



# Evaluation of Yield, Yield Components and Oil Content in *Brassica napus*



A. Heiliger<sup>1</sup>, R. Fletcher<sup>2,3</sup>, P. Byrne<sup>1</sup>,

1: CSU Soil & Crop Science Department 2: CSU Bioagricultural Sciences and Pest Management Department 3: Cargill Specialty Canola Oils  
Colorado State University, Fort Collins, CO 80523 USA

## Abstract

Increasing fuel prices coupled with declining supplies of fossil fuels have affirmed the need for alternative energy strategies both in the United States and globally. *Brassica napus* is a leading candidate in the search for oilseed biofuels, having received much recent attention by agriculturalists and breeders due to its high oil content and potential to be used onsite as a biofuel for farm equipment. However, production of a regionally-adapted variety of *B. napus* would be necessary in Colorado where drought tolerance is a key trait. The objective of this study is to map and analyze yield and yield components as well as plant morphology and maturity characteristics in *B. napus* using quantitative trait loci (QTL) mapping and statistical analyses. A new population of 240 doubled haploid *B. napus* lines, constructed from a cross between an annual and biennial variety, was grown in four replicates of a row-column design under dryland and irrigated conditions in Fort Collins, Colorado in summer 2010. Yield was found to depend heavily on flowering time and siliques per main raceme in the dry condition correlated with yield ( $R^2=0.4215$ ,  $p<.0001$ ) and less so in the irrigated condition ( $R^2=0.01$ ,  $p=.06$ ). Oil content is currently being evaluated along with seeds per silique and thousand seed weight.

## Objectives

To evaluate yield and yield components of a doubled-haploid *Brassica napus* population under rainfed and irrigated conditions in Fort Collins, Colorado. Oil content will later be analyzed using gas chromatography and QTL mapping will be performed on all traits (yield, yield components and oil characteristics).

## Introduction

### Why bioenergy?

- Decrease in world's supply of oil
- Import from politically unstable countries
- Environment
  - Sustainability
  - Renewability



### Bioenergy Feedstocks

- First generation: Ethanol from grains, straight vegetable oil (SVO)
- Second generation: More focus on lignocellulosic biofuels
- Third generation: Algae & selected energy crops (i.e., non-corn ethanol)

### USDA Regional Biofuels Roadmap (USDA, 2010)

- 36 billion gallons of renewable transportation fuels by 2022
- Currently 10.75 billion gallons of ethanol from corn
- "Targets barriers to the development of a successful biofuels market that will achieve, or surpass, the current U.S. Renewable Fuels Standards (RFS2), as set out in the Energy Independence and Security Act of 2007 (EISA)."
- For Colorado, the USDA lists oilseeds such as canola and camelina to be the crops with the most promise
- Expectation of .5 billion gallons of oilseeds by 2022

### Drought in Colorado

- Limited water availability is considered to be the most significant limiting factor to yield across the world (Boyer, 1982)
- Most areas in Colorado receive less than 18" (450 mm) of rainfall per year

## Methods

### Experiment Design

- A Doubled-Haploid (DH) mapping population was produced based on parents that differed for root pulling force. The parents were biennial and annual.
- Lines were produced by microspore donor plant ( $F_1$  generation) at Cargill Specialty Canola Oils (Fort Collins, CO).
- 240 lines were grown under irrigated and rainfed conditions in Fort Collins, Colorado using a row-column plot design (created with CycDesign N 3.0, [www.cycdesign.co.nz/](http://www.cycdesign.co.nz/)) with four replicates.

### Phenotyping

- Flowering time was scored at 50% flowering across individual plots
- Yield components measured included:
  - Length of main raceme (on two replicates in the rainfed condition only)
  - Siliques per main raceme (two plants per plot)
  - Seeds per silique: Ten siliques were harvested from each plot. Collection was as close to the plant's main raceme as possible, two siliques each on five separate plants.
  - Thousand seed weight (TSW): The weights of the seeds used for seeds per silique phenotyping were measured and TSW was calculated from the seed number and weight.
- Yield was measured using a combine harvester after swathing. Swathing was done at harvest maturity for each plot across one month.
- Oil content and profile are currently being analyzed using Agilent 6890 Series Gas Chromatograph at Cargill Specialty Canola Oils.

## Results

Field growth was vigorous and uniform. Flea beetle damage appeared upon emergence but did not affect stands. Flowering time varied over the span of almost two months; each plot was harvested based on its harvest maturity. Damage from house finches appeared at the start of maturity, so a multi-bang propane-fueled detonation cannon was used to prevent further damage after June 20. Drought stress was observed near the first week of July and continued to progress in severity through the end of the trial. Traits appeared to be approximately normal, with the exception of seed yield, which was skewed right (Fig.1).

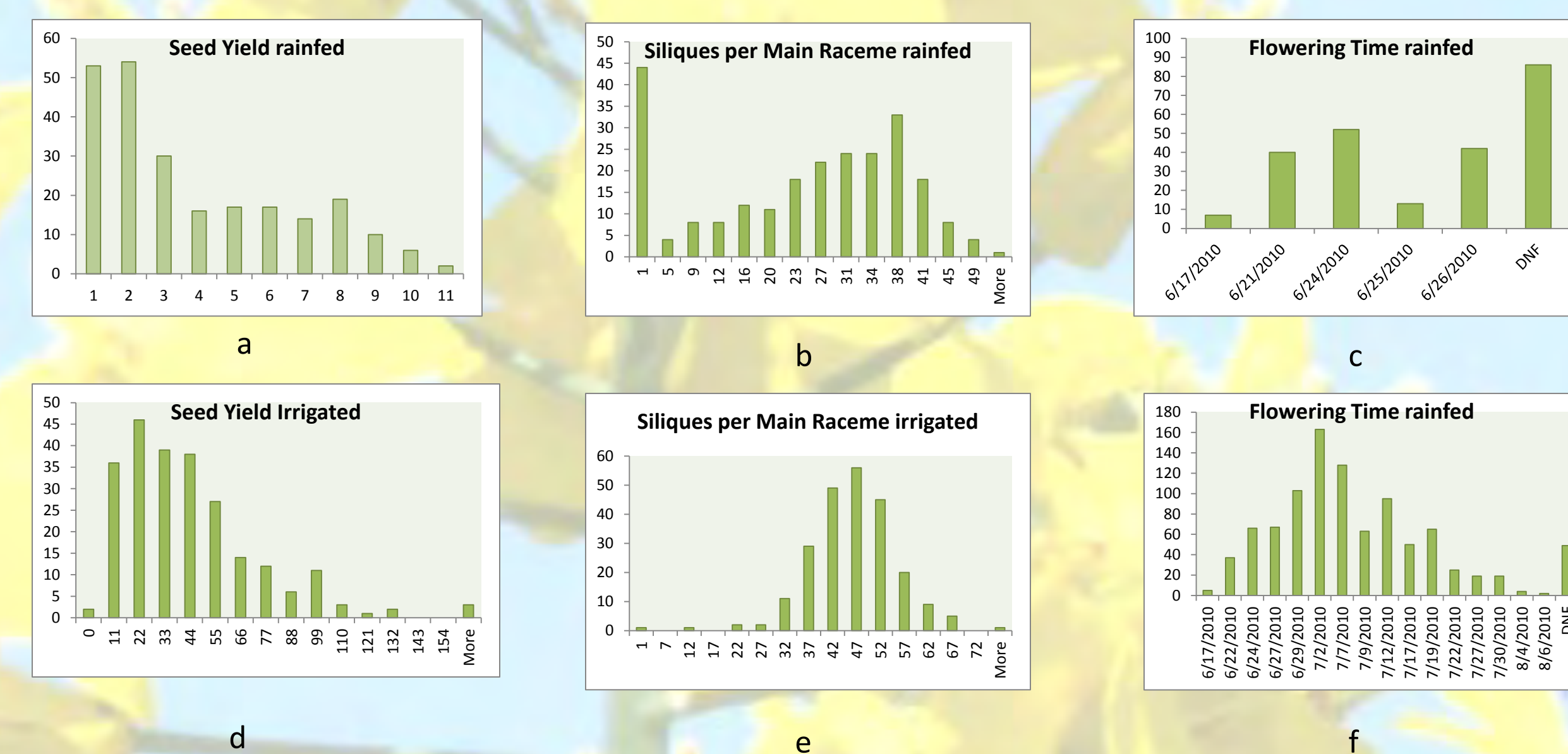


Figure one Frequency distributions of three traits in irrigated and rainfed conditions (a-f).

Source	df	F-value	P-value
Treatment	1	642.81	<.0001
Treatment (rep)	6	8.56	<.0001
Genotype	239	3.02	<.0001
Treatment x genotype	239	1.80	<.0001

Table one Analysis of variance for effect of treatment, treatment (rep), genotype, and genotype by treatment.

### Effect of flowering time and drought stress on yield

- Flowering time (ft) in this population spanned 57 days, which was likely due to the segregation of flowering time alleles in the biennial and annual parents. This variation in maturity had a significant effect on yield in both treatments, presumably due to the heat, insect and bird stress. Drought stress added to the yield decline over time. Yield by treatment was found to be significantly different ( $p<.0001$ ; table one).

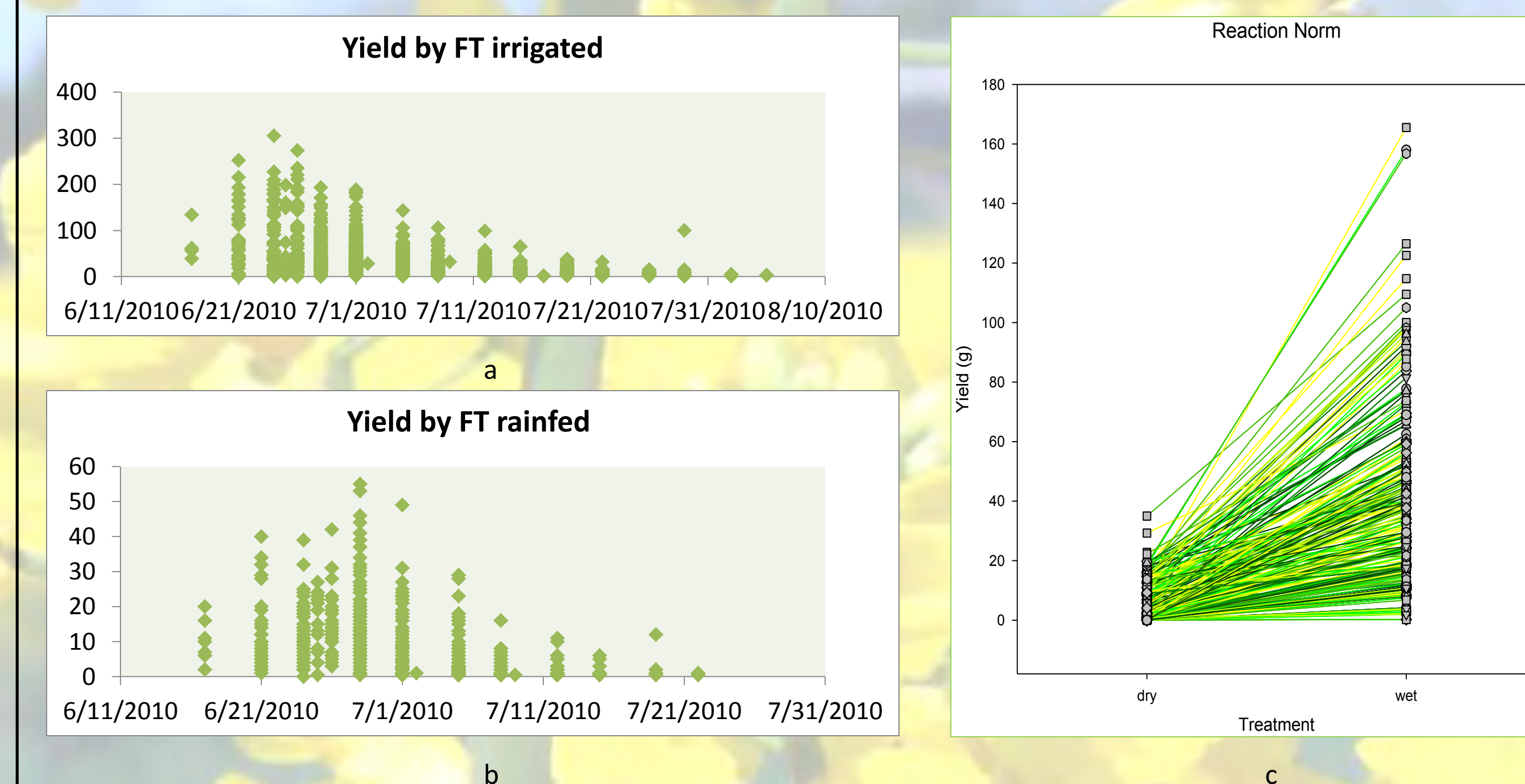


Figure two (a) Effect of flowering time on yield in irrigated treatment (b) Effect of flowering time on yield in rainfed treatment (c) Reaction norm of yield in irrigated (wet) and rainfed (dry) conditions.

## Results (cont.)

Yield components measured in the field were found to correlate positively with yield, indicating that they are a good measure of potential seed yield in a genotype. Components included length of main raceme (rainfed treatment only), number of siliques per main raceme, number of seeds per silique, and thousand seed weight.

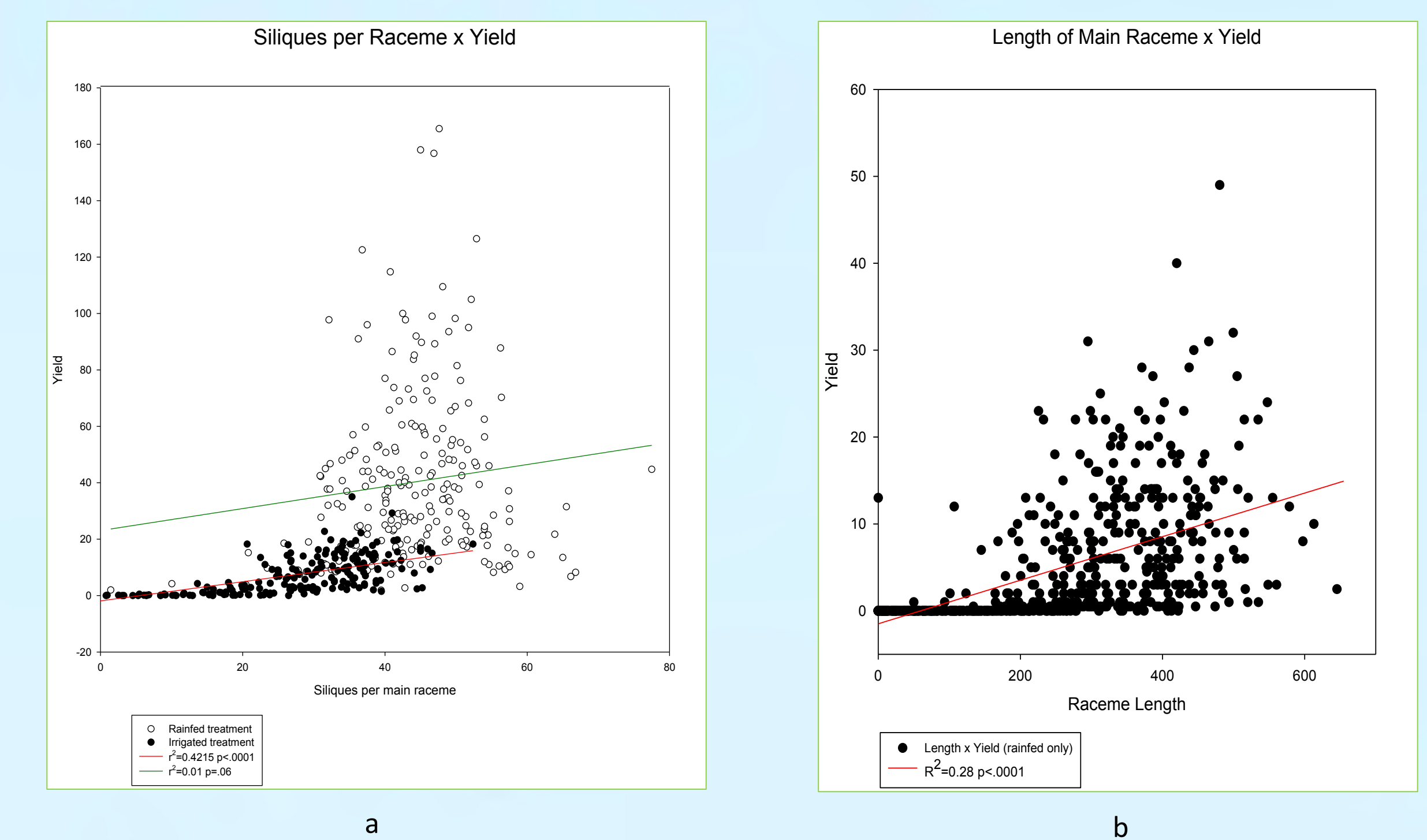


Figure three (a) Siliques per main raceme plotted against yield in both irrigated (closed circles) and rainfed (open circles) treatments. (b) Length of main raceme plotted against yield (dry treatment only).

## Data Analysis

Analysis of variance (ANOVA) was performed on the data to determine genotype and treatment effect. All data were analyzed using SAS software version 9 of the SAS system for Windows (© SAS Institute, Cary, NC, USA, 2010). Histograms were created using Microsoft Excel 2010. Graphs depicting yield components were created using SigmaPlot software for Windows version 10.0 (© Jandel Corporation, 2010).

## Conclusions

This experiment studied the correlations between flowering time and yield components with seed yield in irrigated and rainfed conditions in Northern Colorado. During the field experiment, plant growth was vigorous and stands were uniform. The rainfed condition began to experience drought stress very soon after stand establishment, leading to a significant effect of treatment on seed yield and yield components ( $p<.0001$ ). While siliques per main raceme and length of main raceme seemed to correlate well with yield under non-irrigated conditions ( $r^2=0.42$  and  $0.28$ , respectively), these components were less indicative of yield in the irrigated treatment, perhaps indicating that bird and/or insect damage was significant in the irrigated condition due to influence of environmental variation. Flowering time was a clear predictor of seed yield, with the earlier flowering genotypes producing more seed. *Brassica napus* is typically a cool-climate crop, so it is not surprising that drought-avoiding genotypes yielded more seed. Seeds per silique, thousand seed weight and oil characteristics are currently being analyzed. Quantitative trait locus mapping techniques will allow all of the yield components and oil characteristics to be analyzed to determine areas of the *Brassica* genome that influence these phenotypes.

## References

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