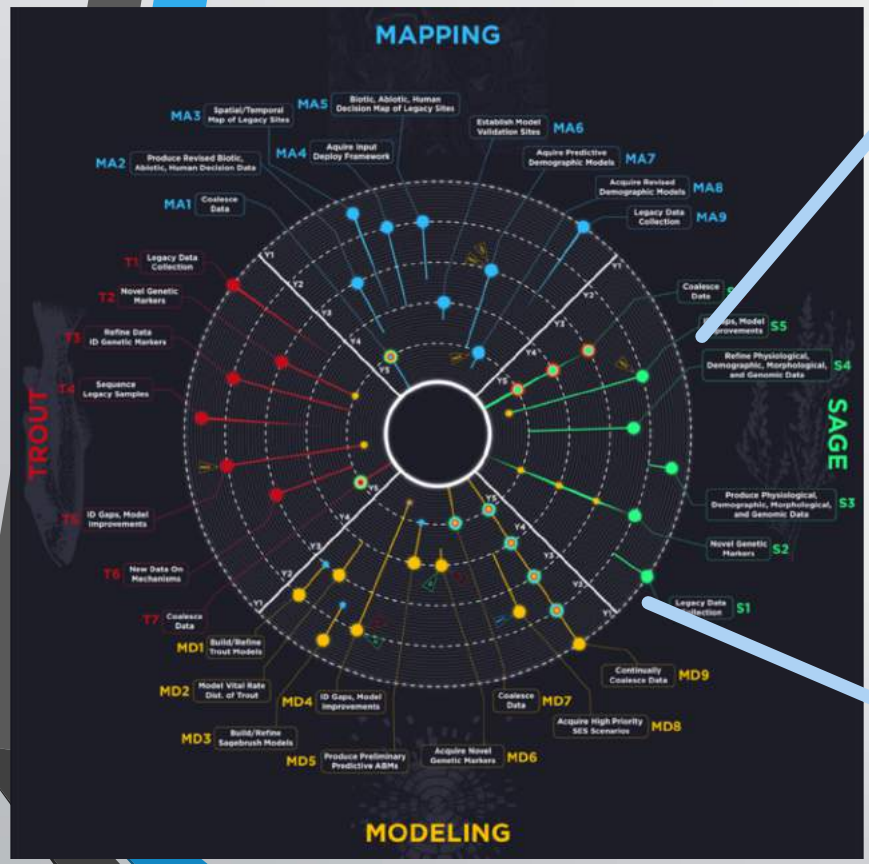
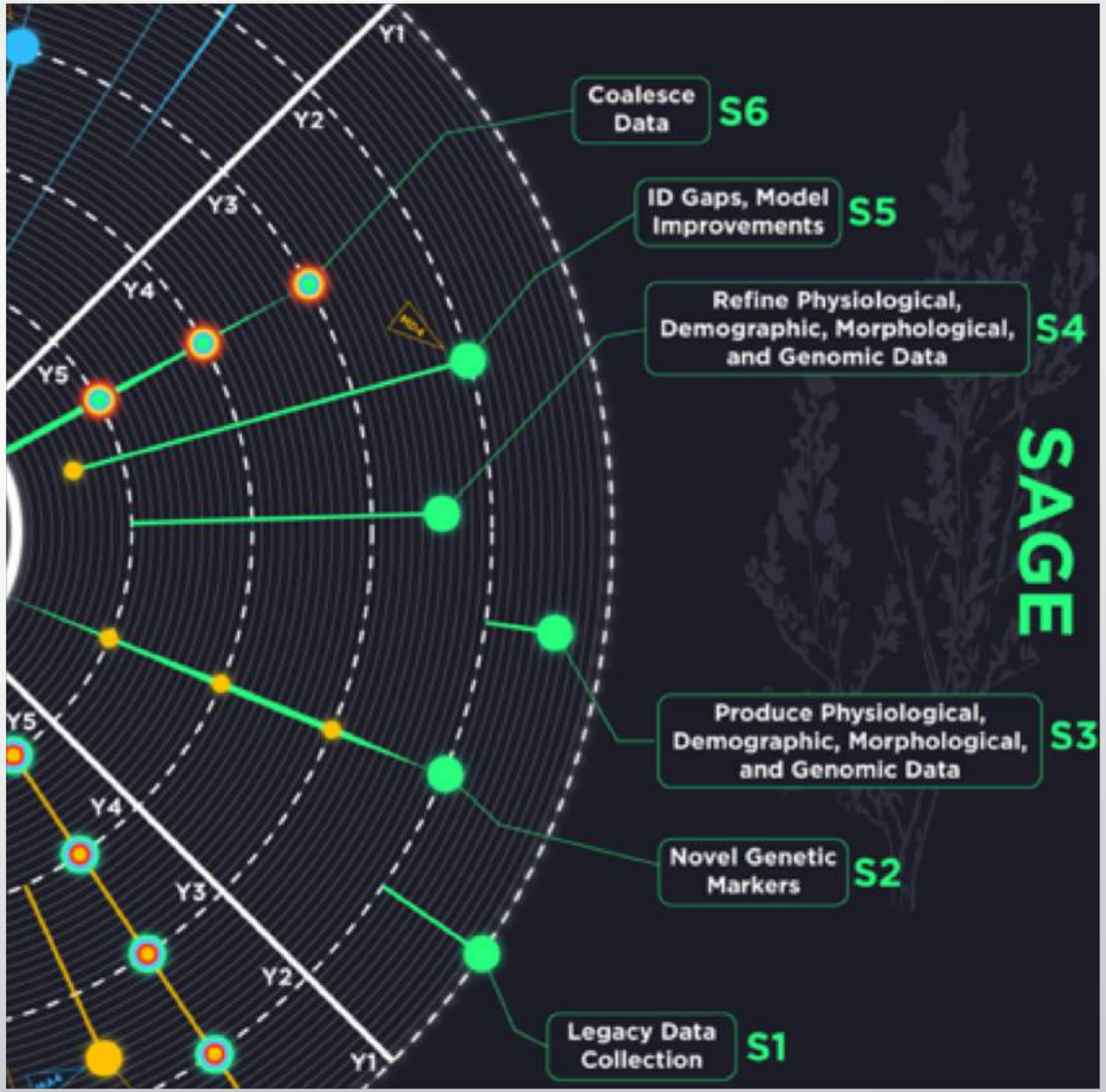
Objective 2: Mechanisms

Sagebrush

IDAHO EPSCoR

GEM3 Genes by Environment Modeling · Mechanisms · Mapping


MAPPING
MA1
MA2
MA3
MA4
MA5
MA6
MA7
MA8
MA9
T1
T2
T3
T4
T5
T6
T7
TROUT
S1
S2
S3
S4
S5
SAGE
MD1
MD2
MD3
MD4
MD5
MD6
MD7
MD8
MD9
MODELING


Y1
Y2
Y3
Y4
Y5
Coalesce Data
S6
ID Gaps, Model Improvements
S5
Refine Physiological, Demographic, Morphological, and Genomic Data
S4
SAGE
Produce Physiological, Demographic, Morphological, and Genomic Data
S3
Novel Genetic Markers
S2
Legacy Data Collection
S1

- **Research Question:** Does genetic variation differ among shrubs of different seed-source locations that translates to differences in adaptive capacity to changing environmental conditions?

- **Overall Goal:** Quantify genotypic X phenotypic mechanisms in common gardens that translate to adaptive capacity of populations,

  in order to

  Provide estimates of G, E, GxE parameters for models

  - G = additive genetic variation, E = random environmental effects, and GxE = gene X environment effects (i.e., phenotypic plasticity)

IDAHO EPSCoR

GEM3 Genes by Environment Modeling · Mechanisms · Mapping

Overall Strategy

- Objective 1: Construct a model genome for sagebrush.
- Objective 2: Measure variation in genotypic and phenotypic responses of shrubs to temperature change (controlled manipulations) in common gardens, due to seed-source-origin

Sagebrush Genomics

- Activity 1: **Generate a draft whole genome for *A. tridentata* subsp *vaseyana***
  - Task 1: Create a community for advancing Whole Genome Sequencing of non-model species
  - Task 2: Generate a draft whole genome sequence

Sagebrush Genomics

- Activity 2: **Utilize genome sequence to identify functional and neutral genetic markers for subspecies and cytotypes of sagebrush**
  - Task 1: Identify and validate functional genetic markers from plants in sagebrush
  - Task 2: Identify and validate neutral genetic markers for assessing demographic processes (e.g., gene flow) in sagebrush

Sagebrush genome X phenome

Identify GxE parameters to explain phenotypic responses of organisms to temperature change

- Activity 3a: **Genotypic expression in common gardens**
  - Task 1: Identify experimental and sampling scheme for linking gene expression and environment
  - Task 2: Investigate role of alternative splicing on phenotypes

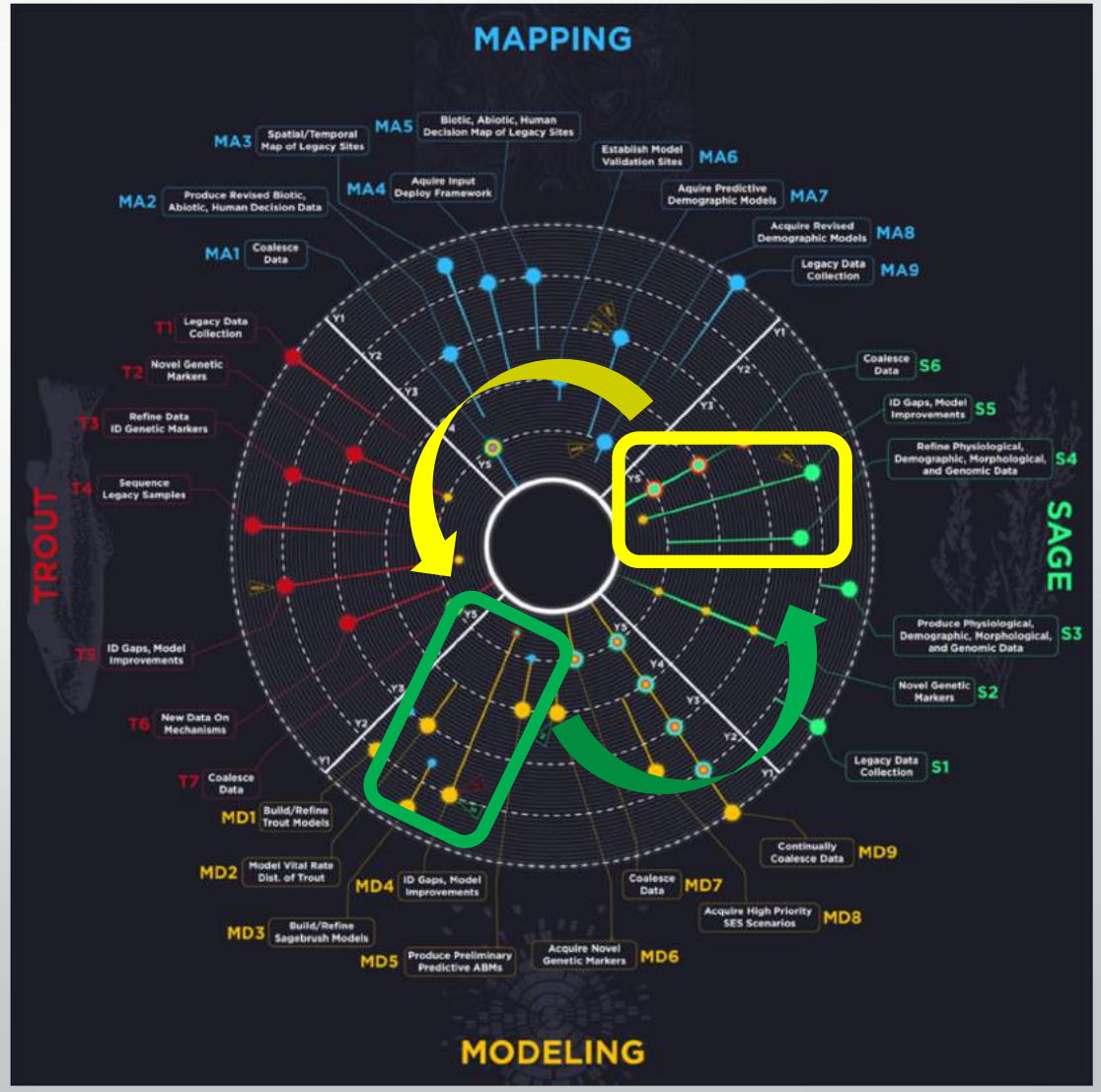
Sagebrush genome X phenome


M. Germino and fellow USGS scientist

- Activity 3b: **Phenotypic expression in common gardens**
  - Task: Quantify phenotypical (=physiological, morphological, phenological and demographic) variation in gardens
  - Task: Quantify phenotypic plasticity in sagebrush in gardens (and test sites)

Integration with modelers and mappers

- Work iteratively with modelers and mappers
- We provide modelers/mappers with data; they tell us what data they need as models develop



Questions?