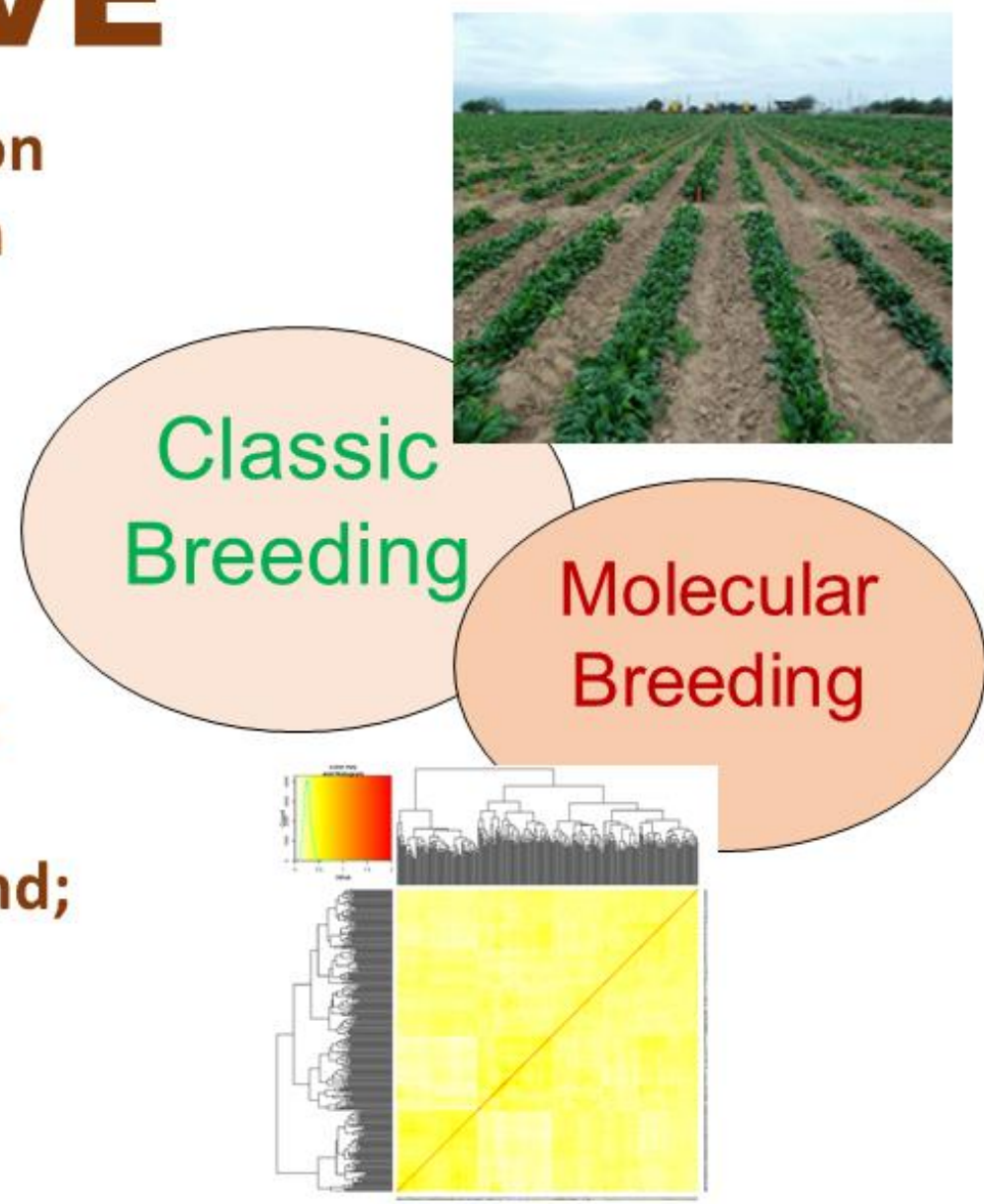


Developing Genetic and Molecular Resources to Improve Spinach Production and Management

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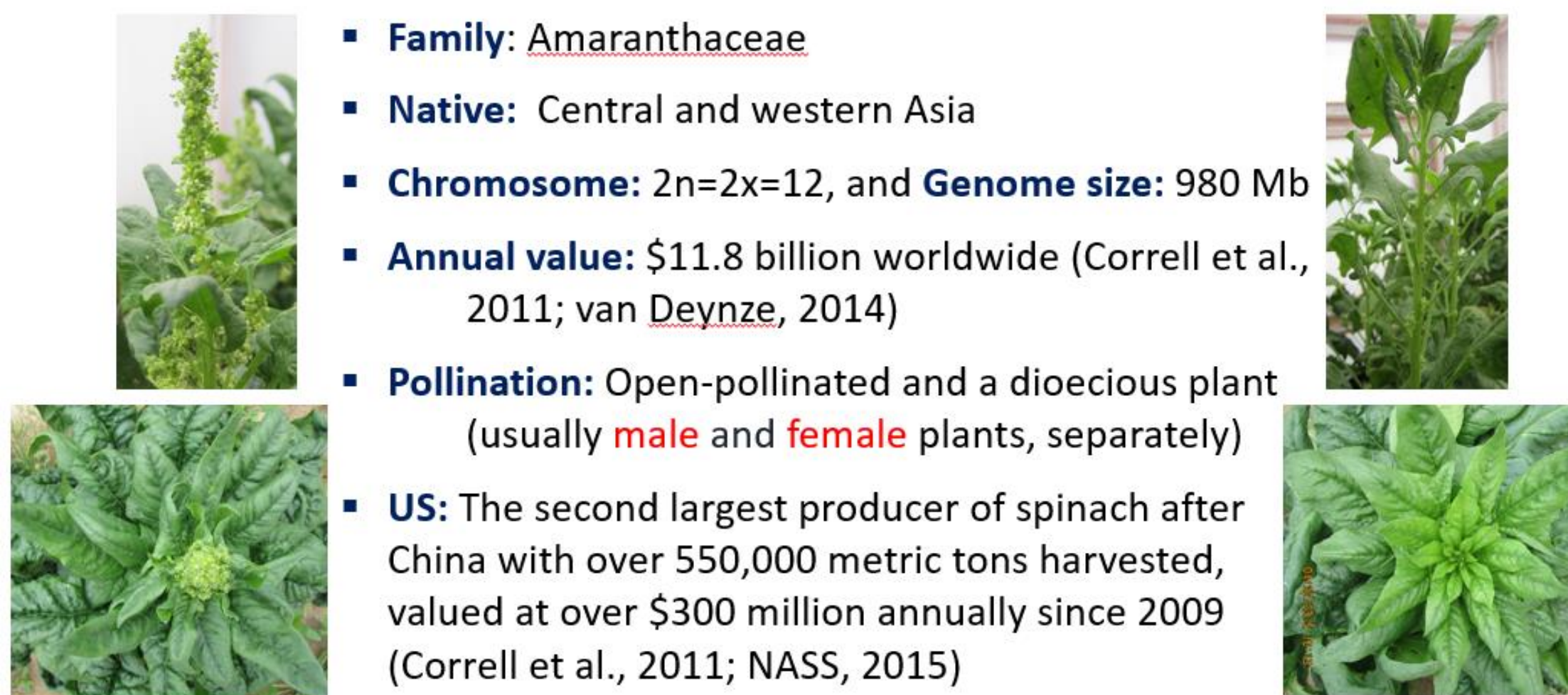
OBJECTIVE

- Genetic mapping and SNP marker identification for downy mildew and white rust resistance in spinach;
- Evaluation, QTL and association mapping and SNP marker identification for Fusarium wilt resistance in spinach;
- Introgression of downy mildew and white rust resistance into spinach lines with diverse leaf quality characteristics to satisfy market demand;
- Construction of high density SNP consensus genetic maps of six chromosomes in spinach using whole genome resequencing.

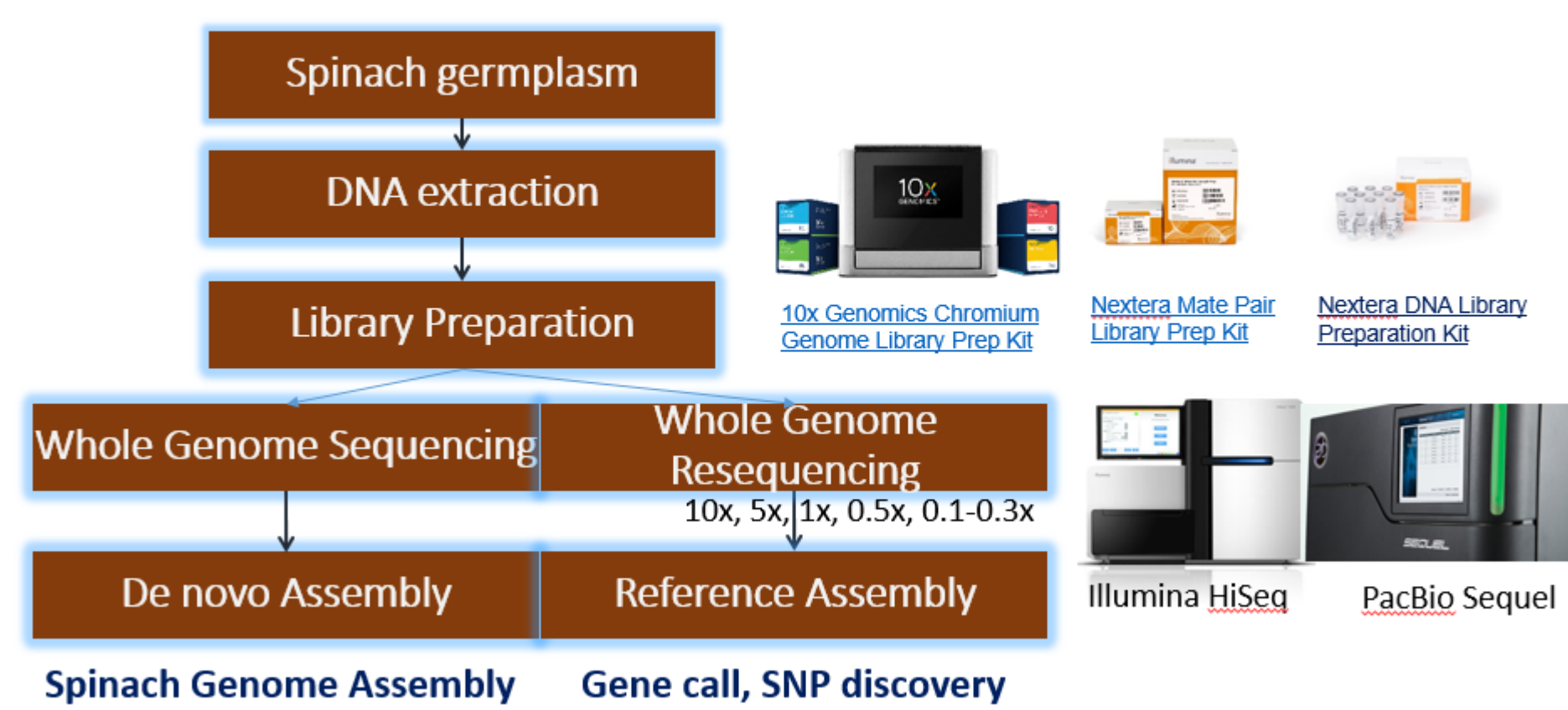


Spinach (*Spinacia oleracea*)

- Family:** Amaranthaceae
- Native:** Central and western Asia
- Chromosome:** $2n=2x=12$, and **Genome size:** 980 Mb
- Annual value:** \$11.8 billion worldwide (Correll et al., 2011; van Deynze, 2014)
- Pollination:** Open-pollinated and a dioecious plant (usually **male** and **female** plants, separately)
- US:** The second largest producer of spinach after China with over 550,000 metric tons harvested, valued at over \$300 million annually since 2009 (Correll et al., 2011; NASS, 2015)



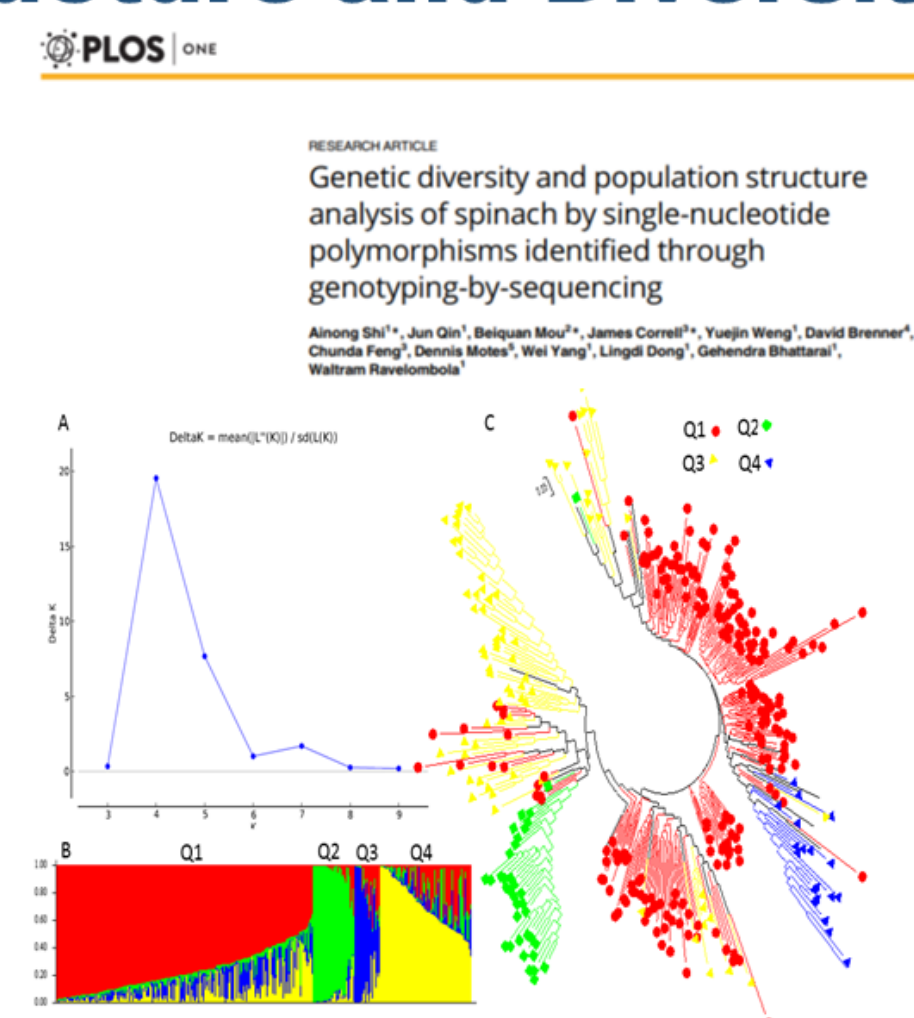
Whole Genome Sequencing and Resequencing



Spinach Genetic Structure and Diversity

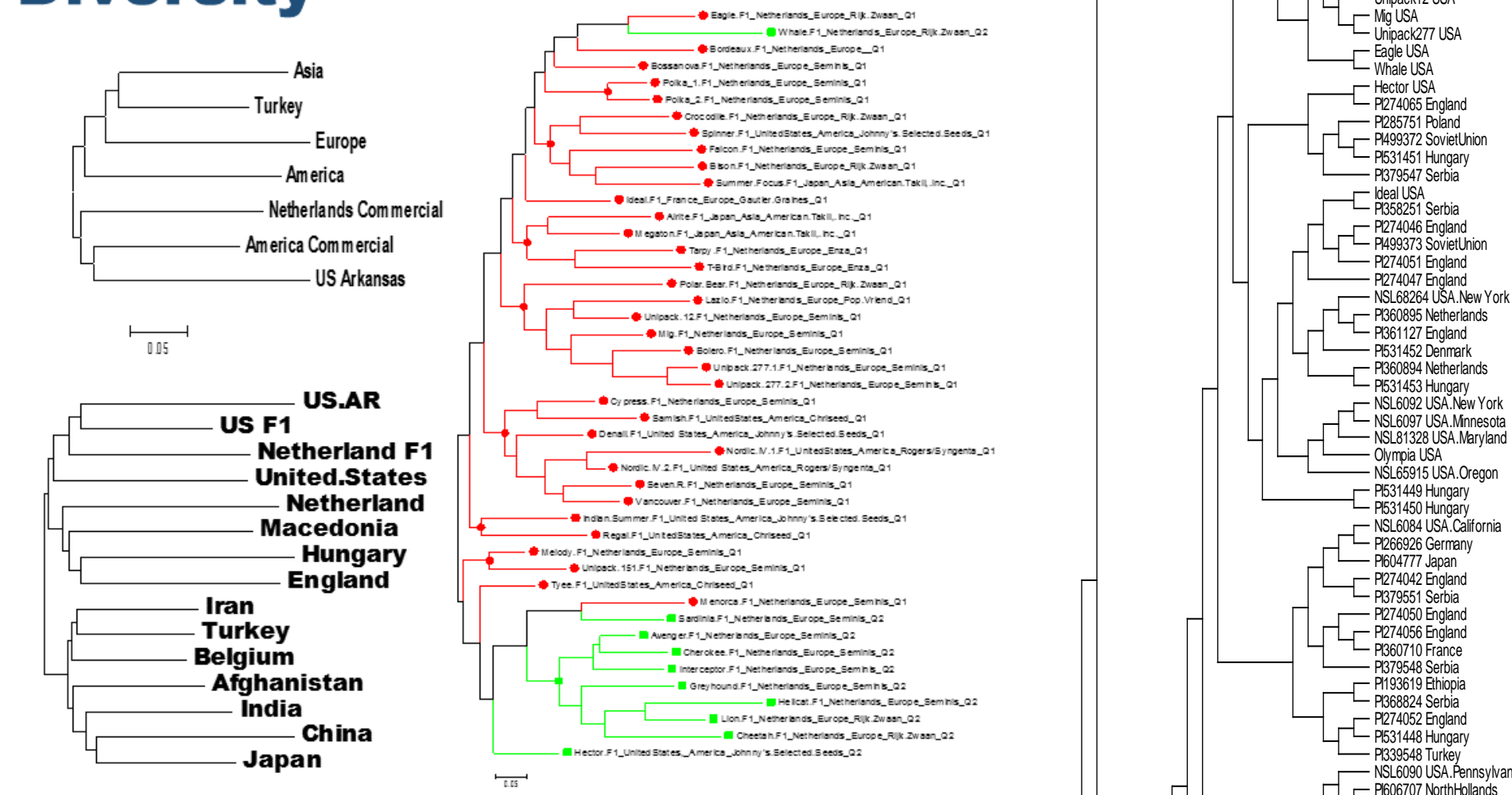
268: USDA GRIN spinach germplasm (30 countries)
 45: commercial spinach F1 hybrids (3 countries)
 30: US Arkansas spinach cultivars

Results:
 The genetic background in improved commercial F1 hybrids and in Arkansas cultivars/lines had a different structured populations from the USDA germplasm
 The genetic diversity was associated with geographic origin and germplasm from the US Arkansas breeding program had a unique genetic background

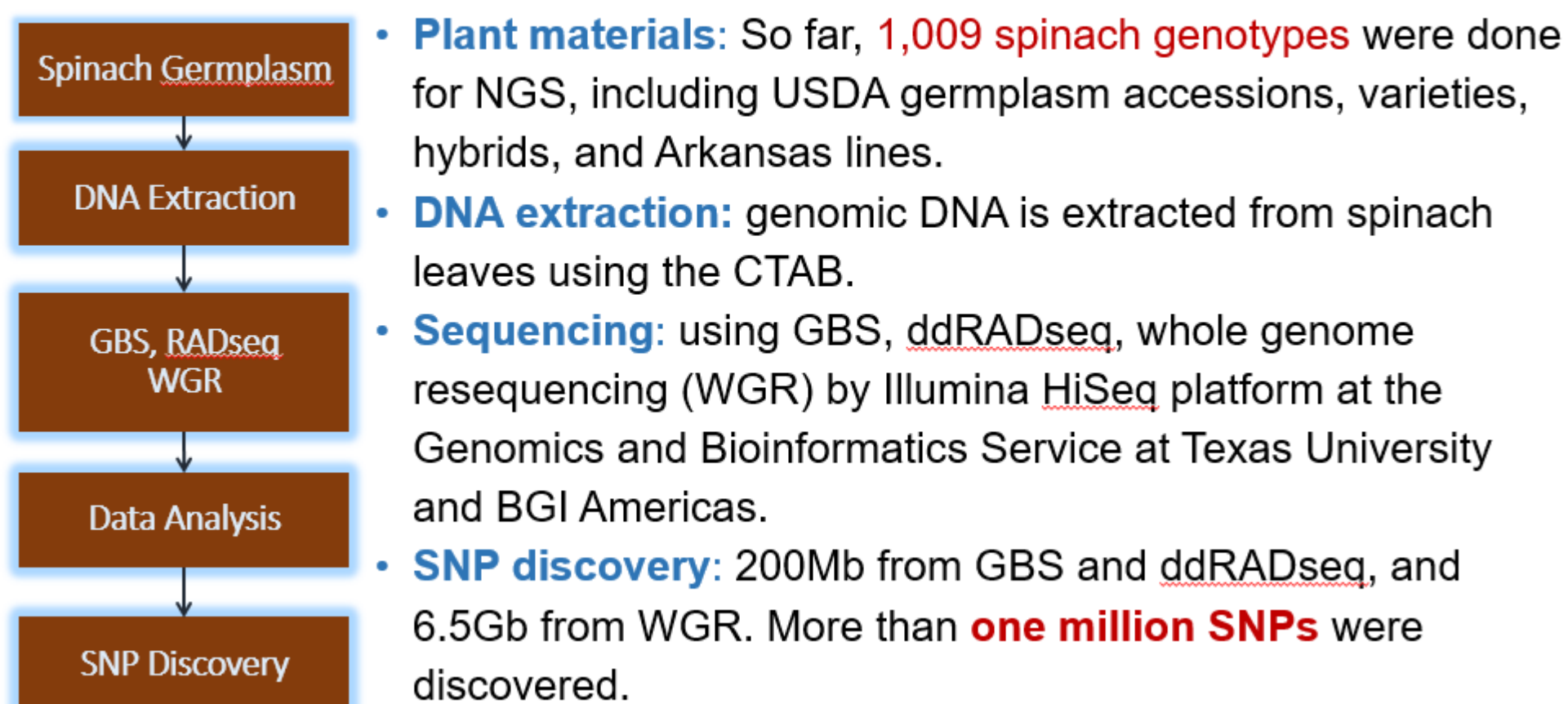


Spinach Genetic Diversity

- Commercial cultivars were separated from germplasm.
- Asia lines are closer to Europe than America.
- US F1 and Netherland F1 are closer to US Arkansas lines than US or Netherland germplasm or from others.
- F1 lines can be divided based on companies.



Genome-wide SNP Discovery in Spinach



Genome-wide association study for white rust resistance

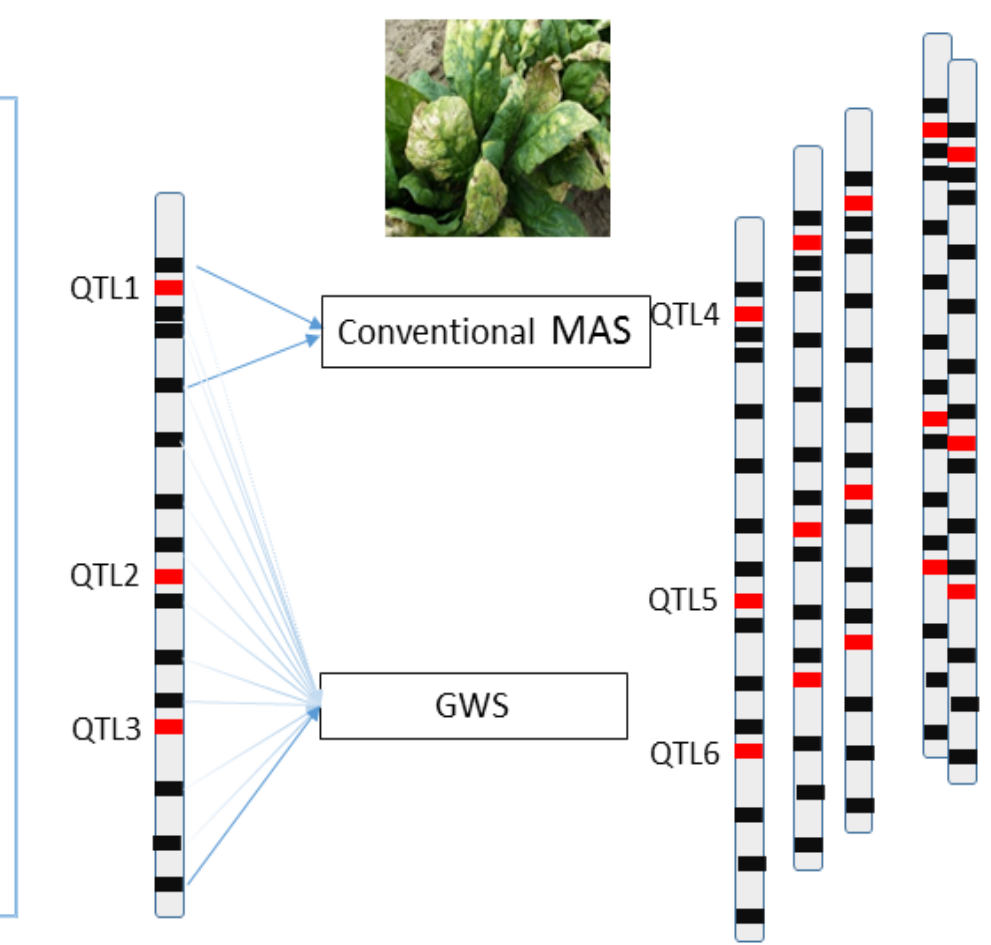
- Four hundred and twelve spinach lines were evaluated for white rust resistance
- Eight SNP markers were identified to be associated with WR resistance.
- The selection accuracy is >80% for each SNP markers.



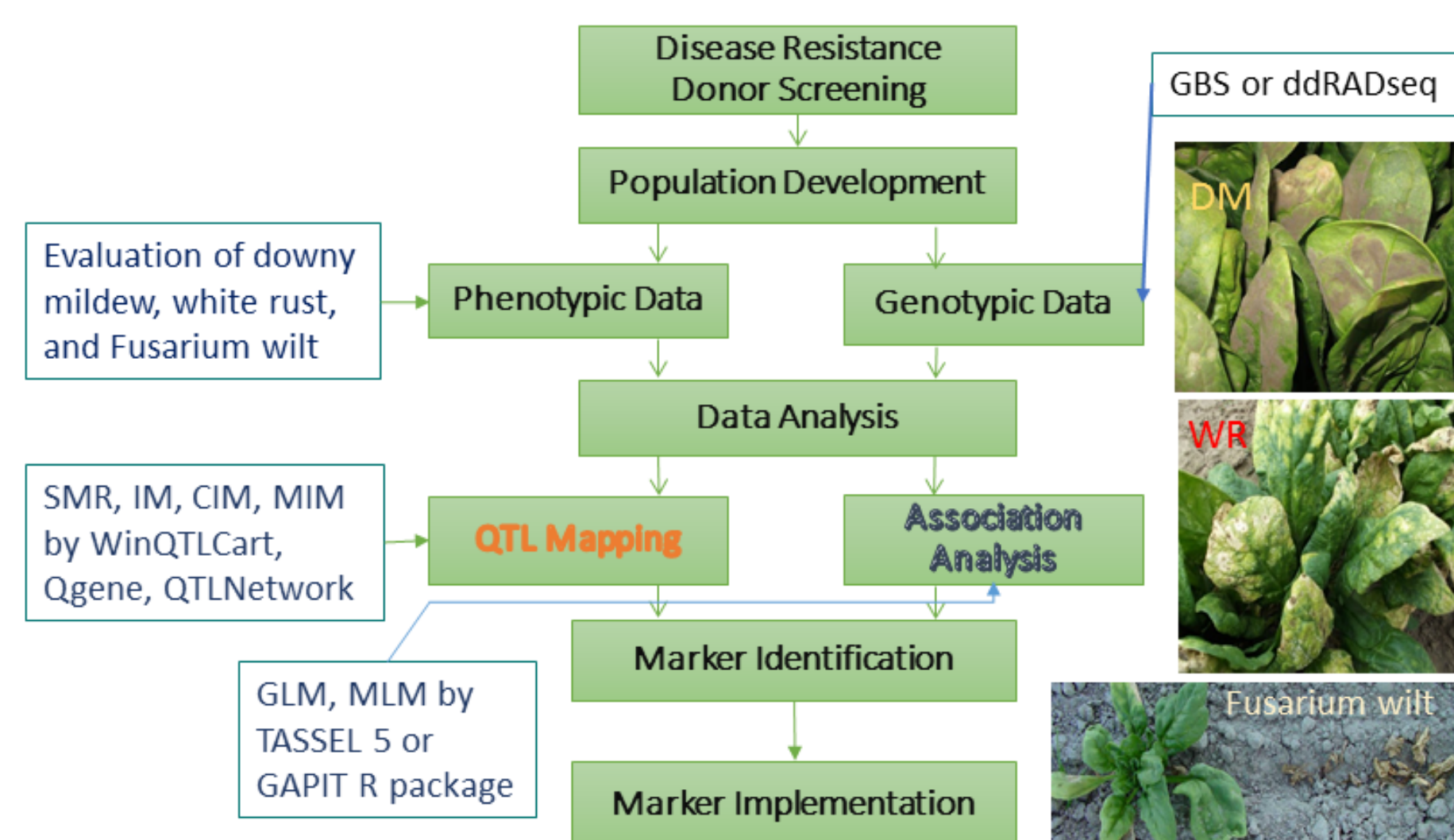
Genomic Selection in Spinach

White Rust Resistance as example

- Genomic Selection (GS), dense SNP genotypes covering the entire genome are used to predict the genetic value of a trait or individual.
- All markers are counted based on genomic estimated breeding value (GEBV) estimated as the sum of the effects of markers across the genome.
- Breeding values are derived from Best Linear Unbiased Predictors (BLUPs) as the sum of BLUPs for all markers.

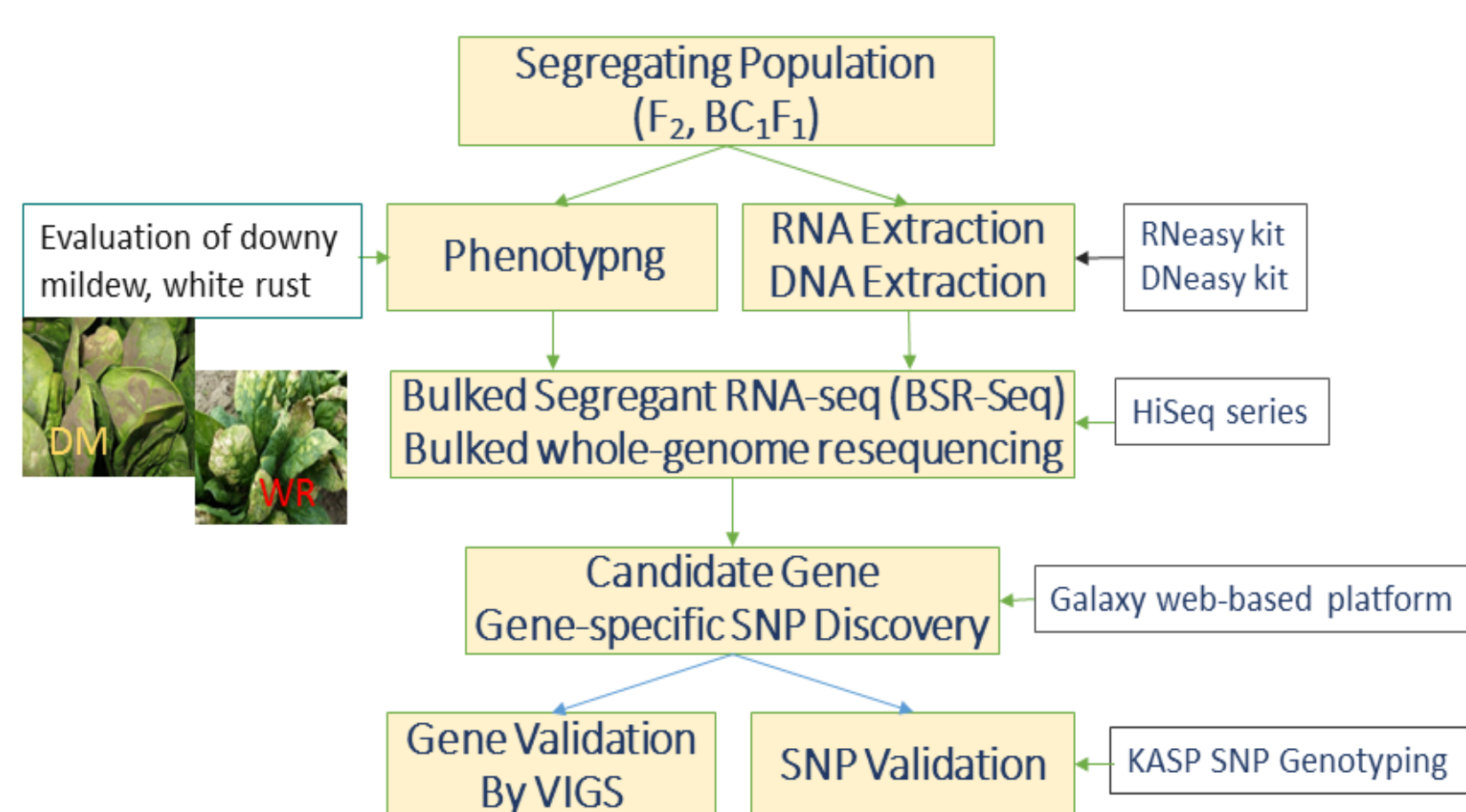


QTL and Association Mapping for Disease Resistance in Spinach

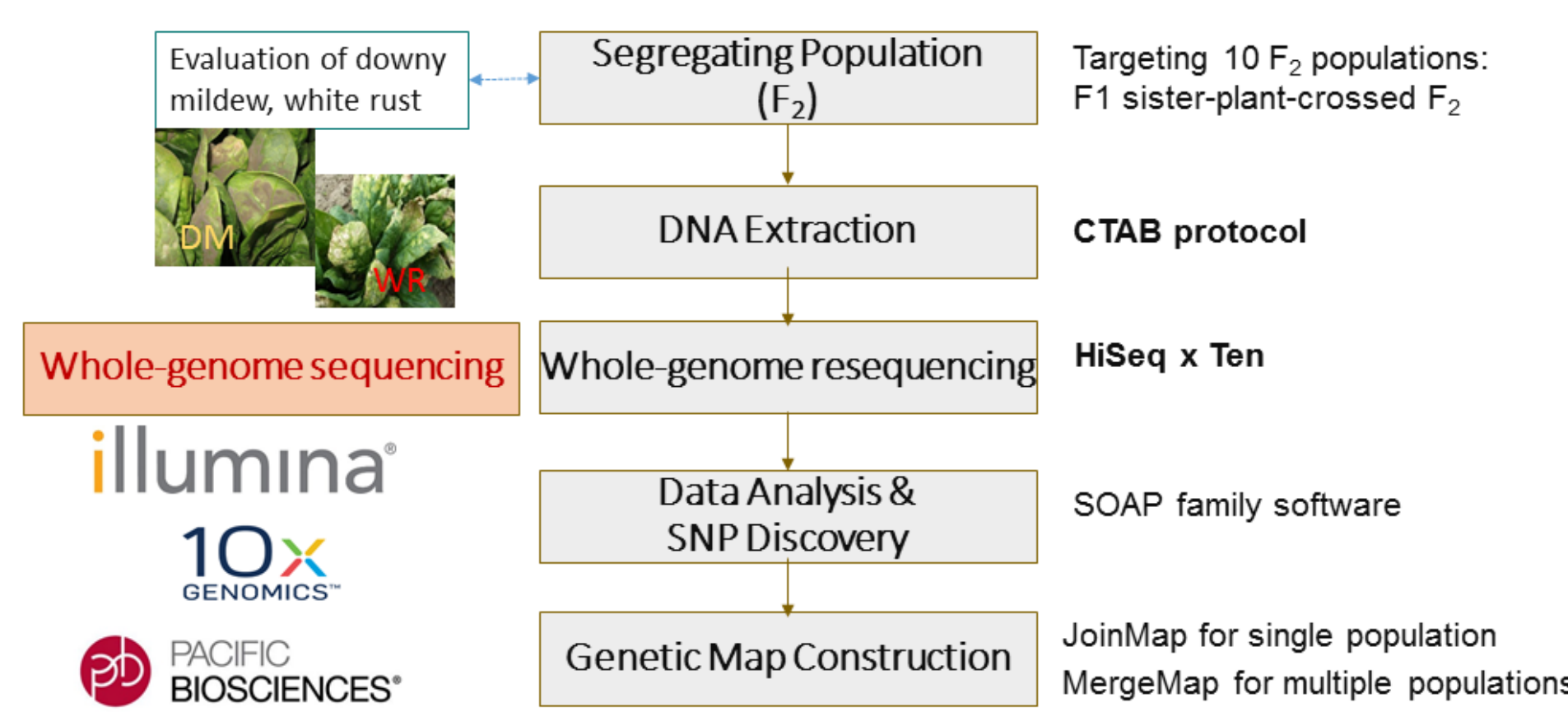


Molecular Breeding

Discovery of Candidate Genes and Gene-specific SNP Markers



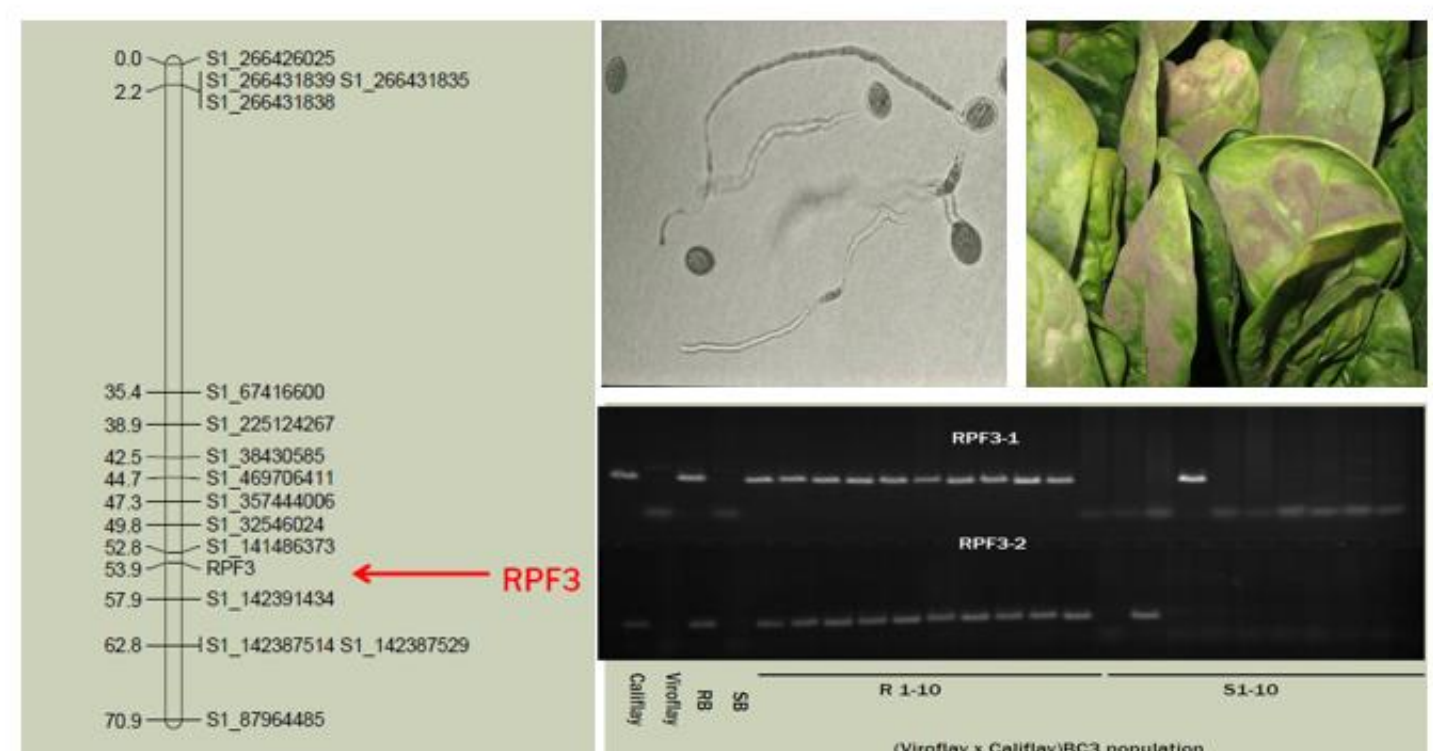
Construct SNP consensus genetic maps of the six chromosomes in spinach



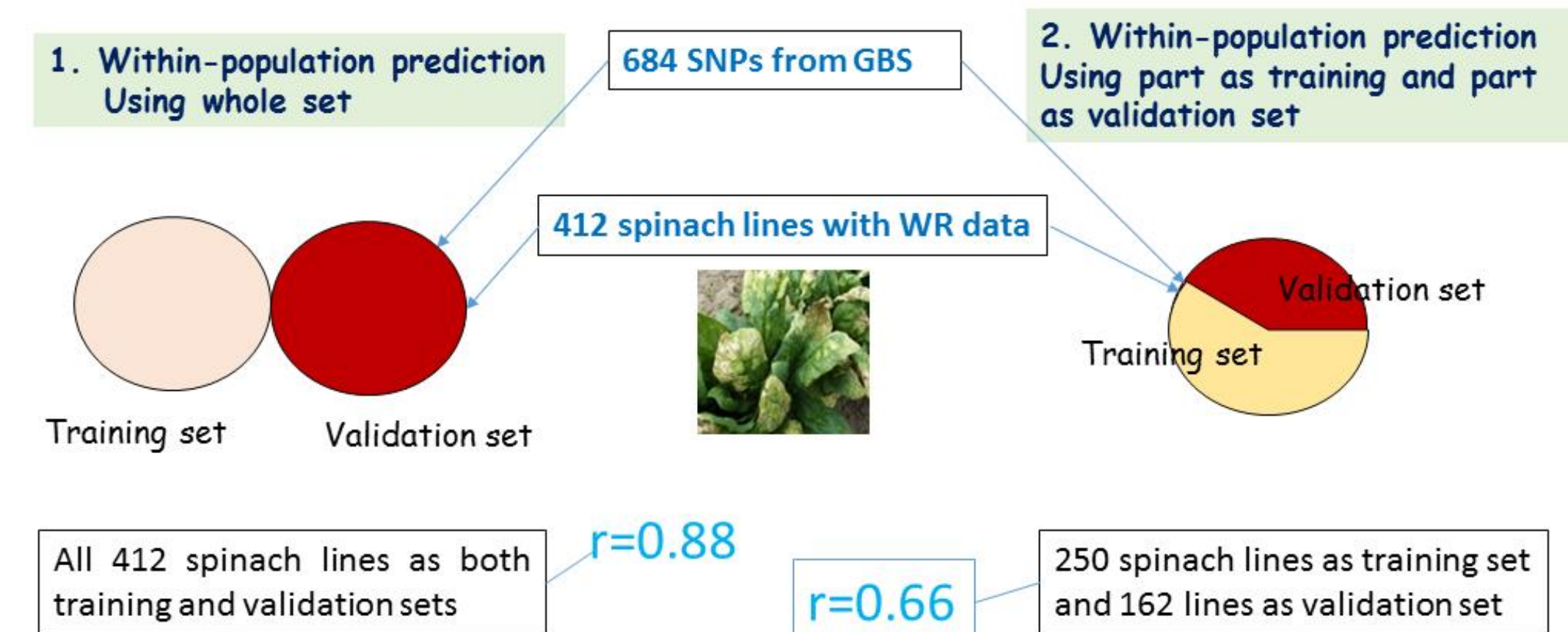
Genetic Map Construction in Spinach

- Plant materials:** Plan to do 10 segregating populations such as F2 populations derived from F1 hybrid sister-plant-crossed or derived from two heterogeneous lines crossed F1 to have a total of 960 individuals with 96 samples each including the populations with rust resistance or downy mildew resistance or Fusarium wilt resistance.
- Genetic map construction:** Linkage maps from single population will be constructed using JoinMap (Van Ooijen 2006) and consensus genetic maps by MergeMap.
- The six genetic maps of spinach will be constructed

Identification of Downy Mildew Resistance in Spinach

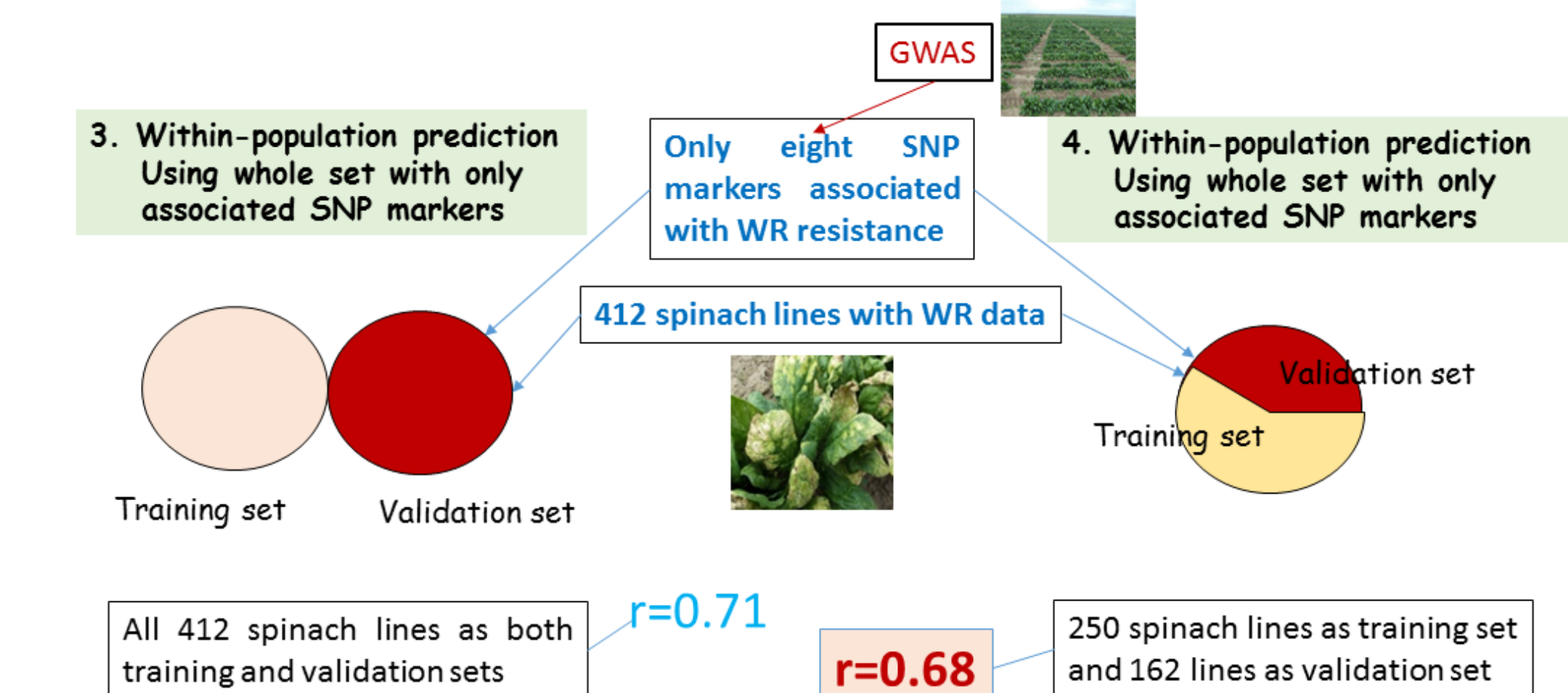


Genome Selection for White Rust Resistance



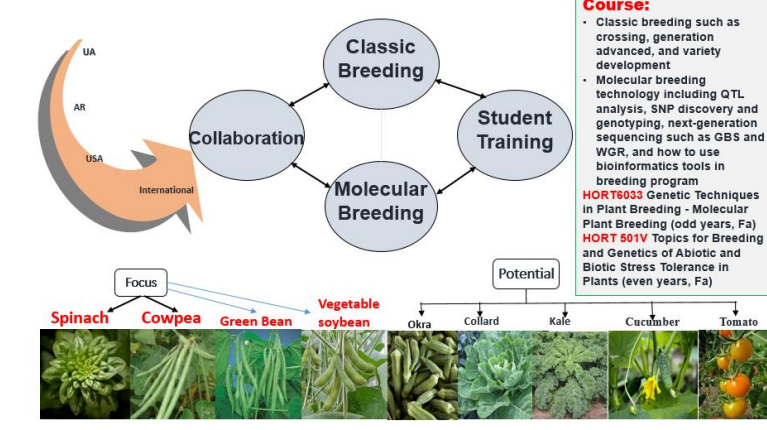
The correlation r is calculated between the predicted breeding value and the phenotypic WR data

Genome Selection for White Rust Resistance



The correlation r is calculated between the predicted breeding value and the phenotypic WR data

UA Vegetable Breeding



Vegetable Breeding and Genetics in University of Arkansas

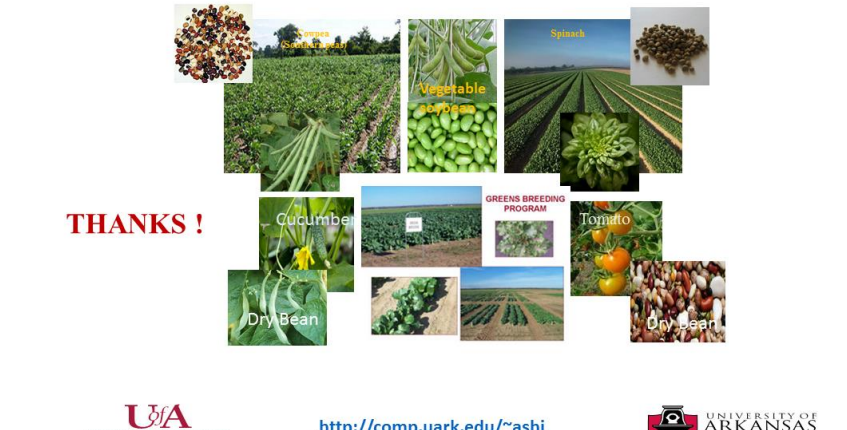


Fig. 1. A Systemic Vegetable Breeding and Genetics Program at the University of Arkansas