Color Space Standardization and Image Analysis for High-throughput Phenotyping of *Sorghum bicolor*

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In plant science, high-throughput phenotyping is an important tool for gene discovery and analysis and improved crop breeding. For the process to be high-throughput, thousands of images must be collected per day. Advances in computational technics have made automated image analysis the most efficient way to process these image sets. Image analysis for high-throughput phenotyping starts with image segmentation, the process of classifying pixels containing plant from pixels representing background. Highly specialized systems for collecting images for phenotyping have been developed, and powerful and flexible tools for analysis of these images for phenotype data exist, such as PlantCV. The biggest challenge to this segmentation process, however, lies in persistent variation between images in a data set. A method for standardizing the color spaces of images was developed and shown to reduce variation in images for easier and more accurate segmentation. This tool is also implemented in PlantCV as a new module, and a new and robust pipeline is developed for segmenting and extracting data from images in a large image set of sorghum collected in the Bellwether Phenotyping Facility at the Donald Danforth Plant Science Center.