

# RosBREED

Enabling marker-assisted breeding in Rosaceae



www.rosbreed.org

**Project Director:** Amy Iezzoni<sup>1</sup> **Co-PDs:** Cameron Peace<sup>2</sup>, Dorrie Main<sup>2</sup>, Nahla Bassil<sup>3</sup>, James Luby<sup>4</sup>, Chengyan Yue<sup>4</sup>, Eric van de Weg<sup>5</sup>, Cholani Weebadde<sup>1</sup>, Gennaro Fazio<sup>6</sup>, Marco Bink<sup>5</sup>, Susan Brown<sup>7</sup>, David Byrne<sup>8</sup>, John Clark<sup>9</sup>, Carlos Crisosto<sup>10</sup>, Thomas Davis<sup>11</sup>, Kate Evans<sup>12</sup>, Chad Finn<sup>17</sup>, Karina Gallardo<sup>12</sup>, Ksenija Gasic<sup>13</sup>, Tom Gradziel<sup>14</sup>, James Hancock<sup>1</sup>, Raymond Jussaume<sup>2</sup>, Vicki McCracken<sup>2</sup>, Nnadozie Oraguzie<sup>15</sup>, Gregory Reighard<sup>13</sup>, Alexandra Stone<sup>16</sup>, Mykel Taylor<sup>2</sup>, Dechun Wang<sup>1</sup>, Kenong Xu<sup>7</sup>

<sup>1</sup>Michigan State University, East Lansing, MI, USA  
<sup>2</sup>Washington State University, Pullman, WA, USA  
<sup>3</sup>USDA-ARS, Natl Clonal Germplasm Repos., Corvallis, OR, USA  
<sup>4</sup>Univ. of Minnesota, St. Paul, MN, USA  
<sup>5</sup>Plant Research International, Wageningen, Netherlands

<sup>6</sup>USDA-ARS Cornell Univ., Geneva, NY, USA  
<sup>7</sup>Cornell Univ., NYSAES, Geneva, NY, USA  
<sup>8</sup>Texas A&M Univ., College Station, TX, USA  
<sup>9</sup>Univ. of Arkansas, Fayetteville, AR, USA  
<sup>10</sup>Univ. of California - Davis, Parlier, CA, USA  
<sup>11</sup>Univ. of New Hampshire, Durham, NH, USA

<sup>12</sup>Washington State Univ., Wenatchee, WA, USA  
<sup>13</sup>Clemson Univ., Clemson, SC, USA  
<sup>14</sup>Univ. of California - Davis, Davis, CA, USA  
<sup>15</sup>Washington State Univ., Prosser, WA, USA  
<sup>16</sup>Oregon State Univ., Corvallis, OR, USA  
<sup>17</sup>USDA-ARS Hort. Crops Res. Lab., Corvallis, OR, USA

**OTHER NON-U.S. PARTICIPANTS:** David Chagné (Plant & Food Research, New Zealand), Jasper Rees (Agricultural Research Council, South Africa), Dan Sargent (East Malling Research, England), Herman Silva & Lee Meisel (Universidad Andres Bello, Chile), Béatrice Denoyes-Rothan, Elisabeth Dirlewanger, Charles-Eric Durel, François Laurens, Jose Quero Garcia & Benedicte Quilot-Turion (INRA, France), Roeland Voorrips, Hans Jansen, & Chris Maliepaard (Plant Research International, The Netherlands), Ignazio Verde (CRA, Italy), Riccardo Velasco (IASMA, Italy)



## Introduction

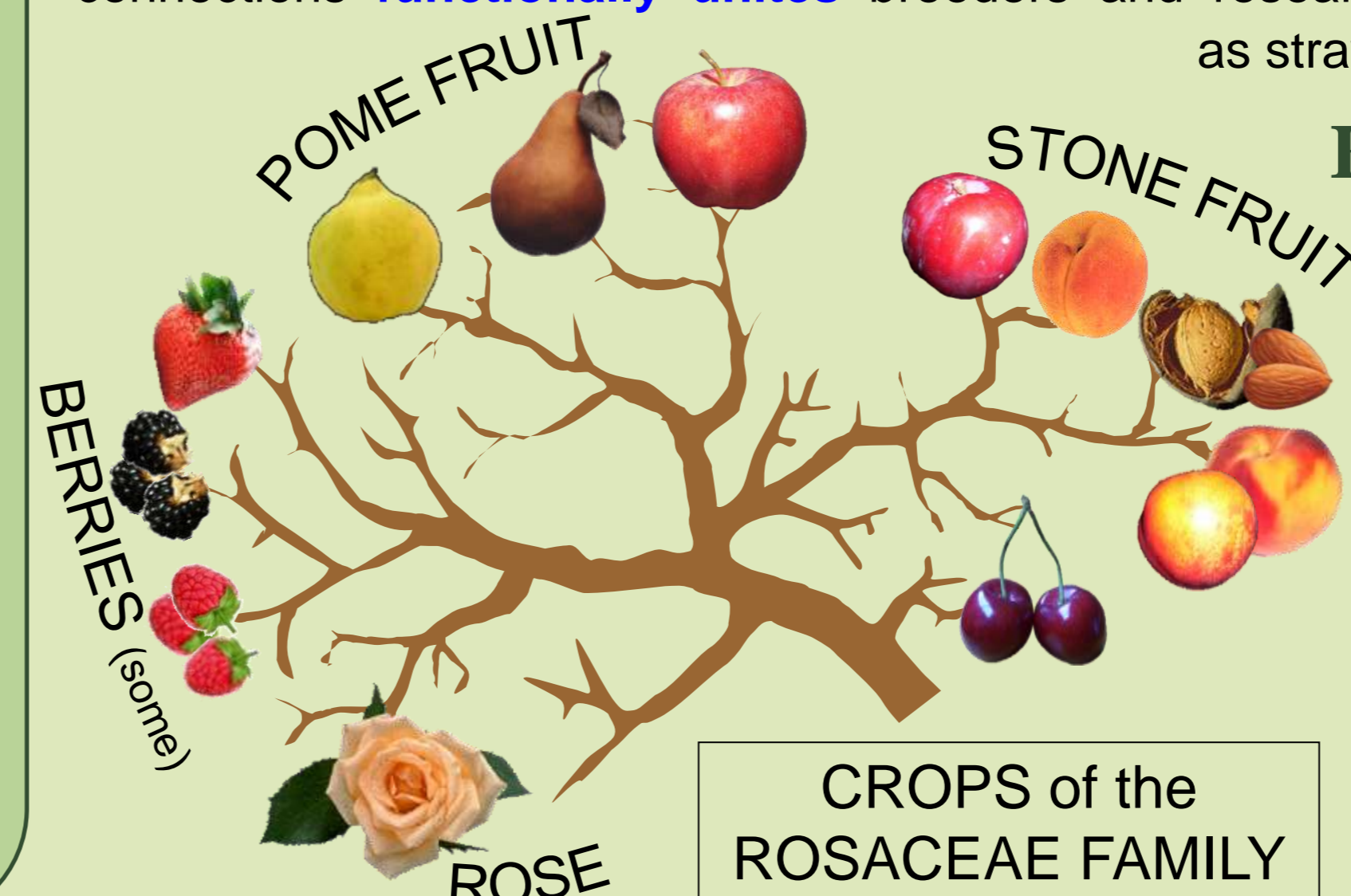
Breeding provides **long-term genetic solutions** to consumer and industry demands (e.g. superior flavor, extended season), challenges (e.g. diseases, climate change), and opportunities (e.g. novel fruit types). Enhancing **fruit quality** of rosaceous crops is a particularly important breeding target, as delivery of consistently excellent rosaceous products will increase consumption and sales, improving human health and well-being and industry sustainability.

The genomics era has provided powerful tools for understanding and influencing the genetic control of crop traits. However, despite a huge investment in fundamental genomics research and the best of intentions by researchers, **practical application is scarce** in Rosaceae breeding. Numerous reasons underlie the skepticism of breeders to using DNA information routinely in their selection decisions, including a perceived extra expense and need for specific technical expertise, and a lack of robust genetic markers for high-impact traits appropriate for their breeding germplasm.

Despite these barriers, the promise remains for marker-assisted breeding (MAB) to **revolutionize Rosaceae genetic improvement**, as it has in other crop families. RosBREED seeks to enable MAB in Rosaceae by addressing and overcoming constraints, via an international network of resources and expertise.

## Exploiting Shared Ancestry

Rosaceae crops share a common ancestral genome. Therefore, genes underlying important traits in one crop may influence similar traits in another crop. Exploiting these genomic connections **functionally unites** breeders and researchers of crops as seemingly different as strawberry and peach, or cherry and apple.



## Exploiting Shared Pedigrees

Individual plants in breeding programs are often related through known pedigrees. Due to repeated use as parents of the same or related cultivars, pedigree connections often extend from one breeding program to another. With **Pedigree-Based Analysis**, these links can be exploited in combining datasets for powerful analyses and for encouraging collaboration.

## VISION

*Integration of modern genomics tools with traditional breeding approaches will transform crop improvement in Rosaceae, significantly improving profitability and sustainability of U.S. rosaceous crop industries and contributing to increased consumption and enjoyment of these fruit, nut, and floral products.*

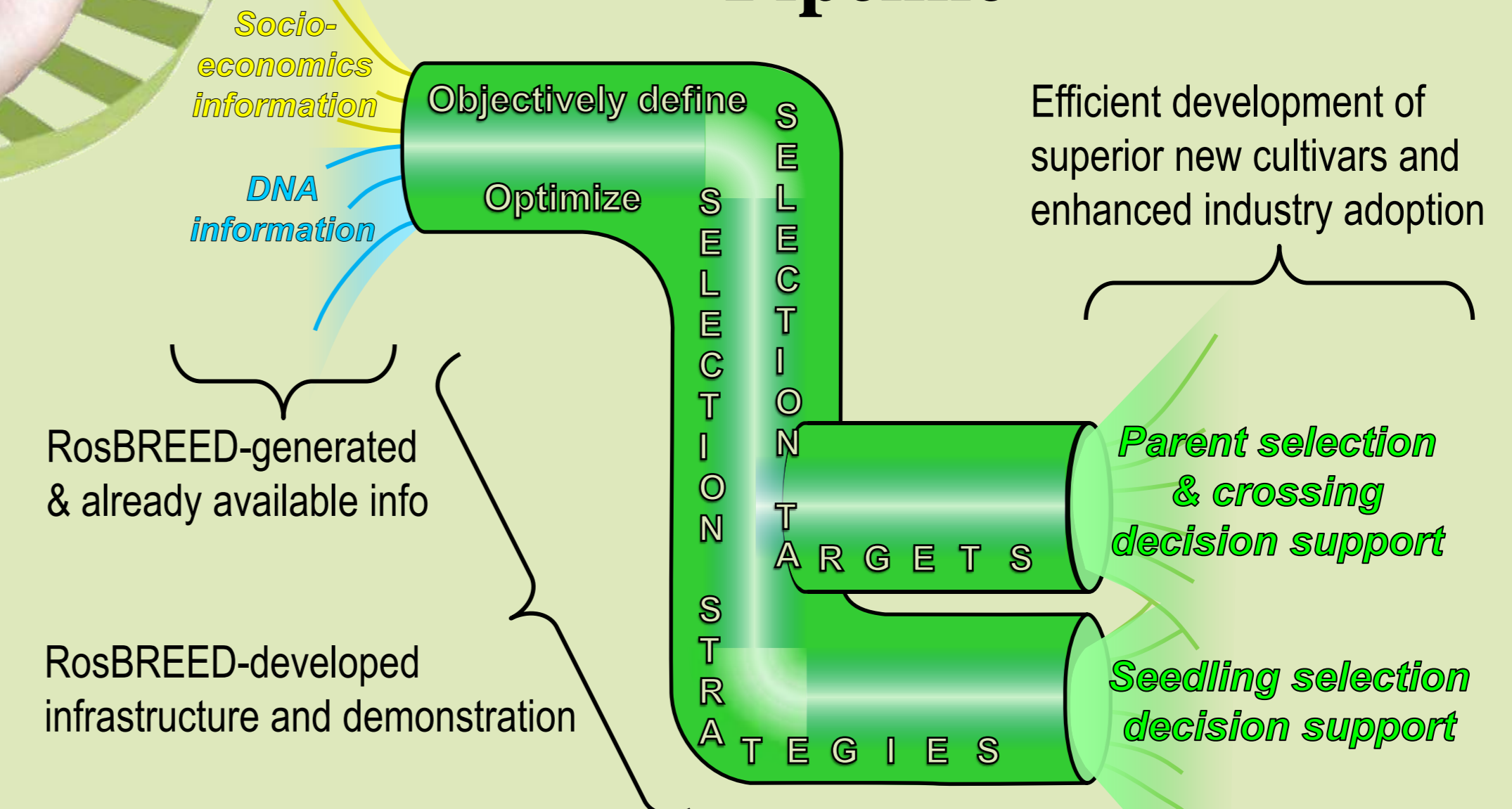
## MISSION

*We will create a dynamic, sustained program in research, infrastructure establishment, training, and outreach for developing and applying marker-assisted breeding based on improved knowledge of industry value and consumer preferences to accelerate and increase the efficiency of rosaceous cultivar release and successful cultivar adoption.*

## The RosBREED Approach

We are establishing a sustainable resource infrastructure to **enable any breeding program** following this approach to integrate the outcomes of genomics research into routine breeding operations, providing **objective decision support**. While RosBREED activities include identification and validation of many high-impact genetic tests, the Pipeline being established is designed to channel any reported marker-locus-trait association into breeding program operations, now and in the future.

## The Marker-Assisted Breeding Pipeline



## Objectives and Activities

- Socio-Economics:** Enhance the likelihood of new cultivar adoption, enlarge market potential, and increase consumption of rosaceous fruits by using socio-economic knowledge of stakeholder values and consumer preferences to inform breeding
- Genomics:** Establish sustainable technical infrastructure for an efficient MAB Pipeline in Rosaceae, including crop-specific SNP genome scan platforms for breeding-relevant germplasm exploiting the shared ancestry of Rosaceae crops
- Breeding Information Management System:** Integrate breeding and genomics resources by establishing a user-friendly U.S.-wide standardized statistical framework and breeding information management system
- Marker-Assisted Breeding Pipelining:** Implement MAB in core RosBREED breeding programs with a common focus on fruit quality traits
- Outreach:** Enhance sustainability of cultivar development by transferring MAB technologies to the public and private community of U.S. Rosaceae breeders through training current and future breeders as well as engaging the production, processing and marketing sectors, allied scientists, and consumers

**4 years**  
(Sep 2009 – Aug 2013)

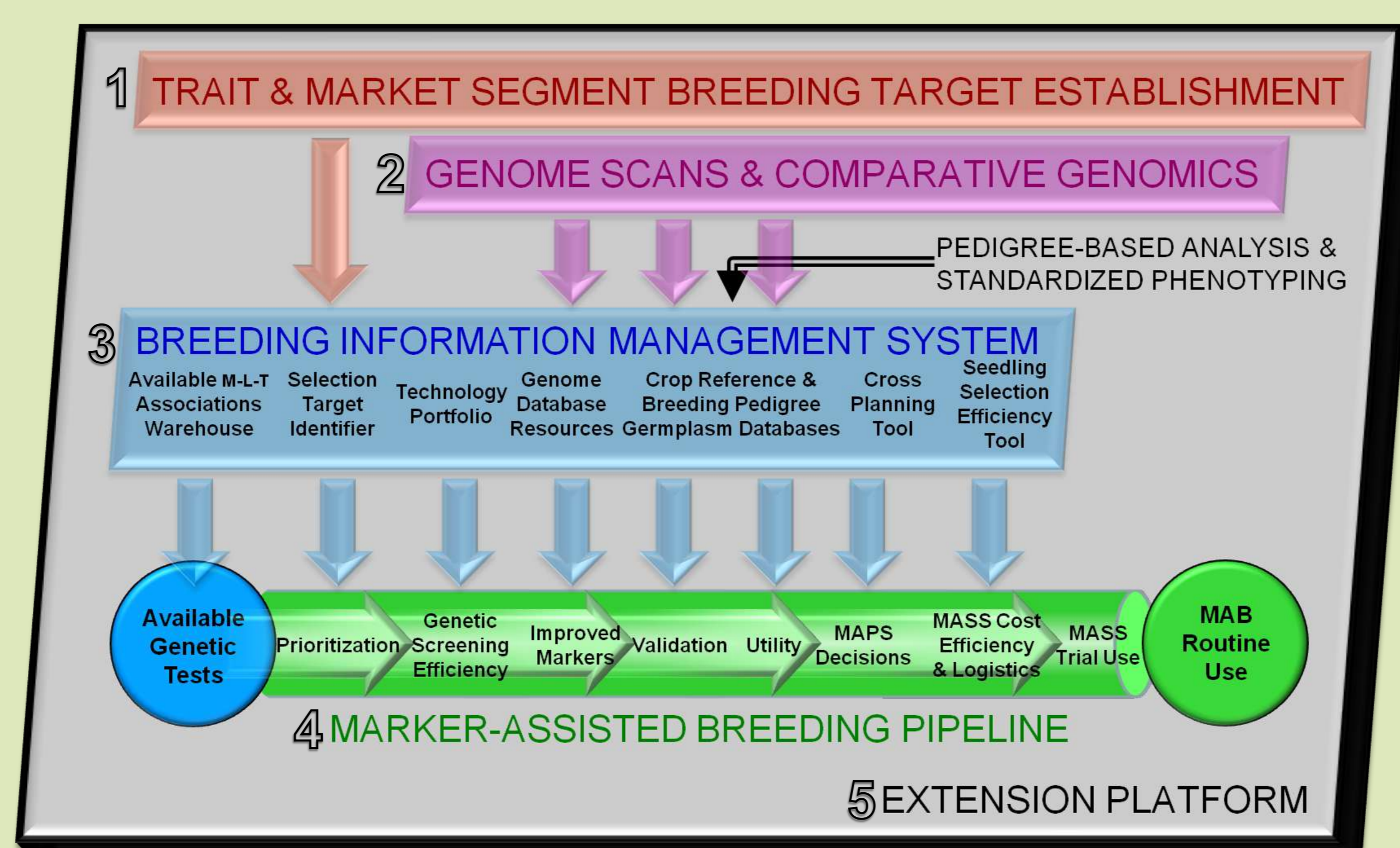
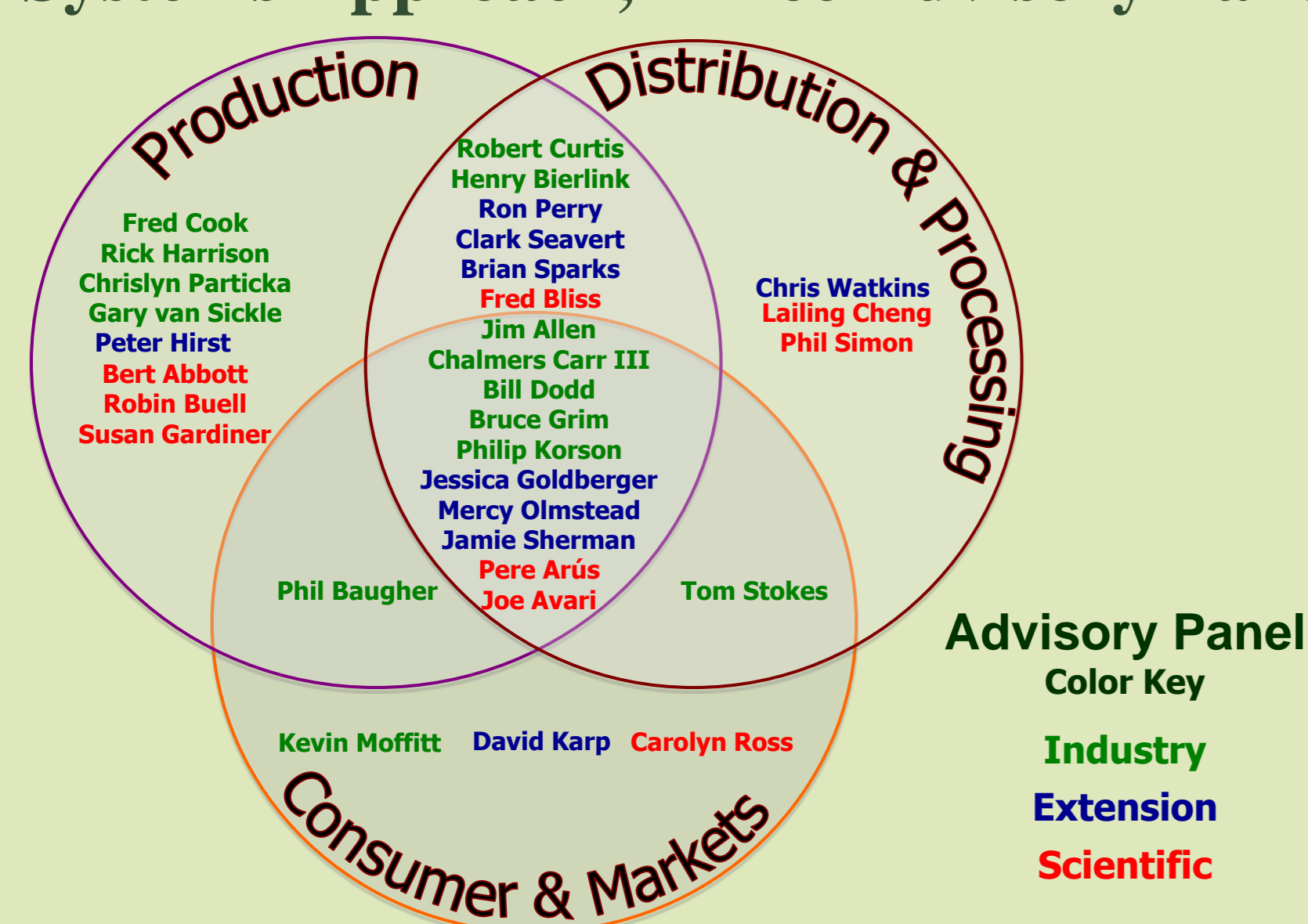
**US\$14.4 M**  
grant funding  
(\$7.2 M federal,  
\$7.2 M in-kind)

## Teams (Team Leaders)

- (all) **Breeding** (Jim Luby)
- (1) **Socio-Economics** (Chengyan Yue)
- (1,5) **Industry** (Jim McFerson)
- (2,3) **Genomics** (Dorrie Main)
- (2,4) **Genotyping** (Nahla Bassil)

- (3) **Breeding Information Management System** (Gennaro Fazio)
- (4) **Marker-Assisted Breeding Pipeline Implementation** (Cameron Peace)
- (5) **Extension** (Cholani Weebadde)
- (5) **Evaluation** (Michael Coe)

## Systems Approach, Three Advisory Panels



## International Network of Participants

