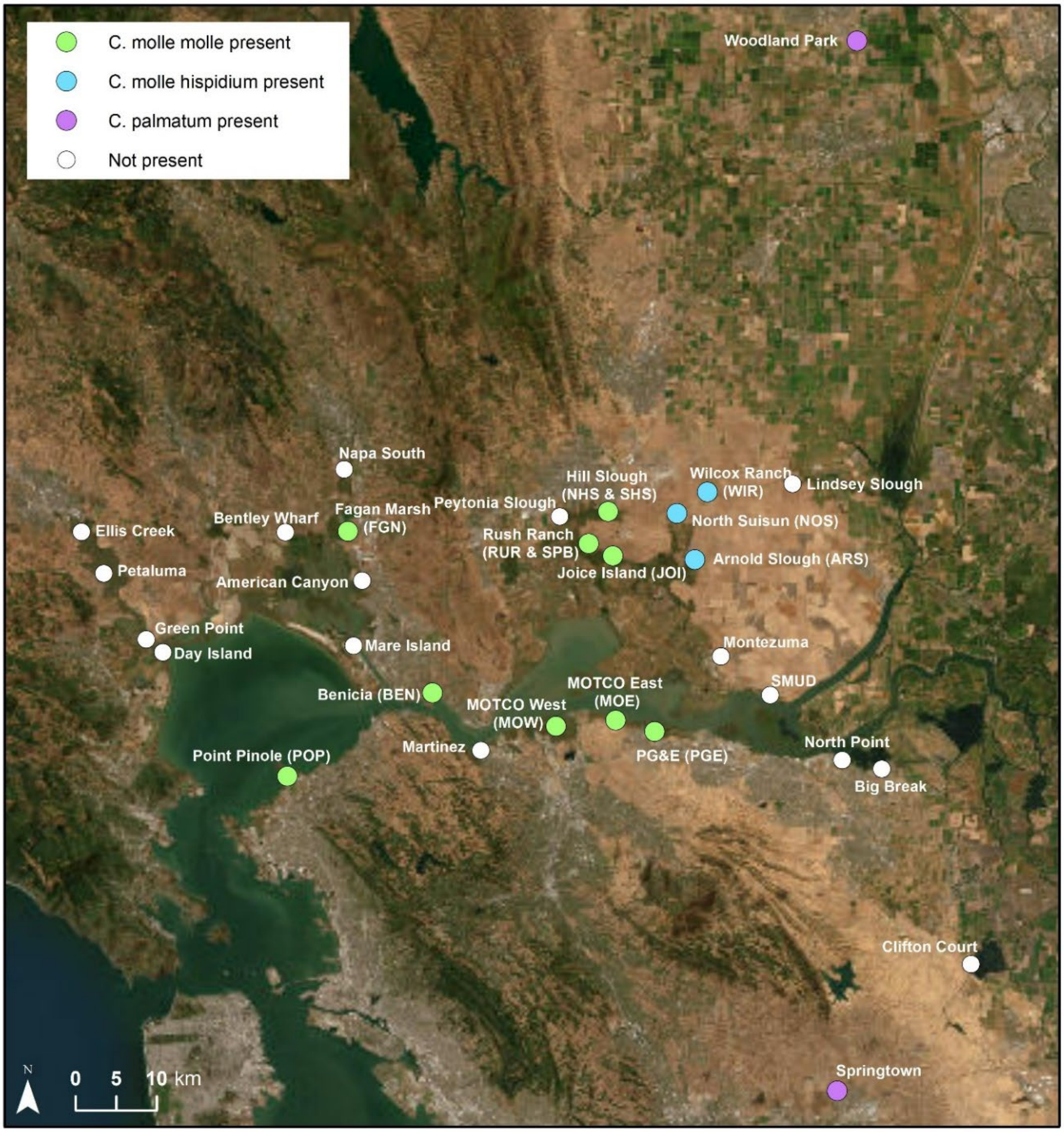


Figure 3. Site map of all locations surveyed by USGS for *Chloropyron molle* ssp. *molle* and where tissue was collected in the San Francisco Bay-Delta, California. This figure is adapted from Figure 1 of USGS Report (Thorne et al., 2023). Colors indicate the presence of *C. molle* ssp. *molle* (green), *C. molle* ssp. *hispidium* (blue), and *C. palmatum* (pink). *C. molle* ssp. *molle* and *C. molle* ssp. *hispidium* sites include three-letter codes used in genetics analysis.

Table 1. Comparison of estimated abundances between 1993 and 2021 range wide population surveys of sites with confirmed *Chloropyron molle* ssp. *molle* presence. Table adapted from USGS report (Thorne et al., 2023). Site name, three-letter code for genetics analysis, 1993 reference name, presence, and abundance, estimated abundance from current 2021 survey, and abundance change for *C. molle molle*. Best estimates were derived during field surveys.

Marsh Site Name	Code	1993 Site Name	*C. molle molle* Present	Estimated Abundance 1993	Estimated Abundance 2021	Estimated Change in Abundance
Hill Slough (North & South)[2]	NHS/ SHS		Yes	141,000	19,522	-121,478
MOTCO East	MOW	Middle Point	Yes	61,725	293	-61,432
Fagan Marsh	FGN		Yes	6,590	550	-6,040
PG&E	PGE	McAvoy Harbor	Yes	23	1,100	1,077
Joice Island	JOI		Yes	5,650	1,157	-4,493
MOTCO West	MOW	Hastings	Yes	5,833	11,000	5,167
Rush Ranch (with Spring Branch)[2]	RUR/ SPB		Yes	2,003	12,735	10,732
Point Pinole	POP		Yes	2,280	12,735	10,455
Benicia*	BEN		Yes	11,576	N/A	N/A

* California State Parks declined USGS surveys at Benicia. This site was resurveyed by Dr. Brenda Grewell (USDA) as part of ongoing efforts by California State Parks and their existing agreement to conduct distribution and abundance estimates and may be available from California State Parks.

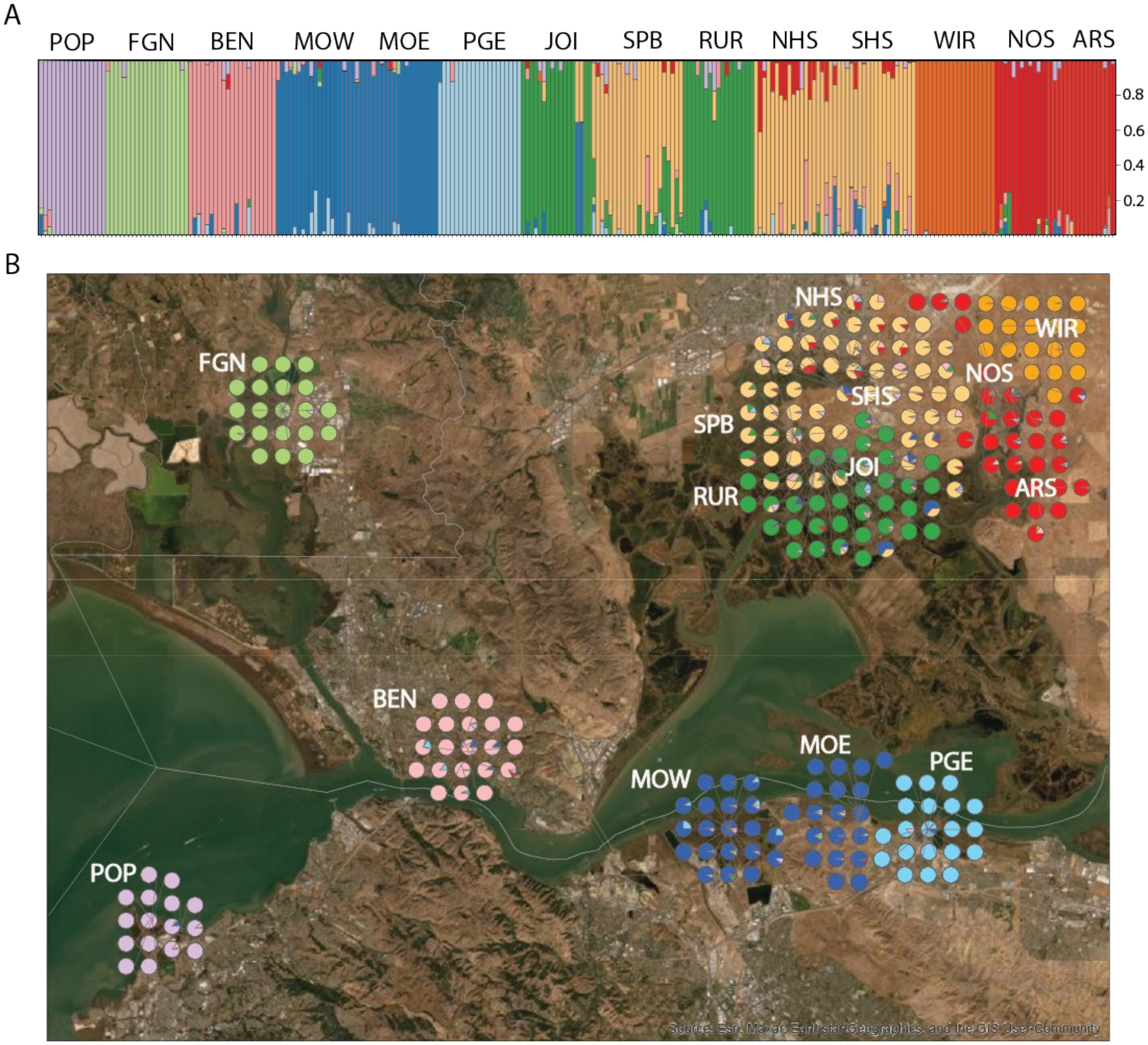
Genomic Diversity:

A primary goal of the USGS' 2021 study of *Chloropyron molle* ssp. *molle* was to assess and describe genomic diversity across the species range. To do this, Thorne and colleagues sampled leaf tissue from 23 individuals at every site surveyed where either *C. molle* ssp. *molle* (found at 11 sites) or its congener, *C. molle* ssp. *hispidum* (found at three sites), was present (Thorne et al., 2023). *Chloropyron molle* ssp. *hispidum* was included in order to better understand whether and how genomically distinct *C. molle* ssp. *molle* is from its closest relative, and how levels of genetic diversity in *C. molle* ssp. *molle* compared to a presumably stable congener. Two-hundred and seventy-nine samples were sequenced using a reduced representation sequencing approach, and a total of 253 were retained for analyses after quality filtering (for details, see Thorne et al., 2023). Broadly, the study supports that these are distinct subspecies by showing clear genetic differentiation between the two congeners (see Fig. 9 in Thorne et al., 2023), although some amount of gene flow was detected where the subspecies boundaries meet in the northeastern portion of the range (see Fig. S1 in Thorne et al., 2023). It is not clear at this time how recent the gene flow might be. Further work is needed in order to determine whether this could be an ancestral signal or, perhaps, evidence of more recent intraspecific hybridization which could have implications for the conservation of genetic diversity in *C. molle* ssp. *molle*.

Genetic structure within Chloropyron molle ssp. molle

Within *C. molle* ssp. *molle*, individuals are generally genetically distinguished by site, with subpopulations within sites being highly genetically similar to one another (Fig. 4A-B; Thorne et al., 2013). For instance, Hill Slough subpopulations reflect highly similar patterns of genetic variation, and MOTCO East and West subpopulations are highly genetically similar to one another. One exception to this is Rush Ranch and the Spring Branch restoration at Rush Ranch that was implemented in 2000 (Service, 2009). In this case, the Spring Branch restoration population is genetically distinct from the Rush Ranch population. Records reflect that the source material for the Spring Branch restoration was comprised of propagules collected from Hill Slough and Joice Island populations (Service, 2009). Hill Slough and Joice Island populations were selected to provide source material based on similarity of environmental and site characteristics to the site at Rush Ranch that was chosen for the Spring Branch restoration (Service, 2009; Jones, 2023). However, details are unclear regarding the sampling design for the collection of the source material. For instance, what was the success/failure rate of propagation efforts, and how/which successful propagants were selected for outplanting. The uncertainty of some details regarding the source material used for the Spring Branch restoration limits our ability to fully interpret the patterns of genomic diversity reported in the USGS study (Thorne et al., 2023). We will be following up with further inquiry regarding the source materials used for the Spring Branch restoration.

Furthermore, few details were provided regarding sampling design for collecting leaf tissue for DNA sequencing (Thorne et al., 2023). It was reported that a maximum of 23 leaf tissue samples were collected per population. But details were not provided on whether consideration was given for the estimated population abundances or the area size of populations, nor was it reported how individual plants were selected for tissue collection within each population (e.g., how nearby were the sampled plants within populations) when determining the total number of plants to sample at each site. *Chloropyron molle* ssp. *molle* predominantly outcrosses and is recorded to disperse over short distances (≤10 meters; Ruygt, 1994; Grewell et al., 2003). Pollinator activity is the presumed primary mechanism underlying reproduction of *C. molle* ssp. *molle* but this has not been confirmed. These factors should be taken into account during sampling design in order to avoid generating patterns in the data that could be an artifact of sampling rather than representative of population level genomic diversity. Thus, this somewhat limits interpretation of the reported patterns of genomic diversity in *Chloropyron molle* ssp. *molle* (Thorne et al., 2023). We will follow-up with further inquiry and future research to clarify these outstanding questions.



Source: Esri, Maxar, Earthstar Geographics, and the GIS User Community

Figure 4. Structure plot showing genetic admixture assignment of each individual (A) and map displaying approximate population locations of individuals that are represented as pie charts of genetic assignment proportions (B). Adapted from Figure 13 in the USGS report (Thorne et al., 2023). Populations are coded as: POP = Point Pinole, FGN = Fagan Marsh, BEN = Benicia State Park, MOW = MOTCO West, MOE = MOTCO East, PGE = PG&E, JOI = Joice Island, SPB = Spring Branch (at Rush Ranch), RUR = Rush Ranch, NHS = Hill Slough North, SHS = Hill Slough South, WIR = Wilcox, NOS = North Suisun, ARS = Arnold Slough. ARS, NOS, and WIR are populations of *C. molle* ssp. *hispidum*. All other populations are *C. molle* ssp. *molle*.

Genetic diversity in Chloropyron molle ssp. molle

Genetic diversity among populations was lower in *C. molle* ssp. *molle* (average pairwise Fst = 0.056) compared to among populations in *C. molle* ssp. *hispidum* (average pairwise Fst = 0.08). This indicates that *C. molle* ssp. *molle* might not be strongly genetically differentiated among populations. And F_{IS} values suggested that very little inbreeding is occurring (Thorne et al., 2023). A strong correlation was detected between geographic distance and genetic distance among populations of *C. molle* ssp. *molle* but there also appeared to be a generalized west-east cline on the distribution of genetic diversity that was observed in both species (see Fig. 10 in Thorne et al., 2023). Levels of genetic diversity were consistent across sites of *C. molle* ssp.

molle, except for the two western-most populations, Fagan Marsh and Point Pinole, which displayed lower genetic diversity (Thorne et al., 2023). Both populations are the most geographically isolated of *C. molle* ssp. *molle*, so this suggests that gene flow between these two populations and the others has been somewhat restricted as seed dispersal is estimated to be around 10 meters or less on average and very little is known about pollination biology or plant-pollinator relationships in this species. Pollinators have been documented interacting with *C. molle* ssp. *molle* but it is possible that the distance between Fagan Marsh and Point Pinole and all other populations is too great for pollinators to travel.

Environmentally relevant genetic variation in Chloropyron molle ssp. molle
The USGS study also reported that approximately 4% of genetic variation was significantly ($p < 0.001$) associated with four environmental variables: mean annual precipitation (MAP), summer precipitation (PPT-SM), average porewater salinity (SAL), and estimated mean higher high water (EMHHW). Patterns in loci heterozygosity varied from one another and from neutral loci, which increases confidence for their potential environmental relevance. This suggests that genetic variation exists in *C. molle* ssp. *molle* that could be important for species response(s) to different environmental conditions represented by the variables tested in the USGS study (Thorne et al., 2023).

Threats Analysis (threats, conservation measures, and regulatory mechanisms):

This section contains a review of the five categories of threat factors, including the known specific threats and stressors, impacting Chloropyron molle ssp. molle. Here, we have reviewed and summarized information from prior Service documents, including the Recovery Plan for Tidal Marsh Ecosystems of Northern and Central California (Service, 2013); the most recent 5-year review for Chloropyron molle ssp. molle (Service, 2009); unpublished agency reports (Thorne et al., 2023); other unpublished resources; and communications with biologists with relevant expertise.

Factor A: The present or threatened destruction, modification, or curtailment of habitat or range

Extensive loss of suitable habitat for *Chloropyron molle* ssp. *molle* has been caused by diking of large tracts of tidal marshes for agricultural purposes, such as vineyard expansion (Service, 2013). Only approximately 15% of the historical area of tidal marsh has been estimated to still exist, and the majority of extant populations of *C. molle* ssp. *molle* are still associated with these areas of relict marshes (Goals Project, 2015; Service, 2013). Despite this low estimation, it is predicted that habitat loss has actually been underestimated because levees were normally constructed directly in sites of high and upper middle tidal marsh zones and along tidal sloughs, which is where optimal habitat has tended to exist for *C. molle* ssp. *molle* (Service, 2013). This was a direct cause of population fragmentation, which remains a contributing factor to increased risk of extinction. Additional human-related activities include levee repair and maintenance, ditch maintenance, grading and stabilization of marsh edges, and inadequate or improper management of grazing. Natural events, such as channel bank erosion, can also have a negative effect on *C. molle* ssp. *molle* habitat quality (Service, 2013).

Tidal marsh modification through large-scale alteration of salinity regimes is another important threat to *Chloropyron molle* ssp. *molle* that degrades habitat (Service, 2013). This is particularly evident in Suisun Marsh, which was targeted with efforts to stabilize low salinity water in order to improve water quality for public use. There were some attempts to address this and also create conditions that favor waterfowl habitat; and some water quality standards in the western part of Suisun Marsh have been revised to allow for more natural, climate-based fluctuation in salinity (Service, 2013). However, the artificially narrow, invariable low salinity range was enforced during fall and winter months for eastern Suisun Marsh up until 2018, at which point a "Summer Outflow Augmentation" was also implemented as part of a flow action experiment to examine effects on the threatened Delta smelt (*Hypomesus transpacificus*, Osmeridae) (Service, 2013; CDWR, 2018). The flow action experiment took place from 2018-2020 and summer operation has been required since 2021 based on the results of that study, which were favorable for creating Delta smelt habitat (CDWR, 2018; Sommer et al., 2020).

Linked to alteration of salinity regimes is the function of delta outflows and drainages of the Suisun Marsh watershed in modifying the ecological character of extant habitat. The operation of salinity control gates alters the natural climate-based patterns of outflows such that establishment and dominance of different kinds of vegetation also become altered in *C. molle* ssp. *molle* habitat. Long-term, progressive salinization in tidal marsh does not appear to be a threat to *C. molle* ssp. *molle*. The species appears to respond favorably to increased salinity by increasing in abundance in areas of tidal marsh with higher salinity, whereas widespread decline of *C. molle* ssp. *molle* has been recorded after years of above-average rainfall (Service, 2013). Together, these observations suggest that fluctuations in salinity, such as those that include variation in fresher waters, in *C. molle* ssp. *molle* habitat could contribute to constraining the species' range.

The current most significant threat(s) to *Chloropyron molle* ssp. *molle* habitat and extant populations are due to the establishment and encroachment of invasive plant species, e.g., *Lepidium latifolium*, into the middle and upper brackish tidal marsh zones (Service, 2013). *Lepidium latifolium* is a tall, clonal herb that grows in very dense stands, and it excludes *C. molle* ssp. *molle* from sites where it invades, as it is not able to survive under the canopy of *L. latifolium*. Previous observations indicated *L. latifolium* to be a threat at four sites with *C. molle* ssp. *molle* populations: Hill Slough, Joice Island, Rush Ranch, and Benicia State Recreation Area (Service, 2013). The most recent survey conducted by USGS does not mention any encroachment of *L. latifolium* into existing stands of *C. molle* ssp. *molle* at any site at this time (Thorne et al., 2023). However, plant surveys were only conducted within specific plots at sites, rather than covering the entirety of every site. It is possible that *L. latifolium* presence in the broader *C. molle* ssp. *molle* habitat was undetected. Surveys focused on invasive species in and around *C. molle* ssp. *molle* habitat would help clarify the current threat to *C. molle* ssp. *molle* of *L. latifolium* invasion.

Other invasive species that were previously identified as threats to *C. molle* ssp. *molle* are *Hainardia cylindrica* (hardgrass) and *Polypogon mospeliensis* (annual beard grass). These two species are problematic because, although *C. molle* ssp. *molle* can parasitize them, they die before *C. molle* ssp. *molle* can complete its lifecycle (Grewell, 2005). However, neither of these species were recorded in the recent survey either (Thorne et al., 2023). *Cotula coronopifolia* (brass-buttons) was also previously included as a potential invasive threat to *C. molle* ssp. *molle*, however, no new information since Service (2013) has been discovered.

Other less consistent threats to *C. molle* ssp. *molle* habitat include rooting behavior (turning over of vegetation) of feral pigs and hazardous waste remediation by military installations (e.g., U.S.

Navy) (Service, 2013). Although such threats generally occur with less frequency, both can result in the total destruction of *C. molle* ssp. *molle* habitat and populations when and where they do occur. While public recreational activities can damage *C. molle* ssp. *molle* habitat because trails are often constructed at the edges of tidal marshes, public trail use along tidal marshes could also have a positive effect by reducing the density and cover of closed marsh vegetation (Service, 2013).

Factor B: Overutilization for commercial, scientific, or educational purposes

Overutilization for commercial, recreational, scientific, or educational purposes has not been determined to be a significant threat to *Chloropyron molle* ssp. *molle* at this time (Service, 2013).

Factor C: Disease or predation

Chloropyron molle ssp. *molle* is a documented target of intense seed predation by insects, specifically by moth larvae (*Sphenista* ssp. in the family Tortricidae, and *Lipographis fenestrella* in the family Pyralidae) (Ruygt, 1994; Grewell et al., 2003). The interaction between the seed-feeding moth and *C. molle* ssp. *molle* is apparently balanced; however, muted tidal regimes can disrupt this balance by increasing moth survivorship, leading to heavy seed-predation and reduced fecundity of *C. molle* ssp. *molle,* which results in population declines (Service, 2013). Seed-predation does not appear to be a widespread problem for *C. molle* ssp. *molle* at this time, but it is a persistent problem at sites with muted tidal regimes where fecundity apparently continues to decline (Service, 2013).

Disease has not been determined to be a significant threat to *C. molle* ssp. *molle* at this time.

Factor D: Inadequacy of existing regulatory mechanisms

The project-by-project approach of Federal and State permitting processes prevents comprehensive impact assessments for threatened and endangered plants (Service, 2013). Impact to threatened and endangered species is often assessed based on the estimated number of acres affected as a proxy for impacts to habitat based on incomplete or inconclusive surveys. This approach has often led to the fragmentation of higher quality continuous habitat into smaller patches. Additionally, survey periods are often brief, which can negatively bias survey results against annual plant species like *C. molle* ssp. *molle*. Sometimes rare plant surveys are foregone entirely in tidal marshes. Such practices increase the risk to threatened and endangered plant populations, particularly annual plants which are not obvious year-round. The Service (2013) notes that regulatory agencies have historically been too permissive across the range of *C. molle* ssp. *molle*, likely because smaller footprint projects tend to take place in the upper margins of marshes and along levees where suitable *C. molle* ssp. *molle* habitat can be found. Therefore, a regulatory bias in favor of projects that impact fewer acres of land can result in greater habitat fragmentation, destruction, and loss for *C. molle* ssp. *molle*.

Factor E: Other natural or manmade factors affecting its continued existence

Sea-level rise and associated flood control responses have been identified as significant long-term threats to *C. molle* ssp. *molle*. Conservation of *C. molle* ssp. *molle* is dependent on preserving adequate land space for the species to migrate along with the suitable habitat as sea level rises (Service, 2013). Much of high tidal marsh land is bordered by levees or has already undergone land-use change and conversion to agricultural, residential, or commercial property. Undeveloped lands exist in Suisun and San Pablo Bays, however, the Service (2013) predicts that such areas will be the focus of conflicting needs for flood protection, agriculture, and preservation as future tidal marsh habitat.

Hazardous material spills have also been identified as a potential threat to *C. molle* ssp. *molle* and its habitat. Crude oil spills, in particular, are a threat as this material tends to deposit along the high tide line where *C. molle* ssp. *molle* is most abundant (Service, 2013). This can affect the species directly by harming seedling emergence in the winter and/or spring, as well as potentially damaging mature, flowering populations during summer. Spill remediation, which often involves removal of oil debris, soil, and sediment of the affected area, can also damage the species by removing an unknown portion of the seed bank. A seed bank is a natural repository of many generations of genetic diversity, some of which may or may not be well represented in contemporary populations, that could be important to the recovery and future survival of a species. Avoiding populations during disaster response could be difficult when plants are not flowering but might be impossible depending on severity and scale of a spill.

Recovery Criteria

Recovery Plan or Outline: Recovery Plan for Tidal Marsh Ecosystems of Northern and Central California, Volume I; August 27, 2013.

Determining whether to downlist or delist a species requires careful examination of the five threat factors (A-E) that were considered during listing of the species, as specified in section 4(a)(1) of the Endangered Species Act. A recovered species is one that no longer meets the Endangered Species Act's definitions of threatened and/or endangered. Recovery criteria define the actionable items against which progress toward species recovery can be assessed. As such, when certain conditions are met (as defined in the 'Recovery Criteria') it can be determined that a species' status may be appropriately changed (i.e., downlisted or delisted). The specific recovery criteria to downlist *Chloropyron molle* ssp. *molle* from endangered to threatened, or to delist, are summarized in Table 2. See Service (2013) for full details and descriptions of the criteria.

Table 2. Downlist and delist criteria for *Chloropyron molle* ssp. *molle*. This information is adapted from Service (2013; see for details).

No.	Code	Brief Description	Units/Approach	Current Status	Downlist Criteria	Delist Criteria
1	A/1	Area inhabited (acres)	Acres	Not completed	≥3,000 acres in Suisun Bay Recovery Unit (RU) and ≥1,000 acres in San Pablo Bay RU for 5 years	6,000 acres in Suisun Bay RU and 2,500 acres in San Pablo Bay RU over 8 years
2	A/2	Area preserved (acres)	Acres	Not completed	≥5,000 acres permanently preserved in Suisuin and San Pablo Bay RUs to encompass ≥80% of species	Permanently preserve and manage ≥9,000 acres in Suisun Bay RU and/or San Pablo Bay RU to encompass ≥80% of species
3	A/3	*Lepidium latifoloium* area (%)	%	Not completed	<10% cover for 5 years	All conditions under A/3 downlisting must have been met; Develop and implement plan for ED&C to prevent future >10% cover in tidal areas; secure permanent funding
4	A/4	* Other non-native plant control (%)	%	Not completed	<10% cover within 50 feet of extant *C. molle* ssp. *molle* populations	All conditions under A/4 downlisting must have been met
5	A/5	Restoration of natural tidal range	Qualitative	Not completed	Restoration of periodic tidal flooding at Hill Slough and Rush Ranch pond area	All conditions under A/5 downlisting must have been met
6	A/6	Elmination of trampling / rooting	Qualitative	Not completed	N/A	Eliminate trampling damage by livestock and feral pigs from all *C. molle* ssp. *molle* and host plants in all populations for 8 years
7	A/7	Propagation and reintroduction methods	Qualitative	Not completed	N/A	Develop and implement reliable propagation and reintroduction methods
8	E/1a	Number of populations	#	7 populations in Suisun Bay Recovery Unit (RU) and 2 populations in San Pablo Bay RU	9 populations in Suisun Bay RU; 4 populations in San Pablo Bay RU	10 populations in Suisun Bay RU; 8 populations in San Pablo Bay RU
9	E/1b	Number of plants	#	Not completed	3,000 individuals per population over 5 years	3,000 individuals in each population over 8 years OR 300,000 individuals around Suisun Bay RU; 300,000 individuals around San Pablo Bay RU
10	E/1c	Minimum number of individuals in full census	#	59,092 individuals (estimated in 2021 survey)	500 individuals in entire species for 2 consecutive years over 5 years	1,000 individuals in entire species for 2 consecutive years over 8 years
11	E/1d	Seed production	#	Not completed	Avg. of >10 seed capsules per plant and avg. of >15 mature seeds per plant	All conditions under E/1d downlisting must have been met
12	E/2	Seed banking accomplished	Qualitative	Not completed	N/A	Seed banking of all extant populations to capture representative genetic diversity
13	E/3	Oil spill response plans prepared to protect populations	Qualitative	Not completed	N/A	Must be completed and include a monitoring plan, if necessary
14	E/4	High marsh / upland transition lands preserved or created and managed	Qualitative	Not completed	N/A	Criterion met when sea level rise modeling indicates sufficient uplands are protected to accommodate landward migration while maintaining acreage criteria

* Other non-native, invasive perennial and winter annual plant species including but not limited to: *Apium graveolens* (celery), *Cotula coronipfolia* (brass-buttons), *Juncus gerardi* (black-grass rush), *Spartina patens* (salt-meadow cordgrass), *Polypogon monspeliensis* (annual beard grass), *Hainardia cylindrical* (barbgrass), *Parapholis incurva* (sicklegrass), and *Crypsis schoenoides* (swamp grass); ED&C = early detection and control

Synthesis

Chloropyron molle ssp. *molle* is an endangered annual plant with a current distribution spanning Suisun and San Pablo Bays. Recent work by USGS confirmed that *C. molle* ssp. *molle* still exists at locations that were first documented in a range wide survey in 1993 (Ruygt). This work also reported that although most populations appear to be stable, at least four populations have undergone significant contractions (Thorne et al., 2023). Some of the variation in abundance might be due to the previously documented phenomena of annual fluctuations in population sizes. In consideration of this, we currently do not know whether the smaller population sizes are sustained and, therefore, a potentially serious threat to the persistence of this species, or ephemeral, such that population abundances might soon recover.

Previously documented threats to *C. molle* ssp. *molle*'s survival include loss of suitable habitat, muted tidal flows, invasive plants and association with inappropriate hosts, trampling by livestock and rooting by feral pigs, hazardous chemical spills/exposure, and habitat degradation and plant damage due to human activities in upper tidal marsh lands. All of these threats still exist, however, the Service (2013) outlined a recovery plan to address the identified threats. This plan also provided clear, actionable items in order to downlist or delist the species. Broadly, these criteria include the identification of a minimum number of inhabited acres in Suisun and San Pablo Bay recovery units for a period of 5 years to downlist and 8 years to delist; a minimum number of preserved acres that encompass 80% or more of the species in Suisun and San Pablo Bay recovery units; a targeted maximum area allowed for invasive species presence within tidal marsh and, specifically, within *C. molle* ssp. *molle* habitat; restoration of natural tidal marsh range, including periodic flooding at two sites; and the elimination of trampling and rooting damage. Additionally, several items in the Recovery Plan focus on addressing the loss within populations and creation of new plant materials for restorations and reintroductions (i.e., propagation and reintroduction methods, seed production and banking).

Recent work determined levels of genomic diversity are mostly consistent across the geographic range of *C. molle* ssp. *molle*. However, intraspecific hybridization with *C. molle* ssp. *hispidum* might be occurring in the northeastern portion of *C. molle* ssp. *molle*'s range. Additionally, the western-most isolated populations of *C. molle* ssp. *molle* (Fagan Marsh and Point Pinole) display reduced genetic diversity compared to other populations, which suggests restricted gene flow is occurring and highlights this area of the range for reintroduction efforts in order to re-establish gene flow to and from these populations. These genetic data will also provide important insights into population diversity, demographics, and dynamics across the range in planning and implementing future restorations and reintroductions. Overall, future work should focus on incorporating the specific criteria outlined in the recovery plan, as well as incorporating new findings from the recent USGS range wide survey and study of the distribution, abundance, and genomic diversity of *C. molle* ssp. *molle*. (Service, 2013; Thorne et al., 2023).

We have determined that *Chloropyron molle* ssp. *molle* remains an endangered species. We base this determination on our review of the downlisting and delisting criteria in the Recovery Plan (2013) in consideration of the most recent range wide survey and abundance estimates (that indicated population persistence at the same locations documented during the last range wide survey but also a mix of stable and declining population abundance estimates) and measured levels of genomic diversity (which indicated little inbreeding across the species' geographic range, but also low genetic diversity in two isolated populations and the potential threat of hybridization with a congener in the northeastern portion of the range).

RESULTS

Recommended Classification:

_____Downlist to Threatened

_____Uplist to Endangered

____ **Delist** (*Indicate reasons for delisting per 50 CFR 424.11):*
____ *Extinction*
____ *Recovery*
____ *Original data for classification in error*

__X__No change is needed

RECOMMENDATIONS FOR FUTURE ACTIONS

The following recommendations for future actions are based on the Service's Recovery Plan (2013) and incorporation of recent research and findings, such as the USGS' 2021 range wide survey and genomics study in *Chloropyron molle* ssp. *molle*.

Surveying and Monitoring:

- Recovery Actions A/1, A/2. Develop and implement an annual, range wide survey and monitoring plan for *Chloropyron molle* ssp. *molle*. As population sizes of *C. molle* ssp. *molle* can fluctuate dramatically between years, surveys that attempt near-exact counts rather than abundance estimates of populations should be the primary focus. Special attention should be given to acquire exact counts, annually, of the populations at regularly inhabited sites. Surveys should also include: the number and location of populations; estimates of area inhabited by each population.
- Recovery Actions A/3, A/4. Work with partners to develop and implement a survey and monitoring plan for invasive species in areas inhabited by *Chloropyron molle* ssp. *molle*. Surveys should be focused on populations of *Chloropyron molle* ssp. *molle* and areas within 50 ft. of each population and they should be conducted based on the development and phenology of the identified invasive plants. These surveys should include: the location of the areas surveyed; survey frequency; invasive plants of interest at each site; abundance estimates of invasive plants found; and proximity to nearest population of *C. molle* ssp. *molle*. Known invasive plant threats currently include but might not be limited to: *Lepidium latifolium*, *Hainardia cylindrica*, *Polypogon mospeliensis*, *Cotula*

coronopifolia. *Cuscuta salina* is native to the Bay-Delta, however, it should be included in such surveys based on the predicted inappropriate plant-host relationship it can form with *C. molle* ssp. *molle*. Survey follow-up and monitoring records should include information on historical, ongoing, and/or planned invasive mitigation and eradication techniques in collaboration with partners.

- Recovery Action A/6. Develop and implement a survey and monitoring plan to focus on trampling and rooting damage by livestock and feral pigs to *Chloropyron molle* ssp. *molle* populations. This plan should cover how to monitor damage, the partners and groups responsible for organizing and conducting surveys and monitoring, the locations to be surveyed and monitored, and the frequency at which surveys/monitoring are needed.

Restoration Activities:

- Recovery Action A5. Develop a plan to restore tidal marsh, including restoration of periodic tidal flooding at Hill Slough and Rush Ranch pond areas. Complete the actions that are achievable within 5 years. Follow-up with a monitoring plan of tidal flooding at Hill Slough and Rush Ranch pond areas.
- Recovery Action A/7. Renew efforts and advance methods for propagation, including a plan to scale-up propagation, of *C. molle* ssp. *molle* to be used in restoration and reintroduction / mitigation efforts.
- Recovery Actions E/1d, E2. Develop and implement a seed banking plan for *C. molle* ssp. *molle* including development of seed storage protocol with estimates of storage effects on seed viability/longevity. Seed collection and banking efforts should be developed based in-part on current knowledge of the range wide distribution of genetic diversity.
- Develop a plan to reintroduce 1-2 populations of *C. molle* ssp. *molle* that might serve as connector populations to promote gene flow between Fagan Marsh and Point Pinole populations in the west and all other populations of *C molle* ssp. *molle* in the eastern portion of the range. This plan should incorporate information from the USGS’ 2021 range wide survey of sites with potentially suitable habitat, as well as in-depth surveys of all existing public lands in the area for currently unknown sites of potentially suitable habitat. Source material for reintroductions should also rely on genotypic information and diversity estimates from the 2021 USGS study.

Additional Future Actions for Consideration:

- Genetic monitoring of populations, particularly those that appear to be at-risk of intraspecific hybridization with *Chloropyron molle* ssp. *hispidum*, and the western-most isolated populations at Fagan Marsh and Point Pinole that appear to be experiencing restricted gene flow.
- Breeding trials between *Chloropyron molle* ssp. *molle* and *C. molle* ssp. *hispidum* to determine what level of threat intraspecific hybridization poses in the northeastern portion of *C. molle* ssp. *molle*’s range.
- Investigation(s) into seed ecology of *C. molle* ssp. *molle* to support seed banking efforts and to inform on the potential use of direct-seeding in restorations.
- Investigation(s) into plant-pollinator relationships to inform on reproductive biology of

C. molle ssp. *molle* and to aid in making predictions regarding current and future gene flow across the species range.

- Quantitative genetics studies to estimate species' phenotypic plasticity (i.e., the capacity to respond to changing environmental conditions) especially to variation in hydrological factors.
- Studies focused on the *C. molle* ssp. *molle*'s plant-host relationships to better determine potential risk from inappropriate host relationships.
- Conduct public outreach and education to develop potential partnerships with private landowners with property where *C. molle* ssp. *molle* might be present.

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Personal Communication

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U.S. FISH AND WILDLIFE SERVICE
5-YEAR REVIEW of *Chloropyron molle* ssp. *molle*

Current Classification:

Recommendation resulting from the 5-Year Review:

____ Downlist to Threatened
____ Uplist to Endangered
____ Delist (Indicate reasons for delisting per 50 CFR 424.11):
  ____ Extinction
  ____ Recovery
  ____ Original data for classification in error
__X__ No change needed

Appropriate Listing/Reclassification Priority Number, if applicable:

FIELD OFFICE APPROVAL:

Donald Ratcliff, Project Leader, San Francisco Bay-Delta Fish and Wildlife Office, Pacific Southwest Region, U.S. Fish and Wildlife Service

Approve DONALD RATCLIFF Digitally signed by DONALD RATCLIFF Date: 2023.08.30 08:41:12 -07'00' Date _________

The lead Field Office must ensure that other offices within the range of the species have been provided adequate opportunity to review and comment prior to the review's completion. The lead field office should document this coordination in the agency record.