



Unmanned aerial system assisted framework for the selection of high yielding cotton genotypes

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ABSTRACT

Recent advances in molecular breeding and bioinformatics have greatly accelerated the screening of large sets of genotypes. Development of field-level phenotyping, however, still lags behind and is considered by many as the main bottleneck to improved efficiency in breeding programs. Unmanned Aerial System (UAS) and sensor technology available today enables collection of data at high spatial and temporal scales, previously unobtainable using traditional airborne remote sensing technologies. Here, we propose an UAS-assisted high throughput phenotyping framework for cotton (*Gossypium hirsutum* L.) genotype selection. UAS data collected on July 24, 2015 were used to calculate canopy cover, and UAS data collected on August 5, 2015 were used to extract open boll related phenotypic features including number of open bolls, average area of open bolls, average diameter of open bolls, perimeter of open bolls, perimeter to area ratio. Using the extracted features, a sequential selection procedure was performed on a population of 144 entries. Entries selected from the proposed framework were compared to the highest yielding entries determined by mechanical harvest results. Experimental results indicated that the selection process increased minimum and average lint yield of the remaining population by 7.4 and 10%, respectively, and UAS-selected entries and genotypes matched 80 and 73%, respectively, the same lists ranked by actual field harvest measurements.

1. Introduction

Currently, cotton (*Gossypium* sp.) is the world's most important natural textile fiber crop, accounting for around 35 percent of total world fiber use. Also, it is one of the biggest crops in the food oil industry (USDA, <http://www.ers.usda.gov/topics/crops/cotton-wool.aspx>). Plant breeding is one of civilization's oldest activities and started with the need of improving plants for human benefit. Today, the world's food, feed, and fiber production relies on breeding programs to create genetic types that excel in productivity and meet population needs. To that end, molecular plant breeding techniques and bioinformatics have significantly evolved in the past few decades (Cabrerá-Bosquet et al., 2012; Hulse-Kemp et al., 2014; Mayes et al., 2005; Yu et al., 2014) to develop cotton genotypes with higher potential yield. The advancement of high throughput genotyping platforms and the access to fast and relatively inexpensive genomic information revolutionized cotton breeding programs. The ability to work efficiently in a genomic level enabled fast advances in innumerable sectors of genetic research. In plant breeding, the use of genetic maps and molecular

markers in marker assisted selection to meticulously target the gene/trait of interest greatly expedites the breeding process. Phenotyping, on the other hand, has not developed at the same pace, despite its important role in plant breeding research (Araus and Cairns, 2014). Lack of high-throughput phenotyping method is known to be the main bottleneck for increased breeding efficiency, and current phenotyping methods still remain relatively low throughput, laborious, and time-consuming. Efficient, rapid, and reliable high throughput phenotyping platforms are much needed to decrypt relationship between the full suite of genetic and environmental factors and phenotypic variations at plant- and population-levels (Cobb et al., 2013; Furbank and Tester, 2011).

Traditionally, a plant breeding program focuses on several major steps. First, breeders establish the goal(s) of his program with a defined objective to focus their attention in gathering and/or creating a breeding population (genetic variability). After a base population has been established, one needs to choose one, or a combination of several available breeding strategies to deal with the segregating populations (e.g. pedigree, modified bulk, backcross, etc). Finally, based on the goal

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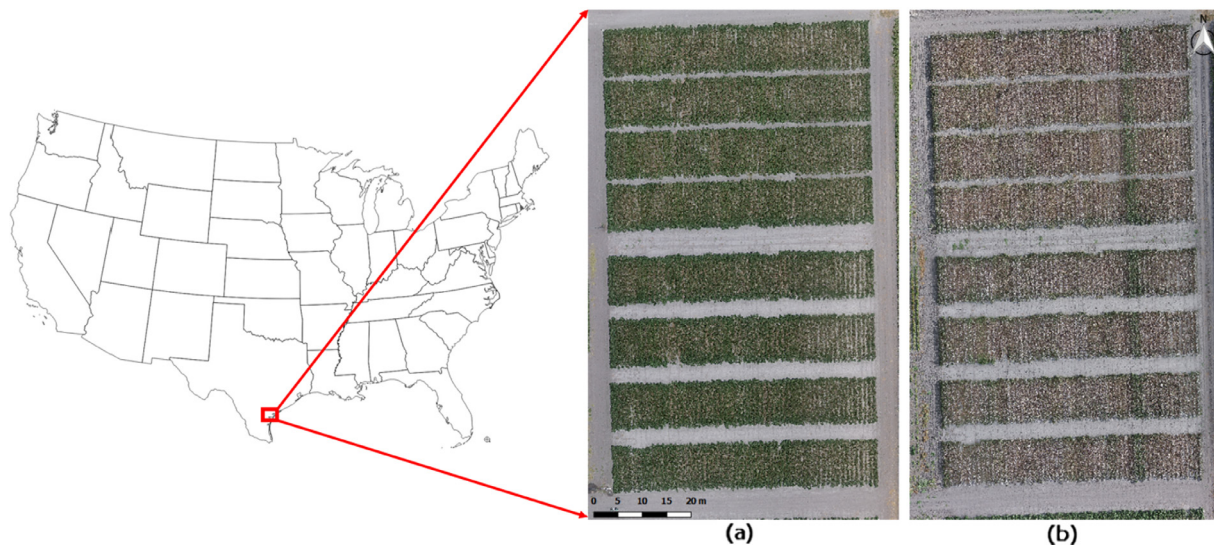


Fig. 1. Location of the study site and orthomosaic images of the field (a) on July 24, 2015 when canopy was fully developed and (b) on August 5, 2015 after defoliation.

(s) of the breeding program, stable non-segregating superior genotypes are identified to be commercially released to the public. Typically, multiple years of intense screening and selection are required to develop and bring new elite genetic types or “cultivars” to market. As a result of the expansion of breeding programs and an increase of demand by the world’s population, breeders are always searching for new methods to increase efficiency, and convenient techniques to facilitate the breeding process.

Although traditional satellite remote sensing technologies have been utilized to address issues in effectively selecting high yield genotypes, the lack of spatial resolution and limited temporal resolution due to their orbital design were mentioned as key hurdles in enabling breeding selection framework using the remote sensing technologies (Berni et al., 2009). Recent advances in sensor technologies now made it possible to integrate small and lightweight sensors into Unmanned Aerial System (UAS). In the early stage of UAS technology for agriculture applications, most research focused on developing UAS data processing scheme and accessing data accuracy. Honkavaara et al. (2013) investigated the processing and uses of UAS image data in precision agriculture. They developed a processing scheme from raw images up to georeferenced reflectance image and digital surface models. The results confirmed that UAS technology has a great potential in precision agriculture and indicated many possible future researches. Gómez-Candón et al. (2014) studied geometric accuracy and crop line alignment while taking into account three different flight altitudes and a different number of GCPs. The results concluded that UAS data collection at a range between 30 and 100 m altitude and using a moderate number of GCPs can result in ultra-high resolution orthomosaic images. Rokhmana (2015) investigated the potential of UAS-based remote sensing for precision agriculture. The system used in the study has the ability to produce imagery with spatial resolution of < 10 cm and the average geometric accuracy can be obtained up to 3 pixels, while the production time can be reached more than 500 ha a day. Primicerio et al. (2012) tested autonomous UAS flight for multi-spectral UAS image acquisition and the acquired images showed good agreement with ground-based spectrometer data.

In addition to the previous literatures, more detailed precision agriculture studies using UASs have been conducted to extract phenotypic features from the UAS data. Gevaert et al. (2015) combined multispectral satellite imagery with hyperspectral UAS imagery for precision agriculture applications for the first time. They constructed spectral-temporal response surfaces for crop phenology monitoring. Gago et al. (2015) compared the performance of different types of UASs

with ground-truth plant data in terms of crop water stress. The results showed that thermal indices have a great potential to determine water stress heterogeneity. López-Granados et al. (2016) generated georeferenced weed seedling infestation maps by analyzing of visible and near-infrared UAS images. Based on the classification map, they investigated variability of herbicide treatments against weed coverage ratio. Bendig et al. (2015) combined selected vegetation indices and plant height information to estimate crop biomass. The correlations between vegetation indices and dry biomass were analyzed and then multiple regression models using selected vegetation indices and plant height were developed.

UAS can perform aerial data acquisition missions without manual control. To address the limitations of traditional remote sensing technologies, we propose to utilize an Unmanned Aerial System (UAS) as a data acquisition platform and develop a framework to select high yield cotton genotypes based on measurements from the UAS data. The main objectives of this study is to develop a systematic framework to select high yield cultivars using data acquired from UAS so that the developed framework can be used to empower breeders to improve their cultivar selection process.

2. Methods

2.1. Study site

A dryland field trial was established at the Texas A&M AgriLife Research and Extension Center (27° 46.948'N, 97° 33.605'W, elevation 16 m above sea level) at Corpus Christi, TX during the summer of 2015 (Fig. 1). The dryland field trial was approximately 35 m in width and 110 m in height. Seeds of 48 different cotton genotypes were planted on March 27, 2015 at a rate of 13.3 seeds/m in north to south oriented rows. Crop emergence occurred six days later on April 2, 2015. Plots were arranged in a randomized complete block design and each genotype was replicated three times, for a total of 144 plots. Each plot consisted of two rows that were 10.7 m long spaced at 0.96 m. Management practices such as fertility, disease prevention, weed and insect control followed the guidelines recommended by local Texas A&M AgriLife Extension specialists. Harvest aids were applied when cotton plants exhibited approximately 60% open bolls, and consisted of a combination of thidiazuron (*N*-phenyl-*N*-1,2,3-thiadiazol-5-ylurea; 0.025 kg a.i. ha⁻¹) and diuron (3-(3,4-dichlorophenyl)-1,1-dimethylurea; 0.013 kg a.i. ha⁻¹) for defoliation, and ethephon (2-chloroethyl phosphonic acid; 0.59 kg a.i. ha⁻¹) and cyclanilide (1-(2,4-

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