

Subprogram 2: Comparative genomics for gene discovery

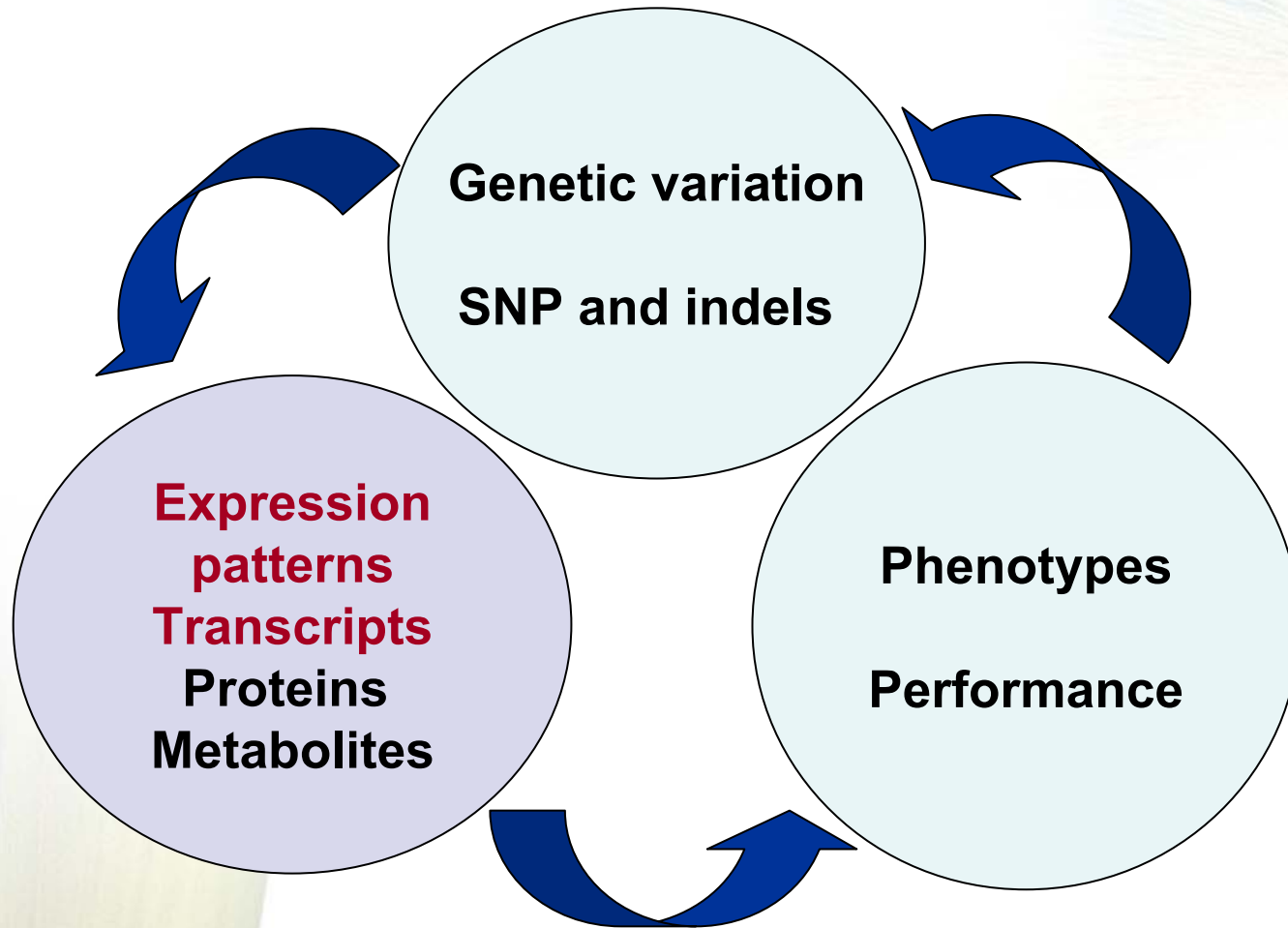


- Acquisition of genetic resources and capacities
- Development of comparative maps *within and between* crop species (increasingly based on gene contents)
- Assignment of genes and pathways to phenotypes
- Validation of genes and pathways

Framework and Objectives

- Technical platform and tools for comparative genomics and gene discovery
- Find genes to alleviate production constraints (stress) in difficult environments
 - “cheapest” and most efficient ways
 - Leverage existing resources
 - Invest if see significant payoffs

Connecting genomic variation with phenotypes and performance

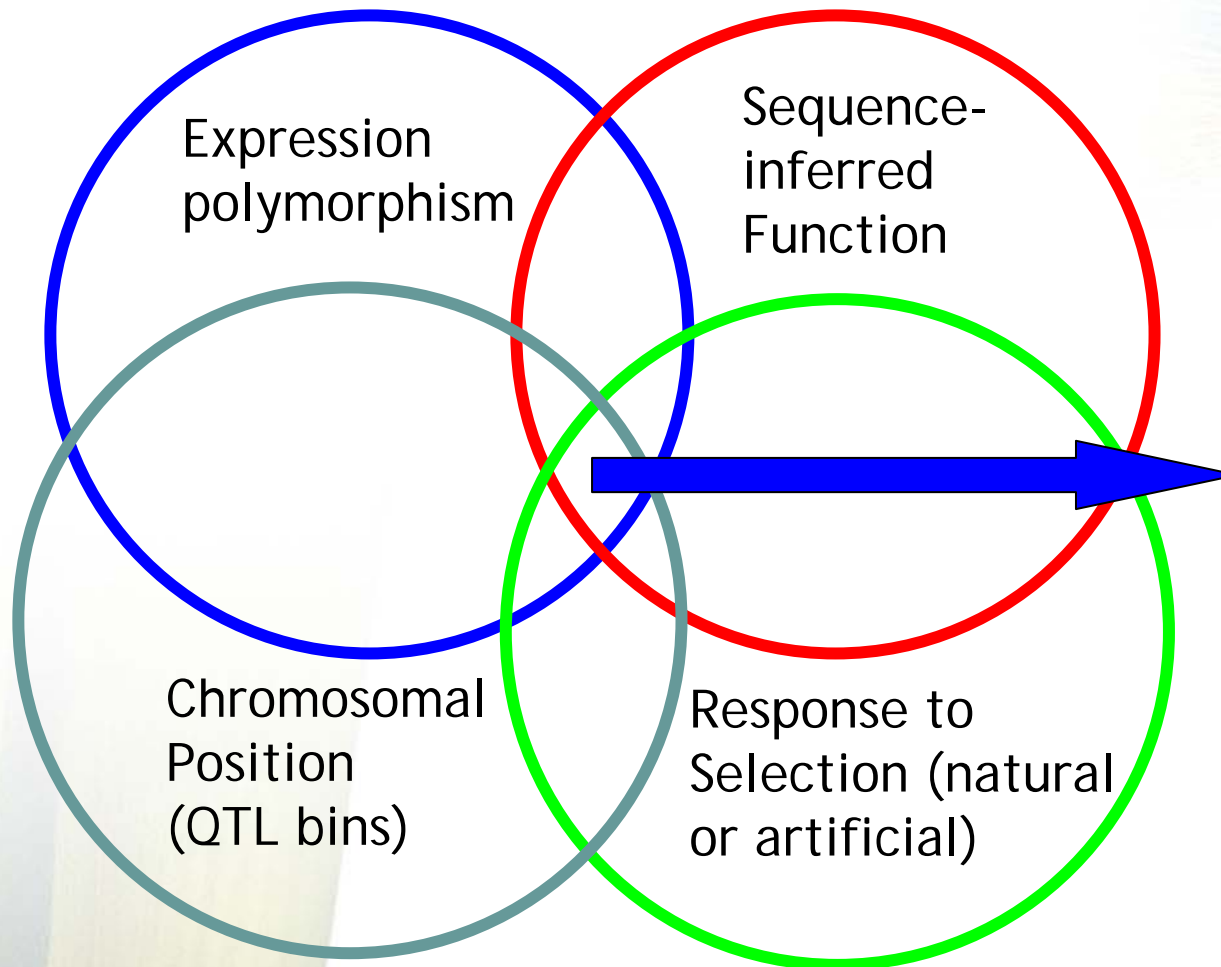


Evolving subprograms



- SP1, 2 and 3 are increasingly integrated
- Gene discovery revolves around field-proven materials—with good phenotypes

4-Ring Circus model of gene discovery



- **Germplasm variation (SP1)**
- **Cross-species comparative analysis (SP2/SP4)**
- **MAS/Pre-breeding (SP3)**
- **MAS/Phenotyping training (SP5)**

Converging evidence for candidate gene validation

Progress in SP2



- **Specialized genetic stocks and resources are shaping up**
 - bean and potato mutant stocks
 - *Musa*-rice syntenic map
- **Biological understanding**
 - Drought response physiology
 - Genetics of stress tolerance (problem soils)
 - Disease resistance (host/non-host)
- **Genome-wide view of regulation of stress response—potential shortcut to pinpoint useful genes**
- **Near-term products**
 - genes for AI toxicity tolerance
 - salt and P-deficiency tolerance
- **“Trait packages” for drought prone-environments**
 - Disease R + P-deficiency tolerance in rice
 - Disease R + AI-toxicity tolerance in maize
- **People-power to analyze data within and between projects→ true synergy**

Examples of genetic/genomic resources



- Specialized wheat stocks
- Common bean TILLING population
- True-seed potato mutant stock
- Application of global collections of rice mutants
- Musa genome sequencing and frame map construction
- EST resources
 - Pearl millet
 - Cowpea → legume project
- Pearl millet
- Cassava
- Sweet potato
- Legume species
 - groundnut
 - cowpea
 - chickpea
 - bean

Gene function

- **Genes with large effects relevant for difficult environments**
 - Phosphorus uptake
 - Salinity tolerance
 - Aluminum toxicity tolerance
- **Complex loci or chromosomal segments with cumulative effects**
 - may contain multiple candidates
 - clusters of genes with aggregated or correlated expression

Lessons Learned



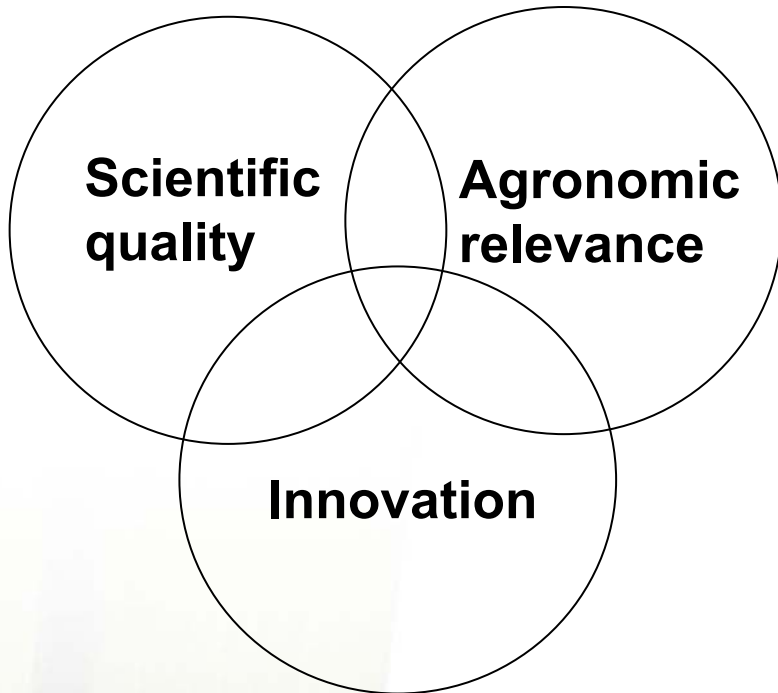
- Specialized genetic stocks useful for gene identification and breeding
 - institutional commitment for stock development, maintenance, and distribution.
 - Feed into networks or existing research consortia
- Transcriptome analysis coupled with fine-scale genotyping
 - new insights of gene regulation in stress responses.
 - bridging the gene-phenotype gap
- Each crop needs genetic resources and genomic tool kits in order to capitalize on knowledge
- Trait packages for drought-prone area
 - Linking activities between projects and across subprograms.
- Leverage resources--GCP community needs to be credible partners
- Strive for better integration of competitive and commissioned projects.

Perspective and outlook



- Successful examples of convergent approaches to narrow down worthy candidate genes
 - Relevant for determining the genes underlying complex traits.
- Breakthroughs from the whole-genome expression analysis expected
 - Strengthen integrated analysis of mapping and expression data
- Several SP2 projects close to delivering practical products
 - advanced germplasm
 - cloned genes (hence perfect markers).
- Focused investment in capacity building to ensure uptake.
- Enhancing the function of existing research and breeding networks.
- “*Patience; stay the course*”—(Gary Atlin, drought breeder)

Gene discovery in GCP



Challenge:

The right alleles or allelic combinations that add tolerance to existing breeding lines/varieties

- Interplay of forward and reverse genetics approaches
- Developing and using smart genetic populations
- Comparative biology

Many thanks to

- **GCP research community**
- **Research teams within Subprogram 2**
- **Advisors to GCP**
- **Staff members of the management team**