



Development and Deployment of Genomics Tools by North American Limousin Foundation



Objectives

- Develop 50K prediction equation suitable for estimation of Molecular Breeding Values (MBV) for Limousin and LimFlex (hybrid) animals
- Use 50K imputed genotypes from LD panel to reduce cost to breeders
- Augment EPDs with MBV
 - NCE
 - Interim Procedures
 - Use Kachman method to weight EPD by MBV using accuracy values of each



MBV Prediction

- Develop 50K prediction equation suitable for estimation of Molecular Breeding Values (MBV) for Limousin and LimFlex (hybrid) animals
 - Using NBCEC production pipeline (GenSel) at Iowa State and GeneSeek
 - Resource populations: ~2,300 PB and FB Limousin (MU), >800 Angus (NBCEC), ~200 LimFlex (NALF and GeneSeek)
 - MBV for all traits in NCE
 - Early results suggest correlations and % genetic variance explained by panel similar to Angus and Simmental
 - Ongoing development of LD panel (GGP) imputation pipeline to produce imputed 50K genotypes



Commercialization

- Fall/Winter 2012
- Genotyping at GeneSeek
 - Initially via Illumina Bovine SNP50
 - Later via GGP (~9K)