



Projet SELGEN 2015-2017: Breed2Last

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Projet SELGEN 2015-2017: Breed2Last

Optimal selection and mating accounting for non-additive genetic effects, genome diversity and Mendelian sampling terms

Context:

- Genome-wide evaluation (GWE) is a disruptive methodology with potential of attaining high accuracies at short generation intervals.
- Last decade has seen a mainstream GWE research focused on factors affecting prediction accuracy, like estimation methods, data integration and design of training populations.
- Comparatively little has been done on the impacts that this extra accuracy might have on the genetic diversity at whole genome scale, on ways to use the wealth of genomic information to reduce these impacts, or how to use efficiently MS variation over the long term.
- There are solutions from the pedigree-based era to optimize breeding for maximum gain over the long-term (optimum contributions), but these rely on average information, and thus variation across markers is neglected when fitting these solutions.

Objectives and approaches:

- The general objective here is to devise a breeding tool to improve coherently long-term gain and diversity management with GWE, by accounting explicitly for the available marker information across genomes in the candidate population.
- We will use quantitative genetics theory, computer simulations and demonstrations via proof-of-concept in poplar, maize and oil palm, for which mating is a key element in their breeding (see species table).
- Three developments will be integrated: (a) GWE models with explicit non-additive components for predicting crosses; (b) gain prospections (simulations) through mate selection while observing diversity and MS terms across genomes; (c) imputation, expected to act synergistically with the other two previous developments.

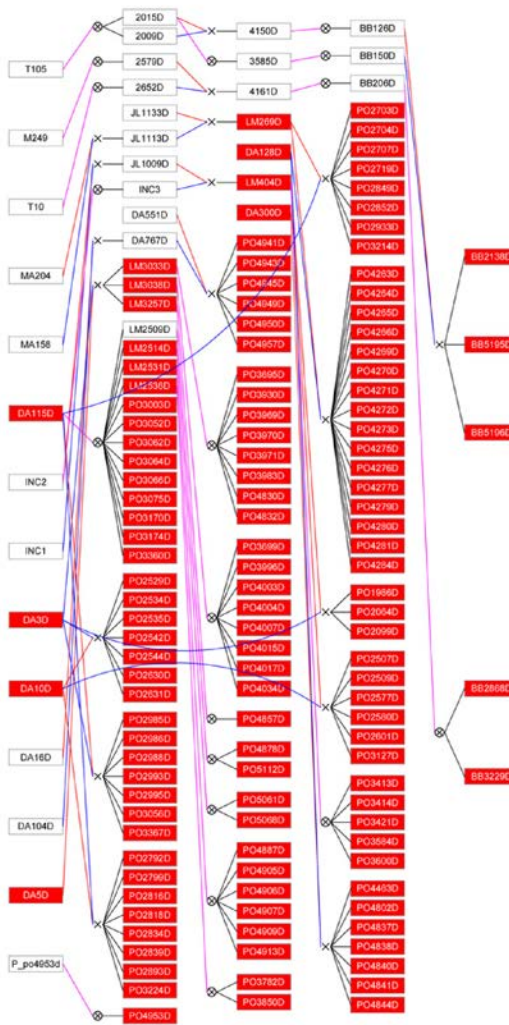


hybrid *versus* parental maize ears

Differences and complementarities of the case studies:
Summary of major characteristics of the studied species and scientific questions

| | Maize | Oil palm | Poplar |
|------------------------------------|--|---|---|
| Major characteristics | | | |
| Biology | Allogamous monoecious annual flowering | Allogamous monoecious Flowering after 3-4 years | Allogamous Dioecious Flowering after 6-10 years |
| Genome size | 2.5Gb | 1.8 Gb | 500Mb |
| LD | +++ | + | - |
| Diversity | +++ (b/ lines), - (w/ lines) | -- | +++ |
| Product of selection | Hybrids between lines | Hybrids | Cloned hybrids |
| Scientific questions | | | |
| Imputation | | X | X |
| GWE with additive/dominant effects | X | X | X |
| Diversity & MS management | X | X | X |

oil palm fruits and breeding pedigree with small Ne



poplar plantations and peeled veneer for packaging



Partners:

The group of partners involves a very comprehensive set of expertise and competences: quantitative genetics, modelling, programming, statistics, genomics and breeding for the three case study species.

P1, P2 & P4: breeding and genomic experience in the species, bring the needed expertise and data for the proof-of-concept phases, developed simulation tools focused on the optimization of breeding. **P1** authored and **P5** perfected tool METAGENE for forest tree species. **P2** authored tool OPTIMAS to optimize mating and selection in Marker-assisted breeding schemes. **P3** brings expertise in quantitative genetics theory and optimization of breeding schemes, and authored tool quantiNEMO. **P6** brings expertise in genome research for poplar case study. **P7** expertise in phasing and imputation approaches (Alphaphase), experience in GWE in animal breeding.

| N° | INRA Unit number | INRA Centre | Division | Main Researchers involved |
|----|-----------------------------------|--------------------|---------------------|---|
| 1 | UR 0588 AGPF | Val de Loire | EFPA | Leopoldo Sanchez, Catherine Bastien, Vincent Segura, Odile Rogier, Véronique Jorge |
| 2 | UMR 0320 GV | Versailles-Grignon | BAP | Laurence Moreau, Alain Charcosset |
| 3 | UMR 1313 GABI | Jouy-en-Josas | GA | Frédéric Hospital |
| 4 | UMR 1334 AGAP | Montpellier | BAP | David Cros |
| 5 | UMR 1345 IRHS | Angers-Nantes | BAP | Hélène Muranty |
| 6 | UMR 1165 URGV | Versailles-Grignon | BAP | M. C. Lepaslier Patricia Faivre-Rampant (currently at URGV she will join the EPGV in January 2015) |
| 7 | University of Edinburgh, Scotland | Roslin Institute | Genetics & Genomics | John Hickey, Gregor Gorjanc |

N° 7 is an external partner.

Impacts:

Bredtolast is expected to impact some ongoing large projects (FP7 ProCoGen, ANR SyBioPop, FruitBreedomics, ATP SEPANG, PalmElit GS2, IA Amaizing, SAMMCR), by providing tools for more efficient long-term breeding and by demonstrating novel aspects of GWE.

Budget:

88K€, 130 ETP / 3 years
1 PhD thesis associated to the poplar case study (funds not comprised in forecited budget)

Coordinator:

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