

Development of locally adapted chenopod genetic, genomic, and germplasm resources in Northern New England



Thomas M. Davis, Madhav Subedi, Haley Nolen, Clayton Ludwig, Erin Neff, Anissa Poleatewich
New Hampshire Agricultural Experiment Station
University of New Hampshire

INTRODUCTION & OVERVIEW

Exploratory plantings of quinoa in the New England region have not performed well, primarily due to either poor seedling establishment, pollen sterility associated with heat spikes, and/or poor seed maturation and fungal disease associated with excess humidity. Thus, breeding of quinoa for production in Northern New England would need to include emphasis on various aspects of local adaptation, as well as resistance to the fungal disease downy mildew (see photo below).



Goal and Rationale: The ultimate goal of our project is to re-invent quinoa as a crop suitable for cultivation in Northern New England. This goal can be pursued via introgression of adaptation-related traits from locally endemic chenopods into existing quinoa varieties, or by *de novo* domestication of a suitable, locally adapted sister species: *C. berlandieri*. Either strategy will benefit from discovering marker-trait associations and identifying genes responsible for domestication traits.



C. berlandieri var. *macrocalyculum*
Growing wild on Appledore Island
off of the New Hampshire coast.



Left: *Chenopodium berlandieri*
var. *macrocalyculum*
Right: *C. quinoa*

Approach: Several locally adapted, wild chenopod species are found in Northern New England, and they have the potential to serve in various capacities as germplasm, genomic, and knowledge resources relevant to the genetic characterization and improvement of quinoa. Our focus is on developing and utilizing locally adapted germplasm, such as quinoa sister species *C. berlandieri* var. *macrocalyculum* ($2n = 4x = 36$: AABB), and diploids *C. foggii* ($2n = 2x = 18$: AA) and *C. ficifolium* ($2n = 2x = 18$: BB).



C. foggii at mountainside
collection site.



C. ficifolium in UNH greenhouse.

Developing the *C. ficifolium* diploid model system

C. ficifolium is a BB diploid ($2n = 2x = 18$), and as such provides a genetic model system relevant to identifying and characterizing genes for domestication traits in quinoa (AABB) and its sister tetraploid *C. berlandieri*. We are conducting marker-trait association studies in an F2 population derived from a cross between *C. ficifolium* accessions collected in Portsmouth NH (P) and Quebec City, Quebec (QC). Initial marker studies have focused on the FTL marker system (Storchova et al., 2015)

Phenotypic evaluations

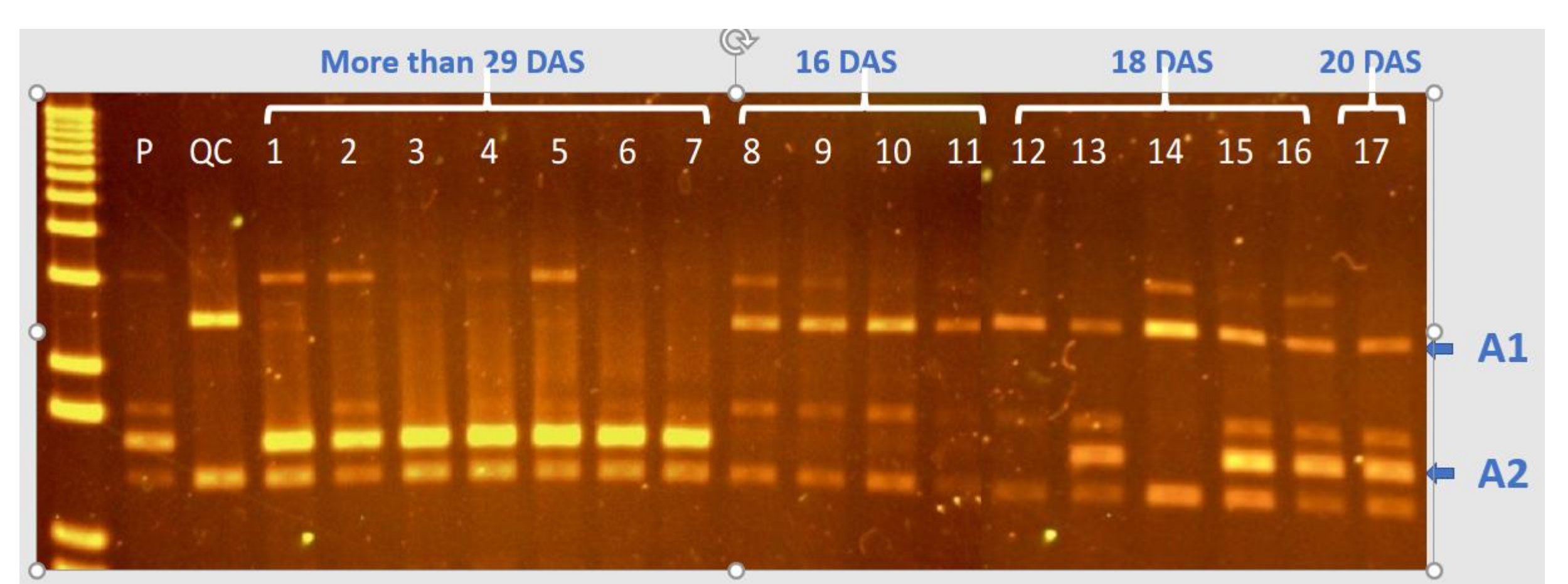
Significant variation in flowering time, plant height, number of branches, branch angle, and chlorophyll content was observed between the parental P and QC accessions. The F2 generation was found segregating for these and other evaluated traits.



Portsmouth (P) and Quebec (QC) accessions and their extreme F2 generation plants displaying variation in branch angle, plant height and number of branches.

FTL genotyping and marker-trait association

Sequencing of FTL amplicons A1 and A2 established that they are alternate alleles of a locus corresponding to the FTL-1 gene located on chromosome 5 (B subgenome) of the *C. quinoa* reference genome assembly (Jarvis et al., 2017).



Genotyping of Portsmouth (P) and Quebec (QC) accession and 17 F2 generation plants through PCR amplification of the FTL marker locus. The F2 generation plants are arranged according to the flowering time in DAS and marker-trait association was found for the amplicons A1 and A2.

CONCLUSIONS

- 1) *C. ficifolium* germplasm from Northern New England is diverse with respect to agronomic traits of relevance to quinoa.
- 2) In an *C. ficifolium* F2 population, variation in flowering time, plant height, and branch number were each associated with FTL-1 genotypes.
- 3) *C. ficifolium* is an appropriate and informative diploid model for genetic studies of quinoa agronomic traits.

References and Acknowledgements

Jarvis et al. (2017) *Nature* 542(7641): 307-312.

Storchova et al. (2015) *Genet Resour Crop Evol* 62:913-925.

This work was supported in part by *New Hampshire Agricultural Experiment Station Project Number NH00632*.