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DOCUMENTING THE EARLY STAGES OF INVASION OF *MATTHIOLA PARVIFLORA* AND PREDICTING ITS SPREAD IN NORTH AMERICA

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ABSTRACT—We identify *Matthiola parviflora*, native to the Mediterranean, as a newly discovered exotic plant in the Sonoran Desert in southwestern United States. We used morphological and molecular characteristics to distinguish *M. parviflora* from its naturalized congener *Matthiola longipetala*. Comparison with Internal Transcribed Spacer sequences from GenBank confirmed identification as *M. parviflora*. To predict the potential for broad-scale invasion, we used repeated censuses and maximum-entropy modeling with MaxEnt software. Censuses from 2008–2010 documented localized spread through an undisturbed biological reserve, and the modeling predicted a large area of suitable habitat in southwestern United States and northern Mexico. This record represents the first reported occurrence of *M. parviflora* in the Western Hemisphere and characterizes the species as well established near Tucson, Arizona, with a significant potential for spread.

RESUMEN—Identificamos a *Matthiola parviflora,* una planta nativa del Mediterráneo, como una nueva planta exótica del desierto Sonorense en el suroeste de los Estados Unidos. Usamos características morfológicas y moleculares para distinguir a *M. parviflora* de su congénere habituado *M. longipetala.* Haciendo comparaciones con secuencias de espaciador transcrito interno (ITS por sus siglas en inglés) de GenBank, confirmamos la identificación de *M. parviflora.* Para predecir el potencial de invasión a gran escala, usamos censos múltiples y modelos de máxima entropía con la programa MaxEnt. Censos realizados de 2008 a 2010 indicaron una diseminación local en una reserva biológica no perturbada. Asimismo, los modelos predijeron que un área grande del suroeste de los Estados Unidos y del norte de México es un hábitat adecuado. Este es el primer registro documentando de la presencia de *M. parviflora* en el hemisferio occidental y documenta que la especie ya está bien establecida en localidades cerca a Tucson, Arizona, y con un potencial significativo para invadir.

Nonnative, invasive species have an enormous impact on ecosystems and economies around the globe (Mack et al., 2000; Pimentel et al., 2000). They displace native species and reduce biodiversity, alter fire cycles and nutrient levels in the soil, act as disease vectors, and can cause huge losses to natural resources (Vitousek, 1990; Vitousek et al., 1996). Managerial strategies for controlling established invasive species are often controversial, and early detection and response provide the most cost-effective and efficient manner for controlling an invasion (Allendorf and Lundquist, 2003; Lambert, 2004; Westbrooks, 2004; Lass et al., 2005; Kaiser and Burnett, 2010). Early detection can be difficult because the introduced species that do become invasive frequently exhibit a lag phase of indeterminate length following initial colonization during which they may persist at low densities without rapidly spreading (Mack et al., 2000; Sakai et al., 2001). Given the high cost of invasions, it is highly desirable to identify potentially problematic introduced species and susceptible regions prior to widespread invasion (Moles et al., 2008).

A variety of tools have been implemented in efforts to identify potential invasions at an early stage. Deoxyribonucleic acid (DNA) fingerprinting has been suggested as a viable technique for use at ports of entry to aid in the early identification of unrecognized species of uncertain provenance (Armstrong and Ball, 2005; Van De Wiel et al., 2009). Ecologists also have worked to develop a set of traits that characterize current invasive species to predict which species may become invasive, such as high growth and reproductive rates and strong dispersal abilities (Baker, 1974; Sakai et al., 2001; Blumenthal, 2005). Modeling tools have been developed to generate habitat-suitability maps that indicate invasible regions based on the current known distribution of a focal species (Arriaga et al., 2004; Welk, 2004; Anderson et al., 2006; Ward, 2007).

Despite the suite of available tools, newly introduced species are often overlooked, even in heavily studied areas. Our study site, the Desert Laboratory at Tumamoc Hill in the Sonoran Desert in Tucson, Arizona, was established as a botanically focused ecological research station in 1903 and has been intensively studied since that time (Spalding, 1909; Bowers et al., 2006; Venable and Kimball, 2013). There are numerous plots for long-term monitoring of vegetation located throughout the reserve (Rodriguez-Buritica et al., 2013; Venable and Kimball, 2013). In 1983 and 2005, efforts were made to document the location of all nonnative species of plants (Bowers et al., 2006). The study in 2005 identified 52 nonnative species, including *Matthiola longipetala* (Vent.) DC [Brassicaceae] (syn. *M. bicornis*); however, *Matthiola parviflora* [Schousb.] R. Br. [Brassicaceae] was not recorded at that time.

In spring 2008, we discovered *M. parviflora*, previously unreported in the Western Hemisphere, growing at the Desert Laboratory. Though the precise timing of the introduction of this species to North America is uncertain, it was likely before 2005. We confirm the identity of *M. parviflora* with morphological and molecular analysis, provide a morphological description of *M. parviflora* as it appears in the Sonoran Desert, describe the distribution of *M. parviflora* in the Sonoran Desert over the last 3 years, and use modeling of its habitat to predict the potential future distribution of *M. parviflora* in North America. Our treatment of *M. parviflora* is one example of how to identify and determine the potential spread and density of a newly introduced species.

MATERIALS AND METHODS—We used the dichotomous key in the most recent monograph of the genus *Matthiola* to tentatively identify our unknown plants as *M. parviflora* (Conti, 1900). However, because the genus has undergone recent taxonomic revision, we consulted more recent regional floras that contained species of *Matthiola* in an attempt to confirm our identification (Coutinho, 1913; Zohary, 1969; Pitard and Proust, 1973; Täckholm, 1974; Maire, 1977; Ball, 1993; Livaniou-Tiniakou, 2002). These regional keys contain only subsets of the genus making definitive identification difficult. We also collected four voucher specimens and deposited them in the University of Arizona Herbarium (ARIZ; Horst 390413, 390687–390689), Tucson, as well as a voucher of *M. longipetala* (ARIZ; Horst 390686).

We were unable to find any previous record of *M. parviflora* in the New World, and some species undergo rapid evolution in a new area (Bossdorf et al., 2005; Buswell et al., 2011). Therefore, we decided to confirm our identification with DNA-sequence analysis. Total DNA was isolated from fresh leaves of *M. longipetala* and putative *M. parviflora*, both collected at the Desert Laboratory, using the DNeasy® Plant Mini Kit (QIAGEN, Valencia, California) according to the protocol from the manufacturer. The partial fragments of the Internal Transcribed Spacer (ITS) region (ca. 750 bp) were amplified using primers N-nc18s10 and C26A (Wen and Zimmer, 1996). Polymerase chain reaction (PCR) was performed in a 30-ml volume containing 15 ml of EconoTaq® PLUS GREEN 2 × Master Mix (Lucigen® Corporation, Middleton, Wisconsin), 1 mM of each primer, and 1 ml of template DNA. We obtained sequences of ITS from Genbank (http://www.ncbi.nlm.nih.gov/genbank/) for other species of *Matthiola* and several species of the closely related genus *Oreoloma* for use as outgroups: *M. fruticulosa* (DQ357566); *M. capiomontiana* (DQ357564); *M. incana* (DQ249848); *M. maderensis* (DQ249849); *M. chorassanica* (DQ518396); *M. farinosa* (DQ357565); *M. parviflora* (DQ357567 and DQ357568); *Oreoloma violaceum* (DQ357576); *O. sulfureum* (DQ357575); *O. matthioloides* (DQ 357574). Sequences were aligned with the computer program Sequencher 4.4 (Sequencher® version 4.4 sequence analysis software, Gene Codes Corporation, Ann Arbor, Michigan, http://www.genecodes.com), and phylogenies were inferred from the sequence matrix using parsimony and maximum likelihood analysis with PAUP 4.0b10 (Swofford, 2002).

Introduced populations of a species frequently exhibit morphological characteristics that differ from those in populations in their native habitat. These differences can result from plastic phenotypic responses to the new environment or rapid evolution under new selective pressures (Bossdorf et al., 2005; Buswell et al., 2011). We compared a compilation of descriptions of *M. parviflora* from throughout its native range with individuals in the Sonoran Desert. We examined specimens and photographs from the full range of reported populations in Arizona to ensure we thoroughly captured diversity within the population. From these records, we created a description that highlights the characteristics of the species as it occurs in the Sonoran Desert.

We discovered *M. parviflora* at the northern edge of the Desert Laboratory in 2008. We surveyed radially from the originally discovered plants until no more individuals were found for 20 m in all directions. Along likely dispersal channels, we extended the search 50 m beyond the last individual. We informally searched the southern sector of the Desert Laboratory, where previous surveys of exotic plants on the property had recorded the presence of *M. longipetala*, to see if the two species co-occurred locally (Bowers et al., 2006). No individual of either species of *Matthiola* was found in 2009 due to a severe winter drought. In 2010, we replicated our 2008 census. In each year, we encountered additional populations around the city of Tucson, and, in 2010, we contacted local botanical societies and distributed a flyer with photos and descriptions of *M. parviflora* to their members asking them to report any populations throughout the surrounding area.

Self-compatibility is a trait that is often associated with invasive plants (Baker, 1974; Sakai et al., 2001). In spring 2010, we tested the capacity for self-compatibility of *M. parviflora*. We located and marked 10 pairs of vegetative (pre-reproductive) plants. We randomly selected one individual from each pair to be completely enclosed in a pollinator-exclosure cage (a cone of organza cloth on a wire frame) while the other remained unmanipulated. At the end of the growing season, mature fruits were harvested, and the number of mature seeds and unfertilized ovules was counted on exclosure and control individuals.

We used MaxEnt, a species-habitat modeling software package that utilizes a maximum entropy approach (MaxEnt 3.3.2, http://www.cs.princeton.edu/~schapire/maxent/) to generate habitat-suitability maps of the native range and the predicted North American distribution of *M. parviflora* (Phillips et al., 2006). This software uses geo-referenced presence data and geographically explicit environmental data to create a

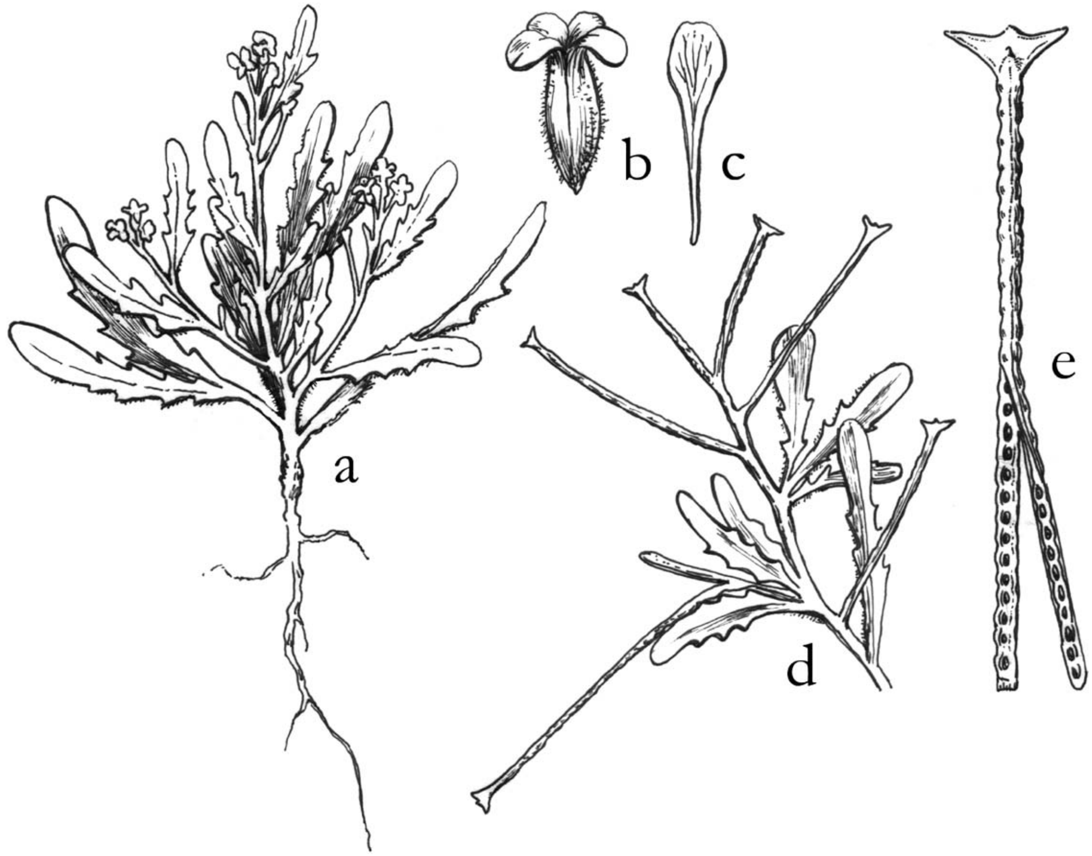

FIG. 1—a) Typical form of *Matthiola parviflora* in flower; b) flower; c) petal; d) branch in fruit; e) silique. Drawing by C. M. Montgomery.

model of requirements of habitat for a species based on its current realized niche (Phillips et al., 2006). The resulting model can then generate a map indicating predicted suitable habitat in a different geographic area (Ward, 2007).

We modeled the native Mediterranean distribution of *M. parviflora* using 261 records of presence from regional herbaria (Appendix). We used an additional 47 points, obtained from regional floras, for underrepresented locations in northern Africa. These additional points decreased the heavy sampling bias of the herbarium records, which favored Spain and Israel. Models from MaxEnt work most successfully when seeded with an unbiased sample of records representing the entire range of the species. However, the effect of sampling bias is negligible once the sample size reaches a threshold of ca. 100 locations of presence (Loiselle et al., 2008). Climatic data were chosen based on our assessment of those layers most biologically relevant for winter-growing plants (precipitation of coldest quarter, temperature of coldest quarter, annual precipitation, and mean diurnal range) from the Worldclim Version 1.4 dataset (www.worldclim.com) at a resolution of 2.5 arcmin (ca. 4 km). We projected the modeled niche onto a similar climatic grid of the southwestern United States and northern Mexico. We selected maximum entropy modeling because its robustness to presence-only data and low rate of omission for seeded data best fit our needs for predicting potential distribution in a new area (Phillips et al., 2006). We configured the model to use 90% of our 112 records of presence to train the model and the remaining 10% as test points for validation of the model, enough for a satisfactory test level (Pearson et al., 2007). The program MaxEnt further reduced presence bias by using only one record per cell of the climatic grid. We used the recommended defaults for the remaining parameters (Phillips et al., 2006).

RESULTS—Our unknown taxon keyed to *M. longipetala* or *M. parviflora* when using regional floras (Coutinho, 1913; Pitard and Proust, 1973; Livaniou-Tiniakou, 2002). Where a key contains both species, it keyed to *M. parviflora* (Conti, 1900; Zohary, 1969; Täckholm, 1974; Jafri, 1977; Maire, 1977; Ball, 1993). The fruit of most *Matthiola*, including *M. parviflora*, is a distinctive long, slender silique with short, curved horns at the tip (Fig. 1). Individuals of *M. parviflora* can be distinguished from *M. longipetala,* the only congener that occurs in North American deserts, by several vegetative and floral morphological traits (Table 1). Characters that are especially useful for differentiating the two species in the field include substantially larger corollas with wavy petals and prefloral scales in *M. longipetala.*

The ITS sequence for our putative *M. parviflora* collected in the field was 100% identical to the published ITS sequence of *M. parviflora* for Spanish accessions in GenBank confirming our identification. Heuristic searches using maximum parsimony yielded a single phylogenetic tree, identical to the one resulting from the search

Table 1—Morphological differences between *Matthiola parviflora* and *M. longipetala*. An asterisk denotes nonoverlapping traits which are the most useful for definitive identification in the field.

Structure	Substructure	*M. parviflora*	*M. longipetala*
Overall plant		Diffusely branched at base; very leafy	Branching from base; rarely leafy
Flower	Petals*	0.6–0.8(–1.2) cm;* obovate;* limb lavender purple or brownish purple	1.5–2.5 by 0.2–0.7 cm;* margin undulate;* limb purple or pink; claw yellow, livid or purple
	Prefloral scales*	None*	Small button-like prefloral scales*
	Scent	Not noticeably scented*	Pleasant perfume in evening*
	Sepals	4–6 mm	8–12 mm
	Nectaries	Very small	Filiform
Silique	Shape	Erect or spreading	Upright, curved or annular
	Size	25–70 by 1.5–2.0 mm	(30–)50–150 by 1.0–2.0(–2.5) mm
	Hairs	Finely pubescent with stellate hairs but at the end glabrous	Densely covered with short branching hairs
	Horns	Straight acute; 1.5 mm	Strongly incurved; (1.0–)2.0–10.0 mm
Raceme	Size	<30 cm (usually <20 cm); often overtopped by leaves	40 cm (usually <50 cm); stems rising from base

using maximum likelihood. The topology of the phylogenetic tree indicated that other species of *Matthiola* are more closely related to *M. parviflora* than to *M. longipetala*, demonstrating that the newly discovered population is quite distinct from *M. longipetala* and is not a hybrid (Fig. 2).

We quote the complete species description of *M. parviflora* from Zohary (1969:272), which most closely represents the species as it grows in the Sonoran Desert. Additional details from other sources are added in brackets. Finally, descriptions in italics designate deviations or specifications of morphological characteristics of *M. parviflora* as it appears in the Sonoran Desert.

"Annual, tomentose with branched hairs, 10–30 cm *7–20 cm* [Basal leaves in a rosette ± fleeting (Maire, 1977)]. Stems almost erect, diffusely branched at base. Leaves 4.5–5 (–7.5) by 0.7–1 (–1.5) cm, crowded at base and along stem, oblanceolate, sinuate-dentate or pinnatifid with acute lobes; lower leaves long-petioled, upper and floral sessile. Racemes short, often overtopped by leaves. Flowers short-pedicelled or sessile. Sepals 5 (–7) mm. Petals 0.6–0.8 (–1.5 cm) cm. [by 0.1–0.2 cm. (Ball, 1993)], purple, *lavender limb with a pale yellow claw*, obovate, [nectaries very small (Ball, 1993) slightly enlarged at the base (Conti, 1900)], [stamens: the large ones 3.5–4.5 mm, the small ones 2.5–3.3 mm; anthers 1.3–1.5 mm (Conti, 1900)]. Fruit 4.5–6 cm. [slightly torulose (Ball, 1993)], erect or spreading; horns 4–5 mm [straight, acute (Ball, 1993)]. [Seeds elliptic with no or little wing, 1–1.2 by 0.6–0.75 mm (Conti, 1900), numerous and pendant in a single series (Maire, 1977).] Fl. March–April."

Surveys conducted in spring 2008 around the initially discovered plants of *M. parviflora* on the north side of the Desert Laboratory yielded 576 individuals with most concentrated in an area ca. 150 m^2 (Fig. 3). On the south side of the Desert Laboratory, we located *M. parviflora* co-occurring with *M. longipetala* in approximately equal densities where the latter regularly occurs. We found *M. parviflora*, by informal searching, at five additional locations in and around Tucson. No reproductively successful adult was found in 2009.

Surveys in 2010 of the north side of the Desert Laboratory yielded 4,018 individuals concentrated in the same location as the base distribution in 2008. The identified boundary of the population had spread 70 m south and 80 m east of the boundary in 2008 following a slight downward slope for an average rate of expansion of 40 m/year. The expansion was more pronounced along slight depressions where water concentrated and then dispersed seeds in a generally linear fashion. A small number of plants dispersed a much greater distance, 225 m, via a small intermittent wash. Information from local botanical societies on location of *M. parviflora* yielded 38 additional populations, groups of plants separated by greater than two city blocks, throughout Tucson and two from Cave Creek, Arizona, 204 km northwest of the nearest population in Tucson.

In its native range, *M. parviflora* occurs in dry coastal regions and deserts. In the Canary Islands, it occupies dry coastal areas below 300 m (Pitard and Proust, 1973). It also is found in limestone hills and areas with hard sandy soil (Jafri, 1977) as well as on steppes, pastures, and floodplains in rocky dry areas from the coast to the mountains (Maire, 1977) in northern Africa. In the Middle East, *M. parviflora* occurs in the Negev Desert and around the Dead Sea (Zohary, 1969).

In Arizona, *M. parviflora* has predominantly been identified along roadsides in areas with little shade; however, observer-bias may be involved. At the Desert Laboratory, the species has spread through an area that is relatively undisturbed and has been an environmental preserve for >100 years. The majority of individuals are growing in rocky and sandy soil adjacent to dry rivulet channels or near the banks of one of the small washes

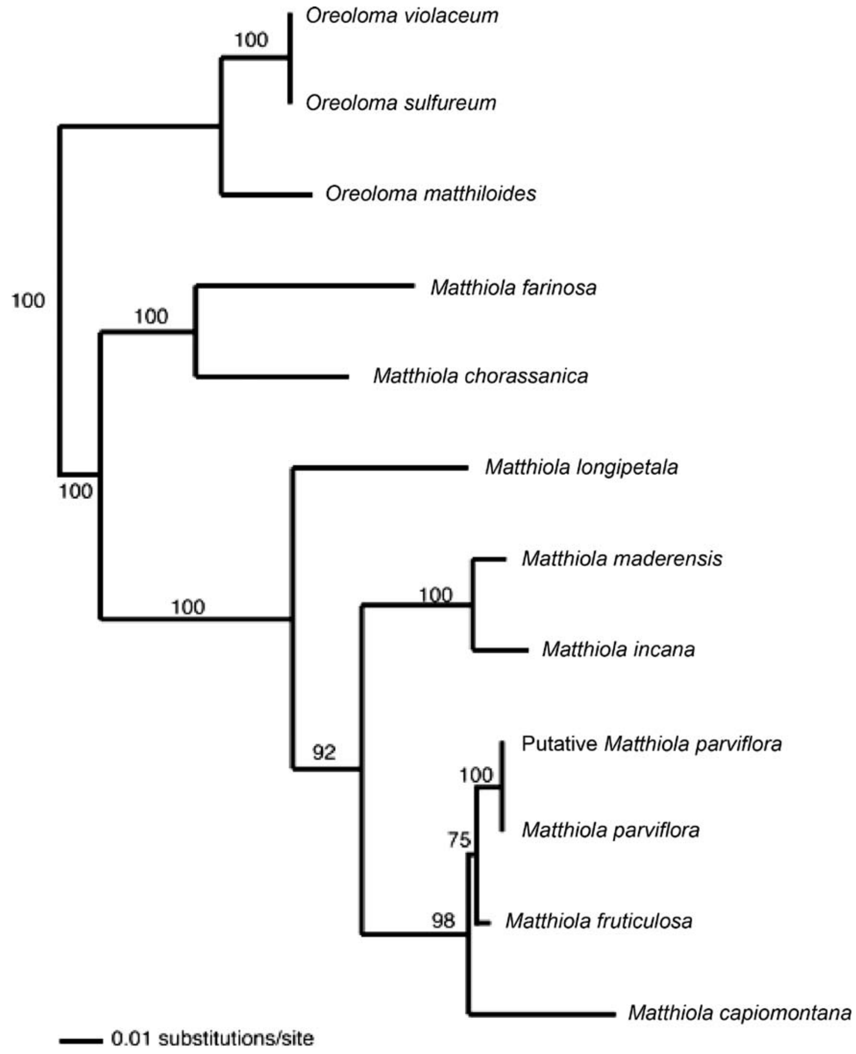

FIG. 2—Phylogenetic reconstruction of several species of *Matthiola* including the putative *M. parviflora* (maximum likelihood tree). Heuristic searches using parsimony produced one single tree which was identical to the maximum likelihood tree. Numbers on branches are bootstrap percentage values for maximum parsimony. The Internal Transcribed Spacer (ITS) sequence for the putative *M. parviflora* was 100% identical to the published ITS sequence of *M. parviflora* for the Spanish accessions in GenBank.

that crosses the site. Individuals growing in the sandy wash itself tend to be smaller and produce fewer seeds than those growing on the banks in finer soils.

An additional factor potentially facilitating the invasion of *M. parviflora* is that it is self-compatible. Only three paired replicates in the self-compatibility study escaped disturbance and could be evaluated. Production of viable seeds was similar for control plants (48.5 ± 40.9%) and those in pollinator-exclosures (33.9 ± 30.7%), indicating that *M. parviflora* is autogamous (self-pollinates without a pollinating agent).

The native-range-niche-suitability map we produced using MaxEnt (Fig. 4a) includes all the described Mediterranean range as well as coastal Sicily, eastern Cyprus, and the eastern Grecian islands, which are areas where *M. parviflora* has not been recorded (Meikle, 1977; Pignatti, 1982; Strid, 1986; Livaniou-Tiniakou, 2002). Predictions from models are scored in MaxEnt by testing presence-location data against the model; random data would score 0.5. Scores evaluating our model were 0.952 for training data and 0.938 for test data. The map indicating suitability of habitat in the southern United States and Mexico identified several large regions with a high probability for being ideal habitat including a 1,200-km long continuous stretch from southern Arizona, USA, to Sinaloa, Mexico, along the eastern edge of the Gulf of California (Fig. 4b). Our study site at the Desert Laboratory in Tucson, Arizona, is well within the predicted range of habitat at a level of 85–99% likelihood for suitability.

DISCUSSION—We positively identified and documented several populations of *M. parviflora*, a Mediterranean species not previously known to occur in the Western Hemisphere, in the Sonoran Desert, Arizona. The genus *Matthiola* contains ca. 140 species native to Eurasia with

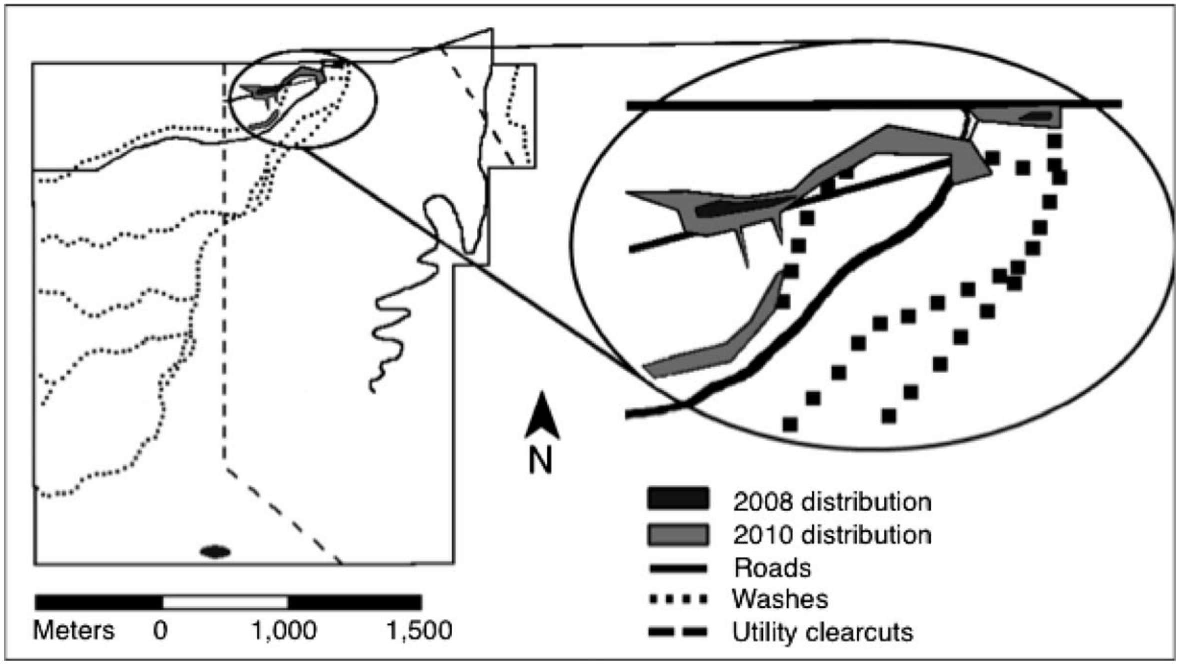

FIG. 3—Map of the Desert Laboratory, Tucson, Arizona, indicating the locations of *Matthiola parviflora* in 2008 and 2010. Map edited from Bowers et al. (2006).

two species previously known to be introduced to the Western Hemisphere (United States Department of Agriculture, 2010) as escaped garden plants. *Matthiola incana* is found in California, Texas, Illinois, North Carolina, and British Colombia. *Matthiola longipetala* (syn. *bicornis)* is known to occur in Michigan, Kansas, Idaho, Alberta, and Saskatchewan and is widespread in the southwestern United States. It also has been documented in Tucson, Arizona since 1902 (Thornber, 1909).

It is difficult to pinpoint when the introduction of *M. parviflora* to the Western Hemisphere occurred. The earliest definitive record (plant is clearly identifiable) that we have found is a photograph by T. B. Kinsey taken at the eastern edge of Tucson in March 2004. The most detailed chronology of its spread comes from the Desert Laboratory, the vegetation of which has been intensively monitored since its founding by the Carnegie Institute of Washington in 1903 (Spalding, 1909; Bowers et al., 2006; Rodriguez-Buritica et al., 2013; Venable and Kimball, 2013). Efforts made in 1983 and 2005 to document the location of all nonnative species of plants by systematically walking grid lines throughout the entire reserve failed to note the presence of *M. parviflora* (Burgess et al., 1991; Bowers et al., 2006). However, *M. longipetala* (syn. *M. bicornis*) was recorded in the 2005 study (but not the 1983 study) at our 2008 site on the northern end of the property where *M. parviflora* was discovered. This was probably a misidentification of *M. parviflora* because we did not find *M. longipetala* at that location in 2008 or subsequently even though it is quite conspicuous. We have searched intensively for it, and two of those years had exceptionally high densities of winter annuals. It is difficult to say if *M. parviflora* was present at the time of the 1983 study but not distinguished from its congener or if it arrived later. If fruiting rather than flowering plants had been encountered during these surveys, the plants would have been readily determined as *Matthiola* from the distinctive fruit but perhaps not distinguished as *M. parviflora*, an unanticipated exotic. The most recent flora for the Desert Laboratory indicates that *M. parviflora* had not been recognized by 1983 even though its floral morphology is quite distinctive (Bowers and Turner, 1985). This suggests that *M. parviflora* arrived at the Desert Laboratory sometime between 1983 and 2005.

The early identification of invasive species is a priority for managers of land and those making public policy (Lodge and Shrader-Frechette, 2003; Blumenthal, 2005). However, early recognition of invasive species is often an elusive goal of management (Pimentel et al., 2000; Simberloff, 2003). One barrier to the goal of early recognition of introduced, potentially invasive species is the lack of a good unified key for identification. Local floras from the original native distribution, which may be fairly recently published, rarely contain all species in a genus, whereas monographic treatments, while complete, are often old (1900 in our case) and may lack important recent information on a genus. Consequently, we were not 100% confident of our initial morphological identification. However, we were able to confirm identification with sequencing and construction of phylogeny, demonstrating the power of molecular methods for quick and

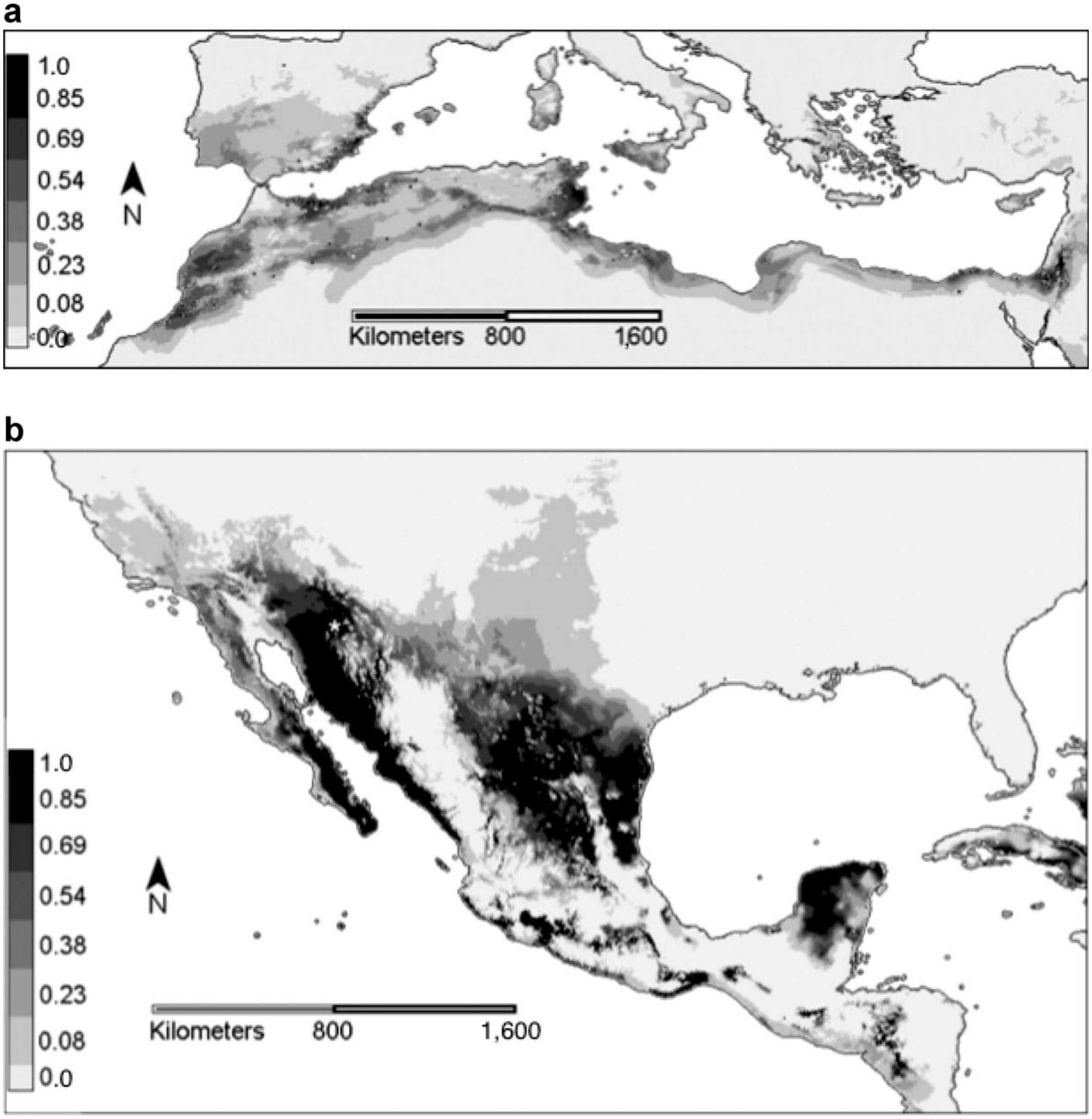

Fig. 4—Probability maps of the fundamental niche of *Matthiola parviflora*. The probability of suitability of habitat is indicated by the gray scale with dark shades denoting a higher probability and light shades a lower probability. White areas are water. a) Native Mediterranean distribution; b) suitable habitat in the southern United States and Mexico. The location of the Desert Laboratory, denoted by the white asterisk, is in an area of high likelihood for suitability of habitat that spreads into western Sonora and Baja, Mexico, with even higher probability.

confident identification of possible invasive species (Armstrong and Ball, 2005; Van De Wiel et al., 2009).

Habitats likely to be invaded include heavily disturbed areas, especially locations that have experienced a recent change in disturbance regime (Moles et al., 2008). We found *M. parviflora* in heavily disturbed, roadside habitats and also in an undisturbed natural area. Many of the roadside populations inspected in Tucson in spring 2010 were high-density monocultures. Though it has not yet formed a dense monoculture, it also has spread rapidly through an undisturbed area of a 100-year-old nature preserve over three growing seasons.

While our surveys in the field demonstrated that *M. parviflora* has spread locally, results of our niche modeling indicate that this species has the potential to spread through a much larger region. Although introduced species may have slightly different niches in their new range (Broennimann et al., 2007), modeling the realized niche of a species in its home range and projecting that model to the area surrounding an introduced population allows predictions about the potential spread of a species in the new area (Welk, 2004). We identified a large area of potentially suitable habitat within North America that *M. parviflora* may already occupy or may expand into in the future. This indicates that *M. parviflora* may soon become a widespread invader over a large range (Richardson et al., 2000; Colautti and MacIsaac, 2004).

The National Park Service has been manually removing *M. parviflora* in Saguaro National Park East and West since 2010 and is considering chemical control. Other local managers of land also are pursuing measures of control in an attempt to prevent or slow the spread of this species in the region.

Data on the initial spread of invasive species are relatively rare but critical for understanding community-assembly, dispersal, and management of invasions (Puth and Post, 2005). The discovery of *M. parviflora* in North America provides an opportunity to document its early dispersal and spread and to determine its potential for invading a larger area. Our treatment of *M. parviflora* demonstrates how molecular techniques, surveys in the field, and niche modeling during the early stages of invasion can be used to accurately identify and determine the invasive potential of newly introduced species. Such data provide critical information for decisions on management.

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