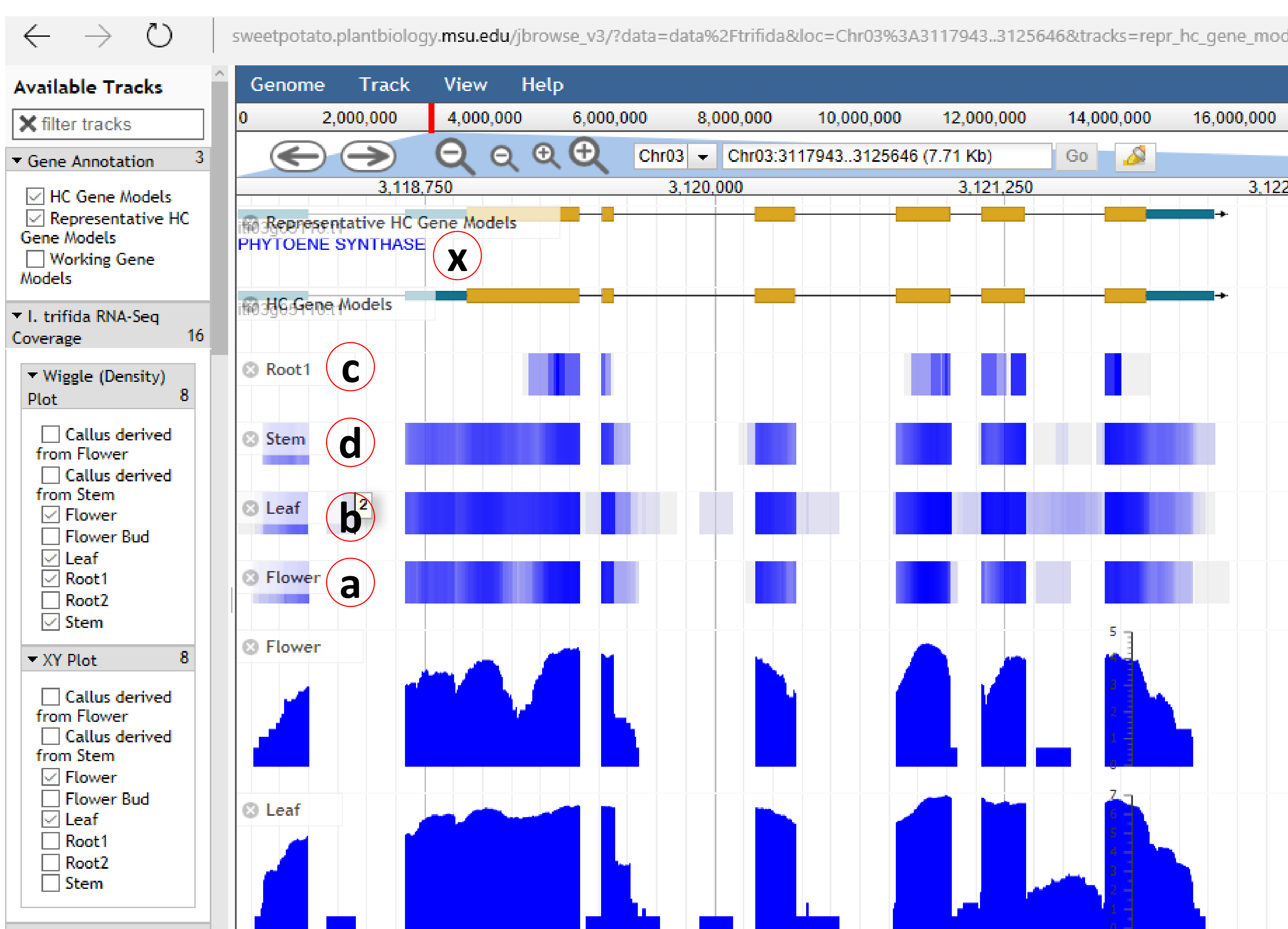




INTRODUCTION

Conventional breeding, is still dependent to a considerable extent on subjective evaluation and empirical selection. The process can be difficult, slow, influenced by the environment, and costly for the economy, as farmers suffer crop losses. Molecular marker assisted breeding (MAS) offers great challenges, opportunities and prospects for conventional scientific breeding, needs less subjectiveness and more science, i.e. practical and accurate [evaluation](#) and effective and efficient selection. MAS allows selection for all kinds of traits to be carried out at seedling stage and thus reduce the time required before the phenotype of an individual plant is known.

High gene expression of the beta carotene gene on sweetpotato Jbrowse, Phytoene synthase (x), in flower (a), leaf (b) and stem (c) and not roots (d)



KEY TABLE OF RESULTS

New genetic resources for sweetpotato many of which are first

- ✓ Sweetpotato reference genomes, *I. trifida* and *I. triloba*
<http://sweetpotato.plantbiology.msu.edu/>
- ✓ High confidence working gene models
- ✓ Genotyping by sequencing protocol and Bioinformatics
- ✓ Sweetpotato database and ontology (SPBase)
- ✓ Trait dissection using high-quality genetic and phenotypic

RELEVANCE FOR DIFFERENT FOOD SYSTEMS

- Assessment of traits expressed at later developmental stages
- Improvement of traits expressed only when favorable environmental conditions present, e.g. [disease/pest resistance and stress tolerance](#).
- Effective selection of minor (recessive) alleles of traits saving time and accelerating breeding progress
- Simultaneous selection for traits controlled by individual or multiple genes (QTLs)
- Discovering new genes and regulatory sequences, their positions, and markers available

Building capacity of the breeders to apply molecular breeding and accelerate improvement



CONCLUSIONS

With genomic tools, sweetpotato has great potential in the light of imminent challenges associated with its genetic complexity, emergence of new diseases and pests and climate change

METHODS

- Clone identification
- Cultivar and variety identification, genetic relatedness and phylogeny
 - Simple sequence repeats and Genotyping by sequencing
- Analysis of population diversity and structure
- QTL and trait mapping population
- Genomics selection
- Gene expression
- High quality phenotyping

RESULTS

- ✓ Reduced breeders time and cost for variety improvement
- ✓ Enhanced breeding of farmer and end user preferred varieties through gene pyramiding
- ✓ Increased availability and utilization of sweetpotato
- ✓ Food, nutrition and income security leading to improved livelihoods and economic stability

