

# Integrating ecogeographic, bioclimatic and phylogenetic analyses for the wild relatives of sunflower (*Helianthus annuus* L.)

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## Introduction

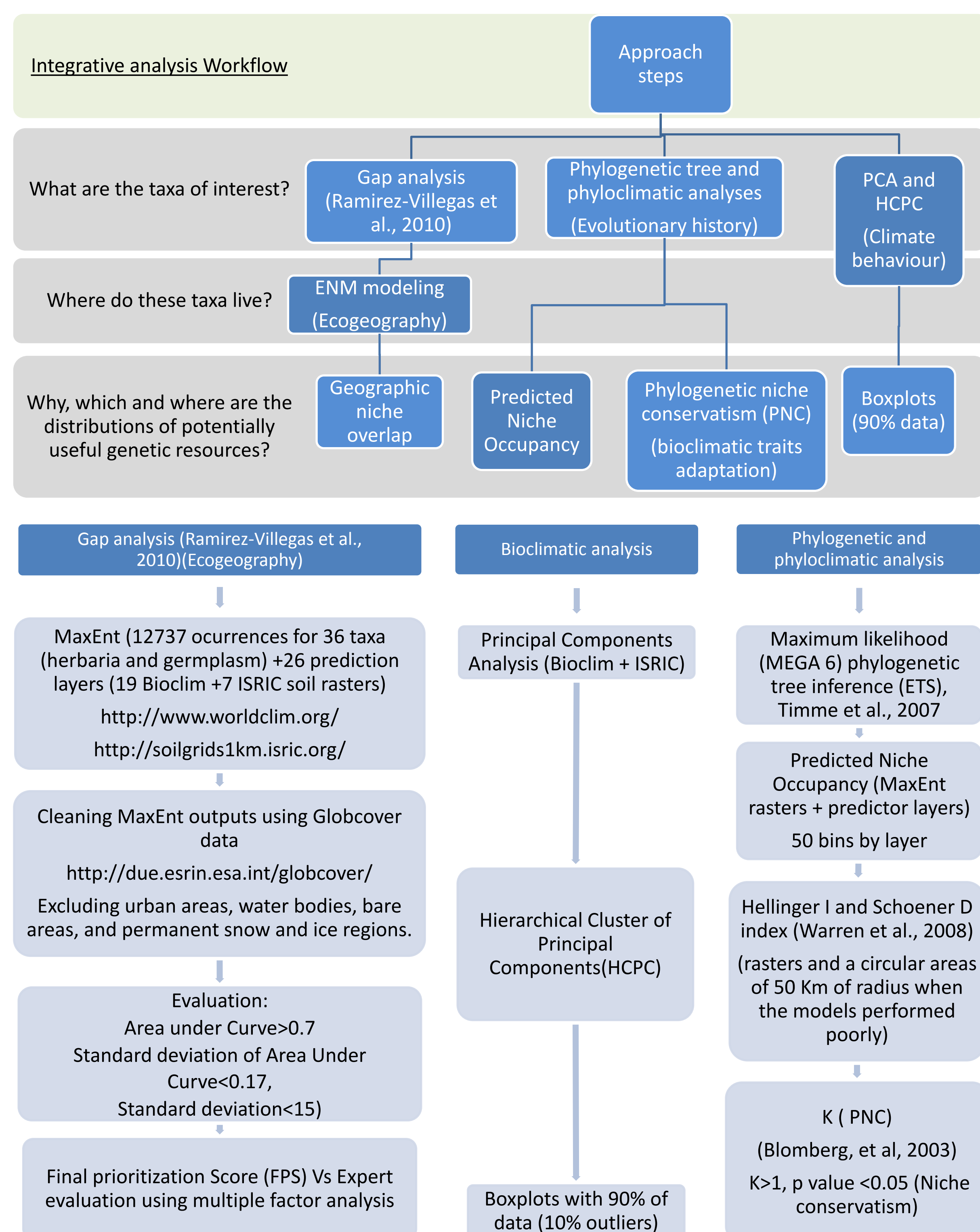
*Helianthus* is a genus composed of 63 taxa, including 12 annual and 37 perennial species native to North America, occupying a variety of habitats ranging from open plains to salt marshes (Kane et al., 2013; Seiler & Marek, 2011). Sunflower (*Helianthus annuus* L.) is the most economically important species in the genus, with ~25 million hectares in production worldwide and a substantial private sector breeding effort (Jan & Seiler, 2006; Berglund, 2007; FAOSTAT, 2012). The genepool of sunflower is well defined with most annual taxa hybridizing well while crosses between *H. annuus* and perennial relatives produces mixed results. There are many taxa with adaptive traits such as drought and salinity tolerance. Investigation of the evolutionary history of such taxa is needed in order to prioritize species for conservation and use in sunflower breeding.

## Objectives

**Prioritize species and geographic areas for further collecting through an examination of 36 *Helianthus* CWR taxa with greatest potential for contribution to sunflower crop improvement**

**Examine species relationships and niche habitation through comparisons of bioclimatic, ecogeographic, and genetic data to identify potential candidates for use in crop improvement**

## Materials and Methods



## Results

### Ecogeography

- 50% of taxa analyzed are in serious need of further collecting
- 28% in moderate need
- 17% were generally well represented in germplasm collections
- There are 5 hotspots of taxon richness (Fig. 1)
- 81% of taxa showed some degree of geographic overlap with wild *H. annuus*

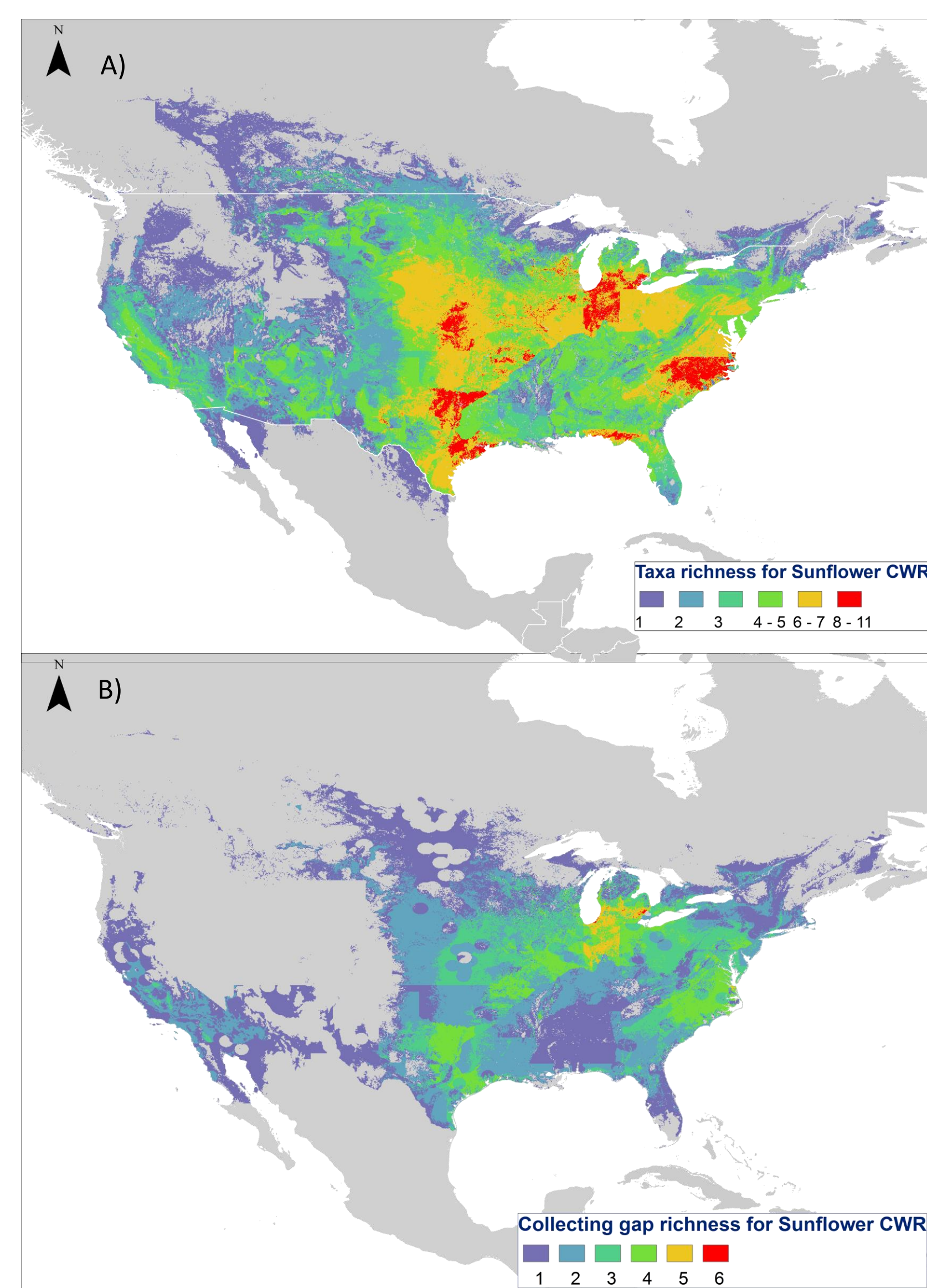


Fig 1. A) Map showing taxon richness for 36 *Helianthus* crop wild relatives (CWR). B) Map showing hotspots for proposed collecting of high priority taxa.

### Bioclimatic analysis

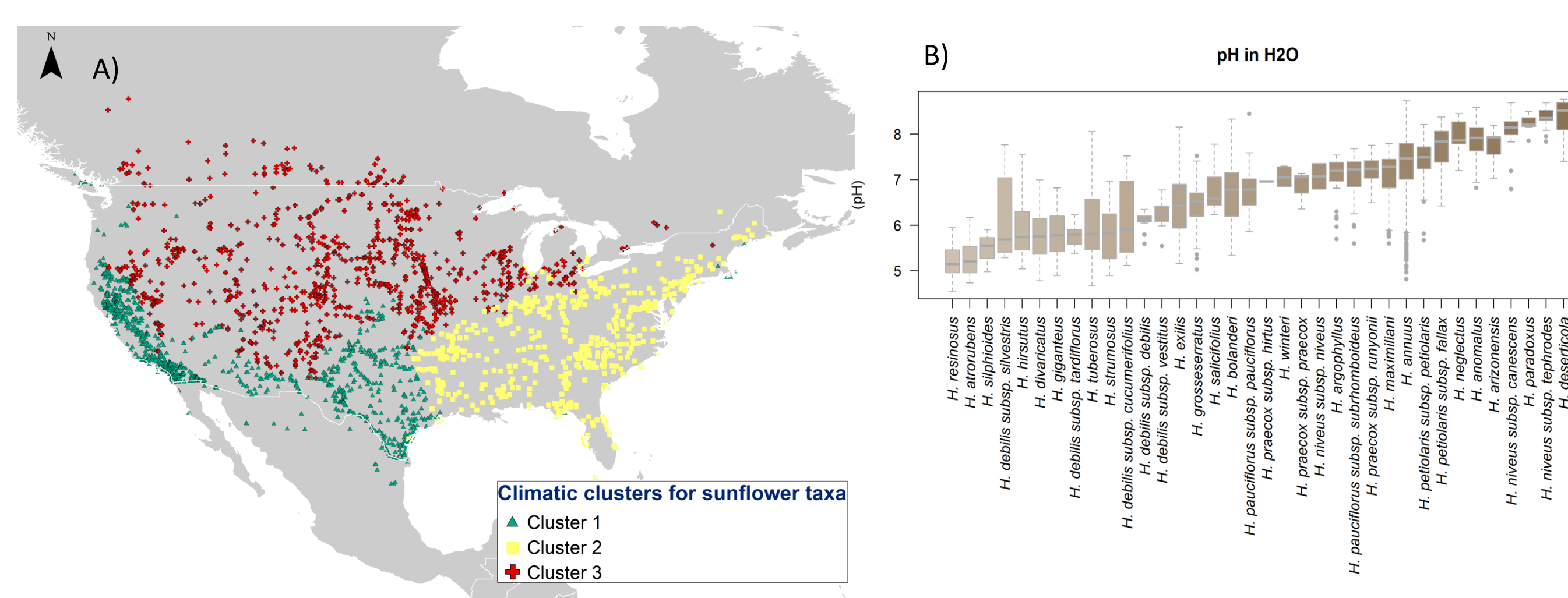


Fig 2. A) Species occurrence points grouped based on the first three principle components of biophysical and bioclimatic variables. Clusters share homogeneous bioclimatic and biophysical conditions. B) Range variable profiles for soil pH. Boxplot displays the median of 90% of occurrence points for each taxon

- We identified three climatic clusters (Fig. 2A):
  - Cluster 1 is defined by dry conditions
  - Cluster 2 shows higher values related with precipitation and soil organic carbon
  - Cluster 3 represents a combination of soil and temperature variables, with a higher than average silt content, a high capacity for cation exchange (CEC), neutral pH, and high soil porosity
- Inclusion of soils variables increased the ability to differentiate species environmental niches
- Niche profiles did display differences between species, e.g. soil pH (Fig. 2B)

### Phyloclimatic analysis

- Mean annual temperature and pH exhibited phylogenetic niche conservatism (Fig. 3)
- The lack of niche conservatism in soil organic carbon and percent sand suggest an important role of soil in the diversification of *Helianthus*

### Potential candidate taxa

- We identified many different *Helianthus* taxa that show extreme environmental adaptation and therefore represent potential candidates for use in breeding for climate adaptation (Table 1). These include both new and complementary findings in regard to traits previously reported

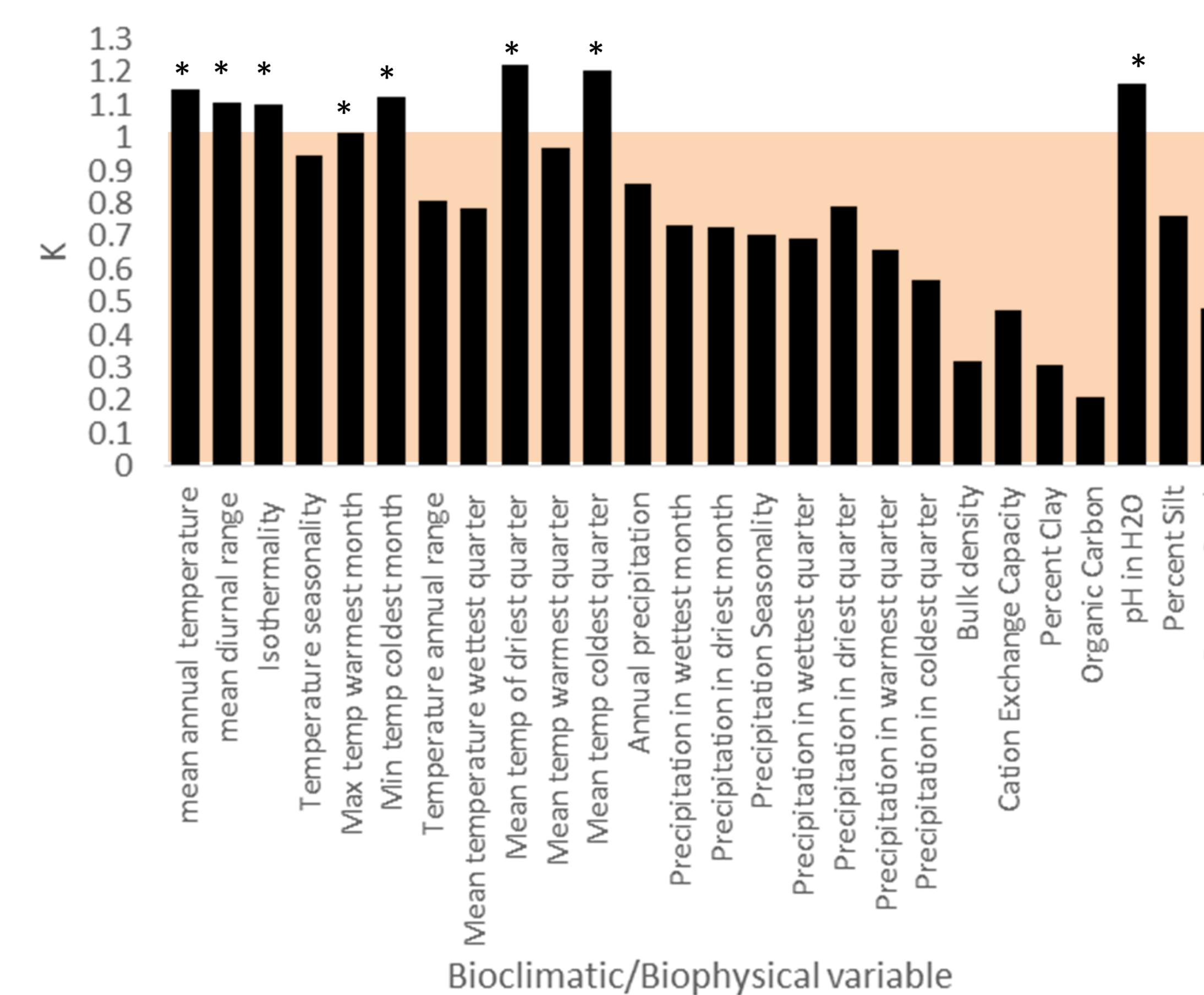


Fig. 3. Test of phylogenetic signal with the Blomberg K measure (Blomberg, et al, 2003) using 25 of 36 taxa analyzed with complete genetic and environmental information. K measures phylogenetic signal in traits, where K values below 1 (orange color) indicates low dependence of traits on evolutionary history and K values above 1 indicates trait conservation over evolutionary history. \* indicates K value greater than 1.

Table 1. Selected taxa with history of introgression and potential new traits found using the integrative approach

Taxon	Traits reported	Recommendation for collection	Position in genepool	Environmental cluster assignment	Life history	Potential extremophile characteristics based on different ecological niche relative to <i>H. annuus</i>
<i>H. anomalus</i>	Fertility restoration	High priority	Secondary	Cluster 3	Annual	Tolerance to low precipitation Tolerance to high pH
<i>H. atrorubens</i>	High linoleic acid concentrations in seed (potential)	Medium priority	Tertiary	Cluster 1	Perennial	Tolerance to low CEC Tolerance to high precipitation Tolerance to low pH
<i>H. maximiliani</i>	Broomrape resistance; Cytoplasmic male sterility	High priority	Tertiary	Cluster 3	Perennial	Tolerance to low temperature Tolerance to erratic temperature
<i>H. paradoxus</i>	Salt tolerance; fertility restoration	Was assessed to be well represented	Secondary	Cluster 1	Annual	Tolerance to low soil organic carbon
<i>H. resinus</i>	Fertility restoration	Medium priority	Tertiary	Cluster 2	Perennial	Tolerance to high precipitation Tolerance to low CEC Tolerance to low pH
<i>H. silphoides</i>	High oleic acid concentrations in seed (potential)	Was assessed to be well represented	Tertiary	Cluster 2	Perennial	Tolerance to low CEC Tolerance to low pH

## Conclusions

•The combination of ecological niche and genetic relatedness studies helps identify candidates for adaptive traits

•Examining bioclimatic and biophysical variables based on phylogenetic and geographic parameters add value in identifying regions and taxa to target for further collecting

## Acknowledgements

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