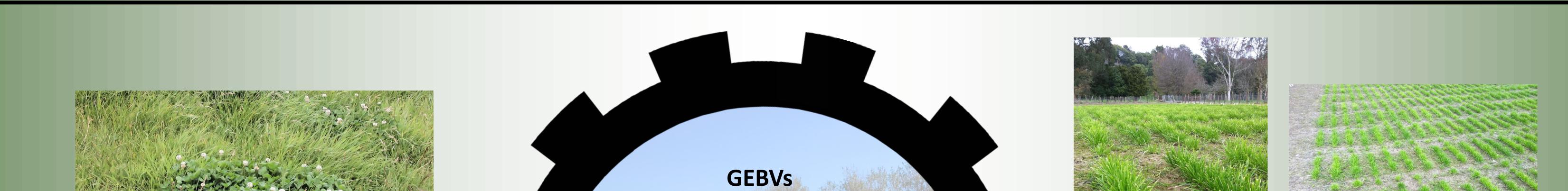# The Pastoral Genomics Plus (PG+) Program: Expanding Forage Breeding in New Zealand

www.pastoralgenomics.com

Hoyos-Villegas, V*., Barrett, B., Cao, M., Crush, J., Faville, M.J., Ghamkhar, K., Griffiths, A., Hussain, S.W., Jacobs, J.M.E., Jahufer, Z., Nichols, S., Conner, A.J

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Pastoral Genomics

agresearch

Breeding Platform

GEBVs
Assemble necessary data resources to establish and deploy Genomic Selection indices in perennial ryegrass and white clover breeding populations with sector partners.

Andrew Griffiths   Marty Faville

Phenomics
Improve the cost-effectiveness of in-field phenotyping, which is currently the rate limiting step in development and deployment of forage genomic selection, to enhance system efficiency.

Kioumars Ghamkhar

Simulation
Develop a robust Forage Breeding Simulator with interactive biophysical and economic model linkages, used to guide, forecast and optimize genetic gain targets and novel breeding strategies including Genomic Selection, in context of NZ pastoral biophysical and economic conditions.

Zulfi Jahufer   Valerio Hoyos-Villegas

GBS and Compute
Establish and improve essential logistics, statistical, and agreements infrastructure to enable the Forage Genomic Selection initiative to deliver to pastoral and seed industry specification.
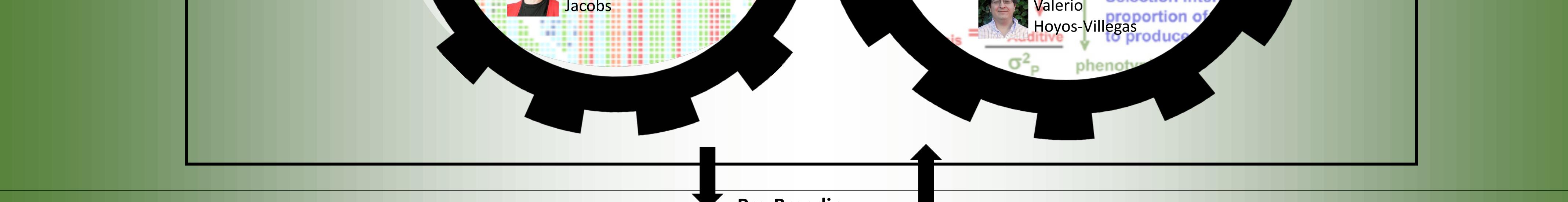
Jeanne Jacobs

Rate of Gain
Gather evidence to document and monitor the relative efficacy of forage genomic selection compared with other breeding strategies, in terms of rate and efficiency of improvement to sector agreed traits as expressed in the New Zealand Forage Value Index or related mechanism.

Valerio Hoyos-Villegas

Inputs (left)
- Training population data
- Germplasm
- Population-specific data
- Model recalibration data
- Existing trait genetic structure background data

Outputs (right)
- Genomic-Estimated Breeding Values
- Refined GS models
- High-throughput phenotyping tools and models
- Genotype x environment interaction information
- Refined genetic structure information

Pre-Breeding

This work will deliver new knowledge and novel clover and grass germplasm to forage plant breeders before 2020 through a pipeline of trait identification, introgression, and proof of function, exploiting valuable nutrient use and stress traits in the primary and secondary gene pools of white clover and ryegrass. Genomic Selection methods (Impact Statement 1), genetic analysis and allele mining will be applied selectively to the germplasm to elucidate the source and genetic control of key traits and, in the medium term, to facilitate faster and wider plant screening. Maximum use will be made of all experimental populations to pyramid benefits into a narrow range of pre-commercial germplasm.

Shirley Nichols   Jim Crush   Valerio Hoyos-Villegas