SUPPORTING INFORMATION

Environmental niche modeling methodology

To avoid overfitting of the distribution models, the geographic extent of the environmental layers was reduced to an area approximately 20% larger than the known distribution of the species (Anderson and Raza 2010). To guard against the inherent difficulties involved in extrapolating distributions into novel climates (reviewed in Alvarado-Serrano and Knowles 2013), an iterative approach was used to generate ENMs for the LGM. Multivariate environmental similarity surfaces (MESS maps) were used to identify which of the 19 bioclimatic variables resulted in areas of low reliability predictions due to the variables being outside of the range present in the present-day environmental data (Elith et al. 2010). MAXENT was rerun excluding these out-of-range variables, and this process of analysis with MESS maps was repeated until no LGM variables were out-of-range compared to present-day bioclimatic variables. Because MESS maps do not indicate changes in the correlations among the environmental variables used for LGM reconstructions (Elith et al. 2010), we checked our LGM ENM using only the most informative variable (Bio5) to ensure we were not reporting errant distributional patterns. Additionally, a present-day ENM was generated for the subset of variables that were not out-of-range and compared to a ENM constructed using all climatic variables with greater than 5% importance (determined by jackknifing) to assess their similarity.

Because our goal was to assess the overall similarity of *C. chalciolepis* and *C. nova's* LGM distributions, and given the difficulties with reconstructing past distributions (Elith and Leathwick 2009), we visualized ENMs by utilizing threshold values based on maximum training sensitivity plus specificity (MTSS). As such, models of past distributions are less likely to be severely constrained, and hence, it is more likely that the habitable area common to *C. chalciolepis* and *C. nova* will be represented in the projected LGM distributions.

RAD library data processing methodology

Potential chloroplast and mitochondrial sequences were filtered from the processed dataset using Bowtie 0.12.8. Because of the lack of sequenced chloroplast and mitochondrial genomes in *Carex*, chloroplast and mitochondrial genomes within Poaceae were used. Specifically, the data were compared to genomes downloaded from GenBank, including *Agrostis stolonifera* (NC_008591.1), *Oryza nivara* (AP006728.1), and *Zea mays* (X86563.2) for identifying potential chloroplast genes, and *Zea perennis* (DQ645538.1) and *Triticum aestivum* (EU534409.1) for identifying potential mitochondrial genes. Given the relative slow rates of molecular evolution characterizing chloroplast and plant mitochondrial genomes (Wolfe et al. 1987), a tolerance of 2 mismatches (-v 2) between *Carex* sequences and these genomes was used to identify chloroplast and mitochondrial sequences that were removed from the dataset.

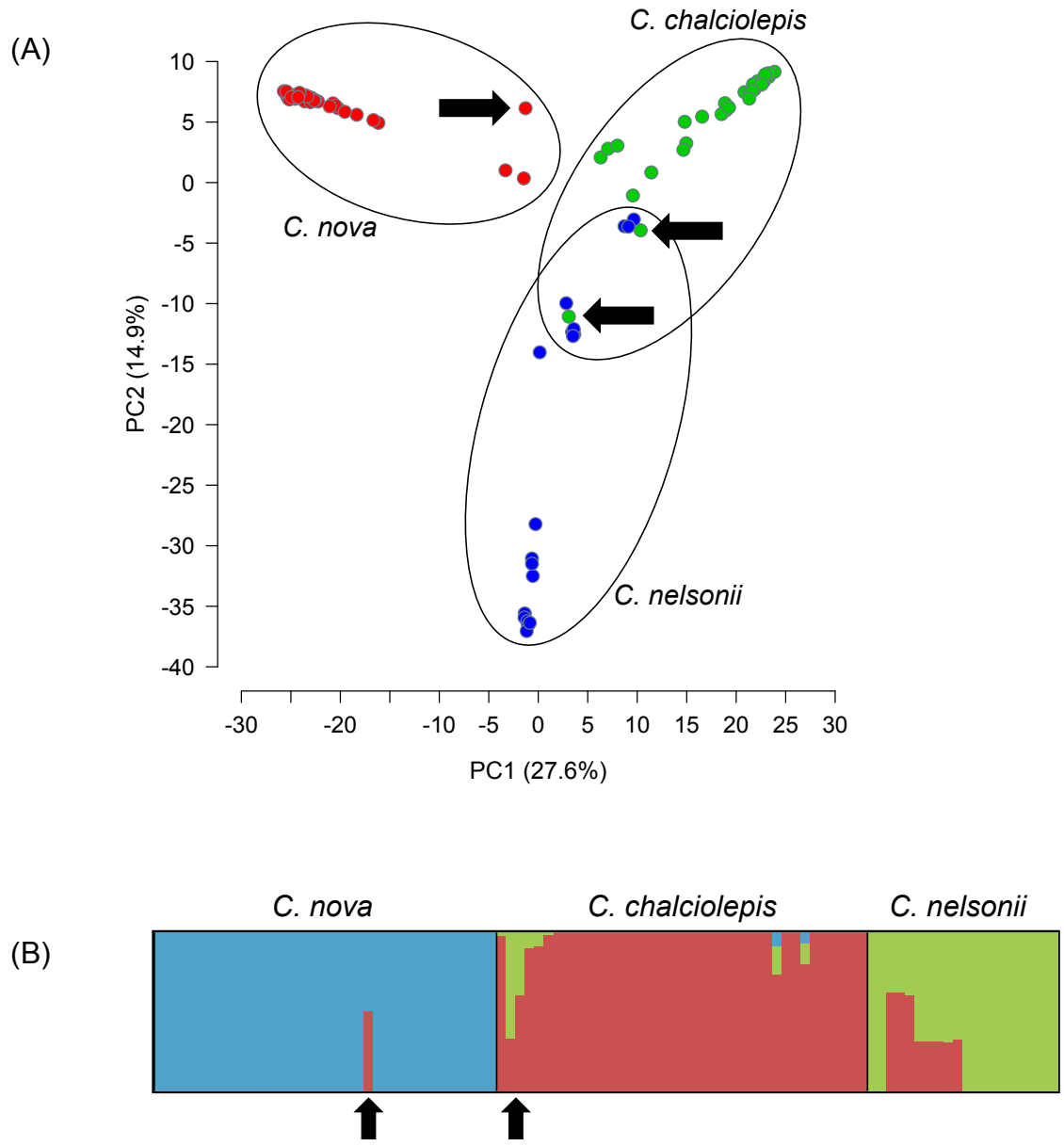

Fig. S1 PCA results (A) and STRUCTURE results (B) identifying three *Carex* individuals with significant contributions of heterospecific genomic material. All three individuals are denoted with black arrows in (A), while the arrow pointing out *C. chalciolepis* individuals in (B) refers to two individuals that are side-by-side.

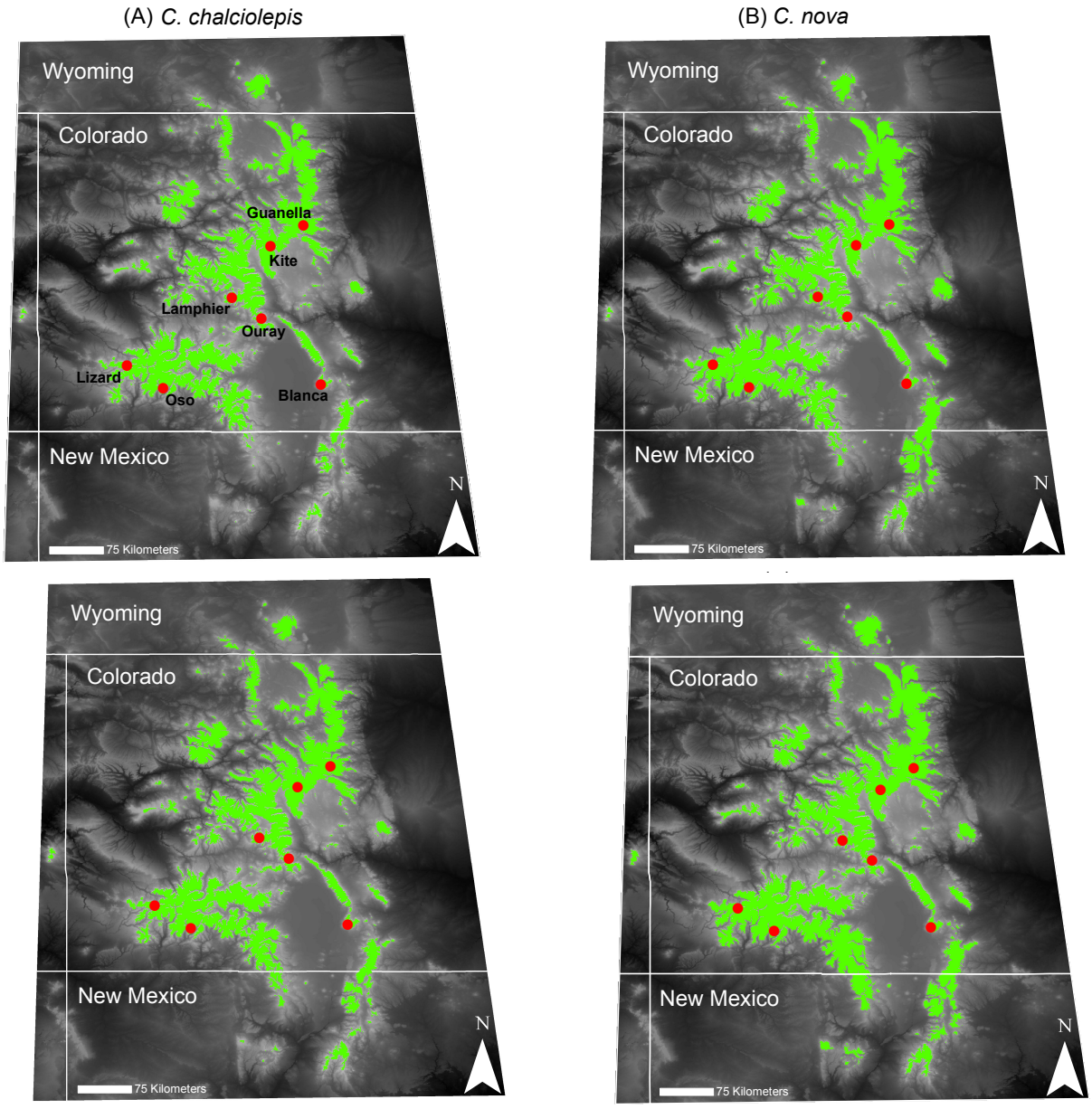

Fig. S2 Present-day ENMs for *C. chalciolepis* (A) and *C. nova* (B). The top row contains ENMs created using all environmental variables with greater than 5% importance, while the bottom row contains models created using only environmental variables that have similar present and LGM ranges (Bio4, Bio5, Bio14, and Bio18). Sampling sites are indicated with red dots.

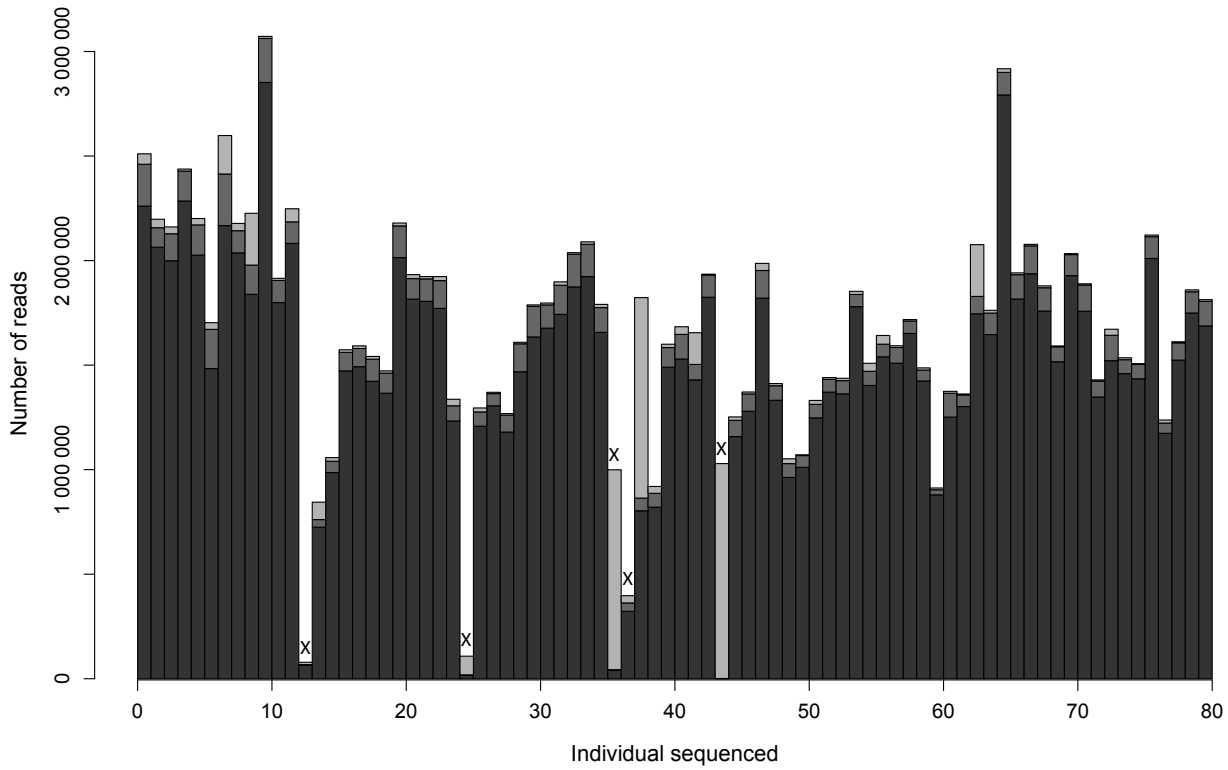

Fig. S3 The number of reads per individual, where individuals 1 through 40 are *C. nova* and individuals 41 through 80 are *C. chalciolepis*. The cumulative stacked bars represent the number of raw reads per individual. Within each individual, the light gray color represents reads discarded due to low quality scores or ambiguous barcodes, the medium gray color represents reads discarded because they aligned with chloroplast or mitochondrial genomes, and the dark gray color represents reads that were available for analyses. Individuals that were removed from all analyses because of insufficient high quality reads are marked with Xs.

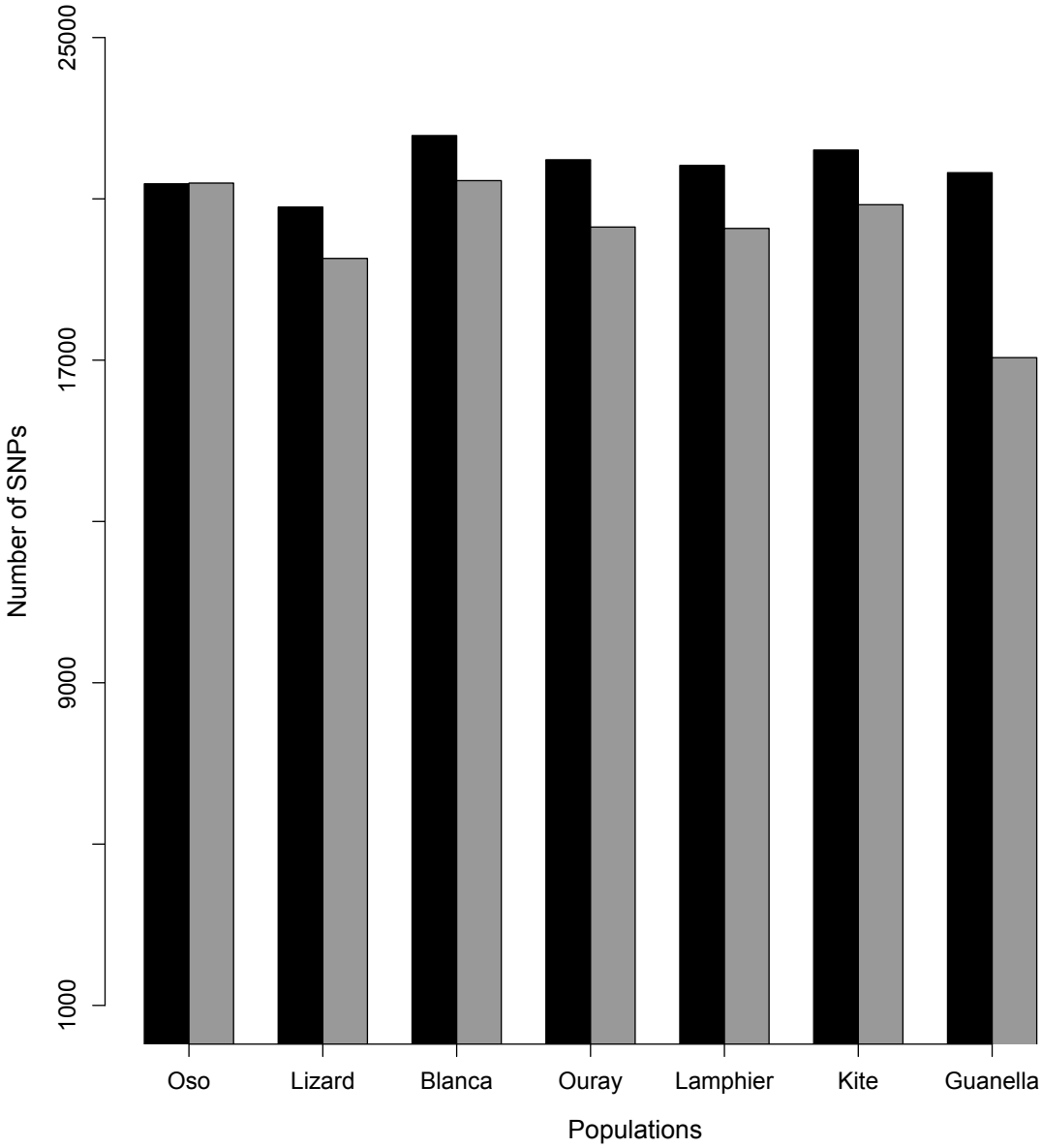

Fig. S4 The number of SNPs present in each population of *C. chalciolepis* (in black) and *C. nova* (in grey). See Table 2 for a summary of genomic data collected in each population, including the average number of reads per population and the number of individuals analyzed per population.

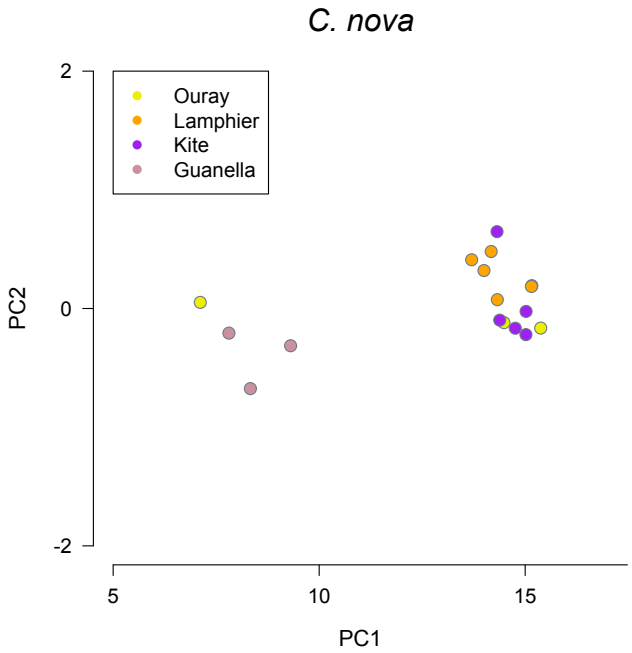

Fig. S5 PCA detail of *C. nova's* Central and North populations (see Fig. 5B). The Ouray individual that groups with the Guanella population was identified as having a heterospecific genomic contribution (see Fig. S1 and Methods).

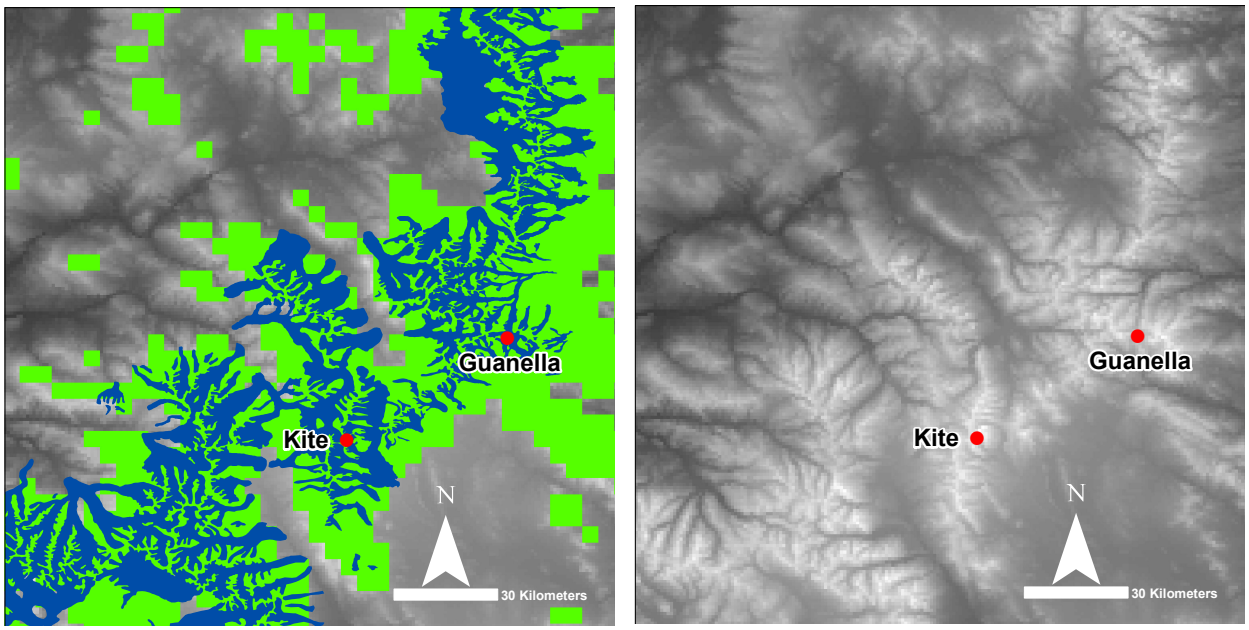

Fig. S6 Detail of the North region (see Fig. 2) to illustrate the interaction of topography, glaciers, and predicted habitat. The left illustration shows a detailed reconstruction of Pleistocene glaciers (blue) based on glacial moraines and glacial till (data extracted from http://geosurvey.state.co.us/geology/Pages/GlacialGeology.aspx). The green polygons represent *C. chalciolepis'* LGM ENM (see above). Potentially suitable habitat within the glacier polygons represents ridges and slopes, whereas glaciers disproportionately affect drainages (where the majority of wetland habitat is located). The right illustration shows the montane landscape, with whiter colors representing higher elevations. For another perspective on Pleistocene glaciers within the southern Rocky Mountains, watch the 'Late Pleistocene glaciers of Colorado' video created by the Integrative Geology Project at the University of Colorado at Boulder (http://igp.colorado.edu/animations.html).

Table S1 Summary statistics for the sampled populations of *C. chalciolepis* and *C. nova*. Results are presented for all nucleotide positions (polymorphic + fixed). Shown are the number of loci, the percentage of loci that are polymorphic, the average frequency of the major allele (*P*), the average observed heterozygosity per locus (H_{obs}), the average nucleotide diversity (π), and the Wright's inbreeding coefficient (F_{IS}).

	Population	Loci	% polymorphic loci	*P*	H_{obs}	π	F_{IS}
C. chalciolepis	Oso	593,856	1.37	0.995	0.004	0.007	0.0061
	Lizard Head	481,613	0.93	0.997	0.002	0.004	0.0039
	Blanca	616,201	0.89	0.998	0.002	0.003	0.0024
	Ouray	586,951	0.60	0.998	0.002	0.003	0.0023
	Lamphier	614,807	0.58	0.998	0.002	0.003	0.0019
	Kite	536,372	1.36	0.996	0.005	0.006	0.0020
	Guanella	590,817	0.79	0.998	0.002	0.003	0.0032
C. nova	Oso	589,187	0.86	0.997	0.002	0.004	0.0045
	Lizard Head	412,113	0.67	0.998	0.002	0.003	0.0028
	Blanca	532,231	0.99	0.997	0.002	0.004	0.0049
	Ouray	589,264	1.22	0.997	0.004	0.005	0.0018
	Lamphier	511,657	0.77	0.998	0.002	0.004	0.0032
	Kite	563,135	0.87	0.997	0.002	0.004	0.0044
	Guanella	399,860	0.49	0.998	0.002	0.003	0.0012

Table S2 Population pairwise F_{ST} values (below diagonal) and Euclidean distances (above diagonal) for *C. chalciolepis* (A) and *C. nova* (B).

(A) *Carex chalciolepis*

	Oso	Lizard	Blanca	Ouray	Lamphier	Kite	Guanella
Oso		51.5	177	148	148	231	276
Lizard	0.083		218	163	150	229	276
Blanca	0.088	0.080		115	155	201	222
Ouray	0.060	0.061	0.061		42	100	137
Lamphier	0.063	0.061	0.064	0.053		83	128
Kite	0.078	0.072	0.072	0.058	0.064		47
Guanella	0.069	0.070	0.076	0.058	0.061	0.062	

(B) *Carex nova*

	Oso	Lizard	Blanca	Ouray	Lamphier	Kite	Guanella
Oso		51.5	177	148	148	231	276
Lizard	0.064		218	163	150	229	276
Blanca	0.062	0.065		115	155	201	222
Ouray	0.061	0.057	0.071		42	100	137
Lamphier	0.052	0.056	0.066	0.056		83	128
Kite	0.058	0.059	0.064	0.064	0.059		47
Guanella	0.041	0.043	0.043	0.051	0.045	0.048	

LITERATURE CITED

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