Chenopodium: A Tale of Two Plant Genomes

[1]Kira M. Falaschi, [2]Nick A. Johnson, [2]Eric L. Patterson

[1]Department of Agriculture, Montana State University, Bozeman, Montana

[2]Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, Michigan

INTRODUCTION

- *Chenopodium quinoa* (quinoa) is a domesticated agricultural crop with a small growth range
- *Chenopodium album* (lambsquarters) is a competitive agricultural weed that grows on every continent except for Antarctica
- Both are allopolyploids, gaining distinct sets of chromosomes, or subgenomes, from different parental plant species
  - Quinoa: tetrapoloid (*2n = 4x = 36*)
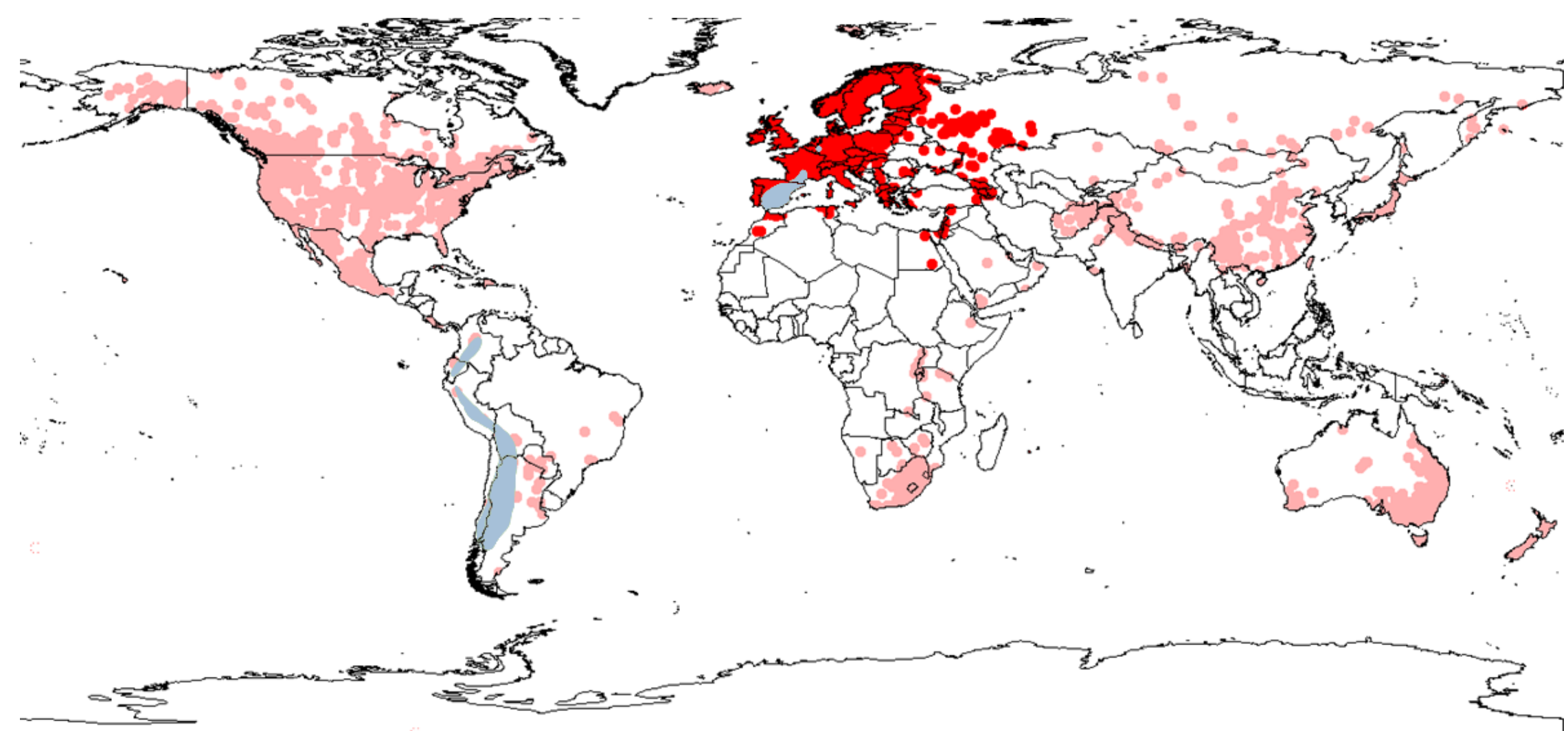 - Lambsquarters: hexaploid (*2n = 6x = 54*)

Figure 1 – Range of quinoa (blue), native lambsquarters (dark red), and non-native lambsquarters (light red). Image modified from *https://www.gbif.org/species/3083838*

HYPOTHESIS

The Chenopods quinoa and lambsquarters have subgenomic similarities that allow for an informative comparison of crops and weeds.

Lambsquarters   **Quinoa**

Figure 2 – Images of lambsquarters (left) and quinoa (right). The quinoa image was retrieved from *https://www.flickr.com/photos/68282140@N04/20074750198*

MATERIALS AND METHODS

Computation:
- Unix: SAMTools, minimap2, RagTag, OrthoFinder, gffread
- RStudio: RIdeogram, ggtree

Genomes/Proteomes:
- IWGC: *C. album* and *B. scoparia*
- CoGe: *C. quinoa* and *S. oleracea*
- Ensembl: *B. vulgaris*

| Genome Preparation	Genome Alignment	Phylogeny
• *C. album* and *B. scoparia* were assembled and annotated by the Patterson Lab • The remaining genomes were downloaded • Unassigned genomic regions were removed from the files	• minimap was used to align the lambsquarters genome to quinoa • Sequences over 5,000 base pairs and 95% similarity were extracted • The aligned genomes were visualized with Rideogram (Fig. 3)	• Proteomes of related species were downloaded • OrthoFinder was ran to determine the phylogenetic tree • The tree was visualized with ggtree (Fig. 4)

RESULTS
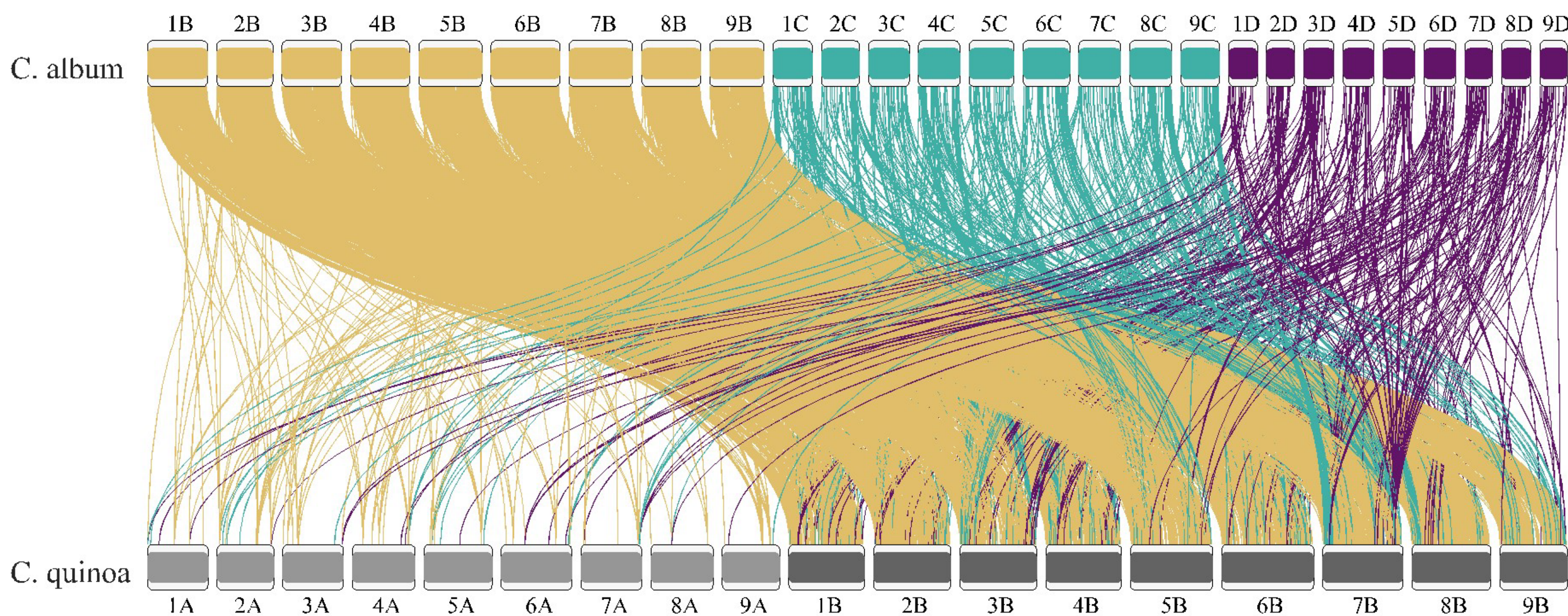
Figure 3 – Alignment of lambsquarters (top) and quinoa (bottom) genomes. Shown are regions of similarity (>95% base pair coverage) that are greater than 5,000 base pairs in length. Subgenomes are divided by color, with link colors corresponding to their subgenome on lambsquarters.
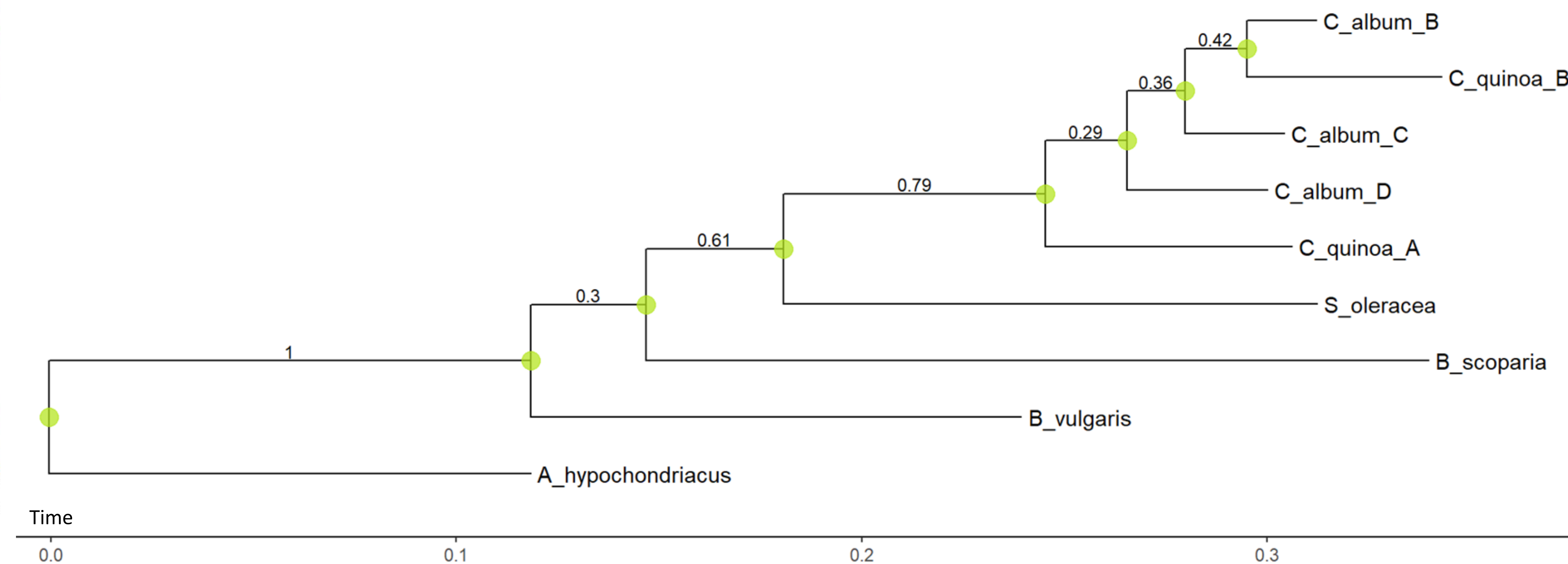

Figure 4 – Phylogenetic tree between the *Chenopodium* subgenomes and four related species. *A. hypochondriacus* is used as an outgroup in the nearest subfamily to the Chenopodiaceae (Amaranthaceae) while *B. vulgaris*, *B. scoparia*, and *S. oleracea* all historically belong in the *Chenopodiaceae* subfamily. The branch values indicate the likelihood that the placement is correct, with a higher value corresponding to higher certainty. The time scale shows how diverged the species are based on relative time between the species.

CONCLUSIONS

- Lambsquarters' B subgenome and quinoa's B subgenome are shared (Fig. 3; Fig. 4)
- Quinoa's A subgenome is not similar to the lambsquarters genome (Fig. 3; Fig. 4)

FUTURE RESEARCH

- Identify gene family expansions and contractions
- How quickly do these genomes obtain mutations in orthologous genes?
- Do the unrelated genomic regions on lambsquarters have features that contribute to weediness in plants?
- Why does quinoa's A subgenome match poorly to lambsquarters?

ACKNOWLEDGEMENTS