

# NOTEWORTHY COLLECTION

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## NOTEWORTHY COLLECTION

### OREGON

LILIUM PARDALINUM Kellogg subsp. PARDALINUM × L. WASHINGTONIANUM Kellogg subsp. PURPURASCENS (Stearn) M.W.Skinner (LILIACEAE). —Douglas County, Umpqua National Forest, above Deer Creek along Toketee-Rigdon Road; 43.31975°, -122.36809°; 945 m; voucher collected July 24, 2021, first observed July 15, 2020; Emma Jaworski s.n. (OSC). Steep slope with a dense overstory of Douglas fir. Associated species include Pseudotsuga menziesii (Mirb.) Franco, Corylus cornuta Marshall var. californica (A. DC.) W.M.Sharp, Rhododendron macrophyllum D.Don, Chrysolepis chrysophylla (Douglas ex Hook.) Hjelmq., Acer circinatum Pursh, Symphoricarpos albus (L.) S.F.Blake, Polystichum munitum (Kaulf.) C.Presl, and Fragaria vesca L. subsp. bracteata (A.Heller) Staudt. Tepals pale orange, suffused with pink along the midvein and towards the base, covered with irregular magenta spots, smaller and more numerous towards the base.

The tepal coloration and spot pattern is intermediate between *Lilium pardalinum* and *L. washingtonianum* (Fig. 1A–C). The tepals are also more strongly reflexed than typical *L. washingtonianum*. These observations,

and the fact that the plants were found growing between individuals of these two species, led the collector to suspect a hybrid origin. A hybrid origin was confirmed with sequences of the nuclear ribosomal internal transcribed spacer (nrDNA ITS), obtained using standard methods (Whittall et al. 2000). Individuals of the two species and the putative hybrid were collected at the above site. The nrDNA ITS sequences of the putative parental species differ at two nucleotide sites in ITS-2 (Fig. 1D). In the hybrid, two nearly equal peaks representing the parental nucleotides are visible in the electropherogram for each site. In addition, L. parda*linum* is polymorphic (two equal peaks) at three sites in ITS-2. At these sites the putative hybrid also has two peaks, but the one corresponding to the unique L. pardalinum nucleotide is 1/2 to 1/4 the height of the nucleotide shared across the three individuals. This pattern is also consistent with hybridization. Based on chloroplast genome sequences of the two parental species (Kim and Lim 2018; Kim et al. 2018), single nucleotide differences were expected in *rbcL* and the spacer between the *psaI* and *ycf4* genes. In order to determine the putative maternal parent of the hybrid, these two chloroplast (cpDNA) loci were sequenced. No variation was found among the three individuals,

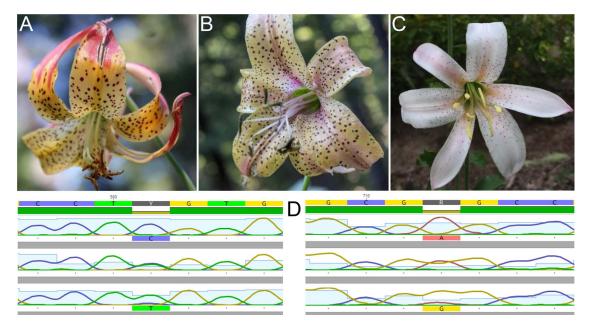


FIG. 1. *Lilium* flowers and DNA sequences. A. *Lilium pardalinum* subsp. *pardalinum* (https://www.inaturalist.org/ observations/145812122) B. Hybrid plant (https://www.inaturalist.org/observations/53218966) showing intermediate tepal coloration and orientation. Both plants photographed at the site of the discovery by Emma Jaworski. C. *Lilium washingtonianum* subsp. *purpurascens* (https://www.inaturalist.org/observations/28213142) photographed 8 km away by Matt Pedrotti (CC-BY-NC). D. Aligned nrDNA ITS sequences for *L. pardalinum* (top), the hybrid (middle) and *L. washingtonianum* (bottom). Single nucleotide additive polymorphisms are visible at positions 561 and 712.

and they all matched the expected sequence for *L*. *washingtonianum*. Thus, the maternal parent could not be determined from these data. Two potential explanations for this are: 1) chloroplast capture has occurred between the two species at this location, or 2) there is geographic variation in the chloroplast genome of *L. pardalinum*.

*DNA Genbank accessions*. Species: nrDNA ITS, cpDNA *psa*I - *ycf*4, cpDNA *rbc*L

*L. washingtonianum*: OP933717, OQ055161, OQ102484

*L. pardalinum*  $\times$  *L. washingtonianum*: OP933718, OQ055162, OQ102485

L. pardalinum: OP933719, OQ055163, OQ102486

*Previous knowledge and significance.* Although hybridization is common among some groups of western North American *Lilium* (Skinner 2002), this interspecific hybrid has not been previously documented. This is despite the fact that the two parental subspecies are broadly sympatric across northern California and southwestern Oregon (CCH2 Portal 2023). It is worth noting that this site is approximately 30 km from the northern distribution limit of *L. pardalinum* subsp. *pardalinum* in southeastern Lane County, Oregon (OregonFlora 2023).

The two parental species differ in habitat preferences, with *L. pardalinum* typically found in moister habitats than *L. washingtonianum* (Skinner 2002). In addition, *L. pardalinum* is primarily pollinated by butterflies and hummingbirds, while *L. washingtonianum* is pollinated by nocturnal moths (Skinner 1988). These ecological differences likely contribute to the rarity of hybridization between the two species.

The L. pardalinum  $\times$  L. washingtonianum hybrid is apparently fertile, consistent with other North American Lilium interspecific hybrids (Lim et al. 2008). Two flowering plants that subsequently produced mature seed were observed in 2020. In 2022, five additional shorter, flowering plants were observed, suggesting that the hybrid has the potential to persist. —AARON LISTON, CELESTE DAX, and NICHOLAS FRANCIS, Dept. of Botany and Plant Pathology, Oregon State University, 2701 SW Campus Way, Corvallis, OR 97331; aaron.liston@oregonstate.edu. EMMA JAWORSKI, 750 Cross Creek Dr., Roseburg, OR 97471.

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#### LITERATURE CITED

- CCH2 PORTAL. 2023. Consortium of California Herbaria CCH2 Portal. Website https://cch2.org/portal/index. php [accessed 29 January 2023].
- KIM, H. T. AND K. B. LIM. 2018. The complete plastome sequence of *Lilium washingtonianum* Kellogg (Liliaceae). Mitochondrial DNA Part B 3:120–121.
- KIM, H. T., P. J. ZALE, AND K. B. LIM. 2018. Complete plastome sequence of *Lilium pardalinum* Kellogg (Liliaceae). Mitochondrial DNA Part B 3:478–479.
- LIM, K. B., R. BARBA-GONZALEZ, S. ZHOU, M. S. RAMANNA, J. M. VAN TUYL. 2008. Interspecific hybridization in lily (*Lilium*): taxonomic and commercial aspects of using species hybrids in breeding. Floriculture, Ornamental and Plant Biotechnology 5:146–151.
- OREGONFLORA. 2023. OregonFlora. https://oregonflora. org/index.php [accessed 29 January 2023].
- SKINNER, M. W. 1988. Comparative pollination ecology and floral evolution in Pacific coast *Lilium*. Ph.D. dissertation. Harvard University, Cambridge, MA.
- SKINNER, M. W. 2002. Lilium. Pp. 172–197, in Flora of North America Editorial Committee, eds. Flora of North America North of Mexico, Vol. 26. Oxford University Press, New York, NY.
- WHITTALL, J., A. LISTON, S. GISLER, AND R. J. MEINKE. 2000. Detecting nucleotide additivity from direct sequences is a SNAP: an example from *Sidalcea* (Malvaceae). Plant Biology 2:211–217.