



HAL
open science

Performance of a multi-species-plant illumina beadchip

Marie-Christine Le Paslier, Aurélie Berard, Aurelie Chauveau, Elodie Marquand, Anne Boland-Auge, André Eggen, Dominique Brunel, Patricia Faivre-Rampant

► To cite this version:

Marie-Christine Le Paslier, Aurélie Berard, Aurelie Chauveau, Elodie Marquand, Anne Boland-Auge, et al.. Performance of a multi-species-plant illumina beadchip. PAG XXIV - Plant and Animal Genome Conference, Jan 2016, San Diego, United States. 2016, PAG XXIV - Plant and Animal Genome Conference. hal-01301786

HAL Id: hal-01301786

<https://hal.science/hal-01301786>

Submitted on 12 Apr 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Performance of a Multi-Species-Plant Illumina BeadChip



EPGV : Etude du Polymorphisme des Génomes Végétaux / Study of Plant Genome Polymorphism

Marie-Christine Le Paslier¹, Aurélie Bérard¹, Aurélie Chauveau¹, Elodie Marquand¹, Anne Boland-Augé², André Eggen³, Dominique Brunel¹ and Patricia Favre Rampant¹

1 - INRA, Unité EPGV - US1279, CEA-Institut de Génomique / Centre National de Génotypage, F-91057 Evry, France

2 - CEA-Institut de Génomique / Centre National de Génotypage, F-91057 Evry, France

3 - Illumina, EMEA-Ag, San Diego, CA, USA

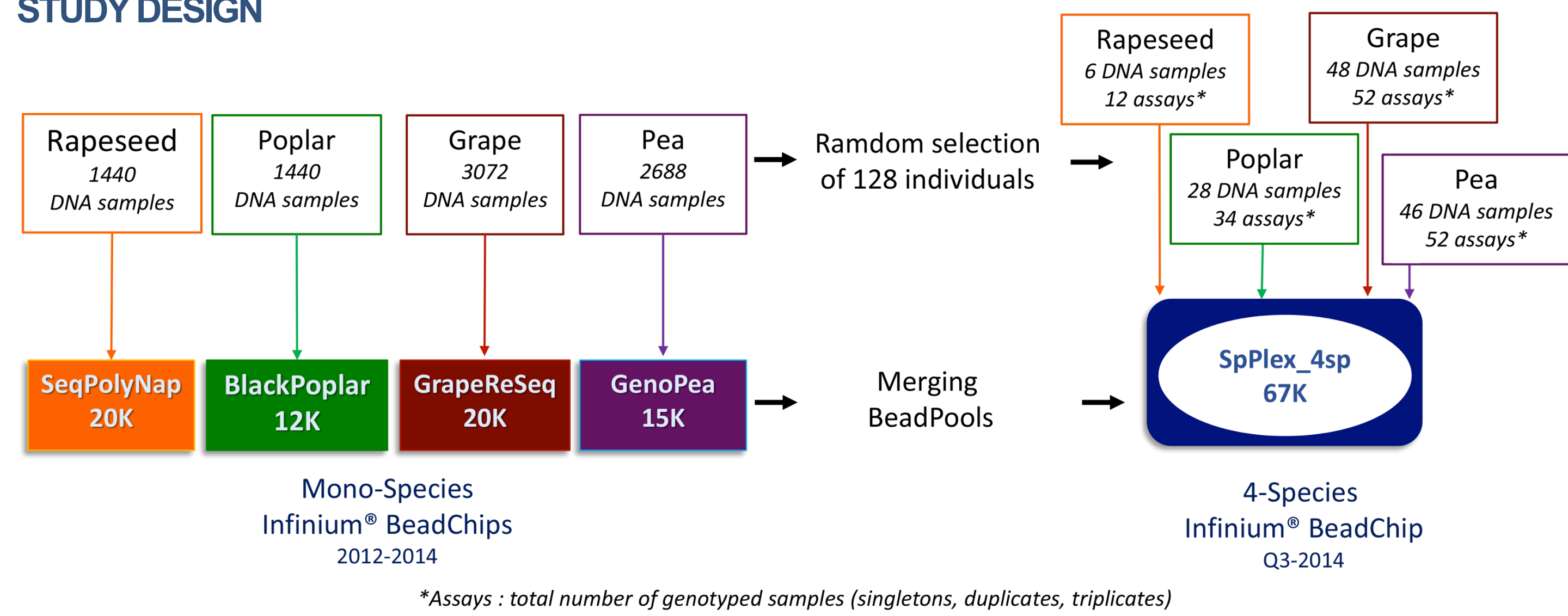
Since mid-2005, Illumina Infinium® genotyping arrays provide data with good accuracy for thousands of SNPs (single nucleotide polymorphism) in thousands individuals for many organisms including plants. These extensive data used in large studies gave new insight in population and molecular genetics. Nevertheless, flexible high density genotyping tools at reasonable costs are still to be developed. Low cost genotyping assays would allow many applications including control of individuals, marker assisted management and genetic approaches in species where molecular developments have a comparatively low value relative to the cost of SNP arrays. The initial cost and/or the minimum sample number requirement are limiting factors for developing a new genotyping tool. An add-on option on already existing product gives a first opportunity to reduce the cost of a beadchip. Designing a multi-species array could be another alternative to increase the number of SNPs and decrease the minimum number of samples for each species, reaching lower genotyping cost assay per species.

DESCRIPTION

To get a lower cost genotyping, animal and plant scientists are already using genotyping on a 2-species beadchip : they choose a commercial cost effective species-LD array and use the add-on option for SNPs of their species. No doubt that a such beadchip gives good results.

For the first time ever, this study evaluates and validates the genotyping accuracy of a 4-species plant beadchip.

STUDY DESIGN



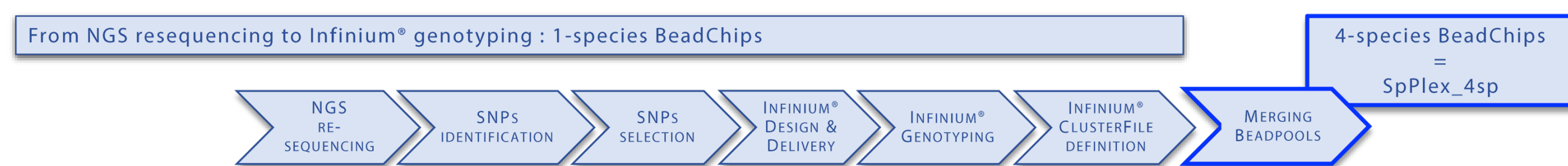
4-SPECIES BEADCHIP DESIGN

An Infinium® multi-species beadchip, SpPlex_4sp, was constructed by merging 4 independant existing beadpools previously designed to genotype rapeseed, poplar, grape and pea individuals in the frame of the projects SeqPolyNap, BlackPoplar, GrapeReSeq and GenoPea respectively.

These 4 mono-species beadchips were developed between 2012 and 2014 either for genetic mapping or QTL identification or genetic diversity analysis. Depending on each project, the SNPs selection strategy from NGS resequencing data was defined to design a highly successful chip.

Due to the presence of same Illumina codes in the 4 existing beadpools, this 4-species chip finally comprises 54 347 SNPs, i.e. 96.5% of the total of markers of the 4 mono-species chips.

Characteristics and performances of 1-species and 4-species beadchips



Project	NGS Re-seq	Infinium® Beadchip	Infinium® Beadchip	Infinium® Design	Infinium® Deliver	Infinium® Success	Infinium® Deliver
Coordinator	Grants	Sample #	Application	Name_Kbeads Sample #	SNPs #	SNPs # %	SNPs # % vs 1-species
SeqPolyNap B.Chaloub, INRA	ANR-09-GEMN-021	5	Genome A/C scaffolds anchoring	SeqPolyNap_20K 1440 samples	17 607	15 932 90%	13 267 83%
BlackPoplar P.Favre Rampant, INRA	EU-FP6-16322 : EVOLTREE project EU-FP7-211868 : Novotree project	52	QTL & Diversity analysis	BlackPoplar_12K 1440 samples	10 331	9 127 88%	8 259 90%
GrapeReSeq A.F.Adam Blondin, INRA	ANR-08-KBBE-008	41	Diversity analysis	Grape_20K 3072 samples	20 000	18 071 90%	12 815 71%*
GenoPea J.Burstin, INRA	ANR-09-GMNE-026	16	Genetic map & Diversity analysis	GenoPea_15K 2688 samples	15 000	13 204 88%	13 156 99.6%**

**33% to 67% depending on RIL population

DNA SAMPLES

To validate the genotyping accuracy of the 4-species array, a subset of the same DNA samples, i.e same DNA stock tube, of each species project was used. Some of these samples were also HT-resequenced. Furthermore, 4-species array beadchip reproducibility was examined using duplicates and triplicates.

GENOTYPING & SNP ALLELE CALLING

Infinium® genotyping was performed on 7 BeadChips (24-sample BeadChip format) by following the Infinium HD Assay Ultra Protocol. Genotyping data were analysed using the Genotyping Module v1.9.4 of Illumina Genome Studio® software 2011.1.

In this study, SNP allele calling was directly generated by applying the appropriate clusterfile previously developed and related to each project and to the samples / populations specifications.

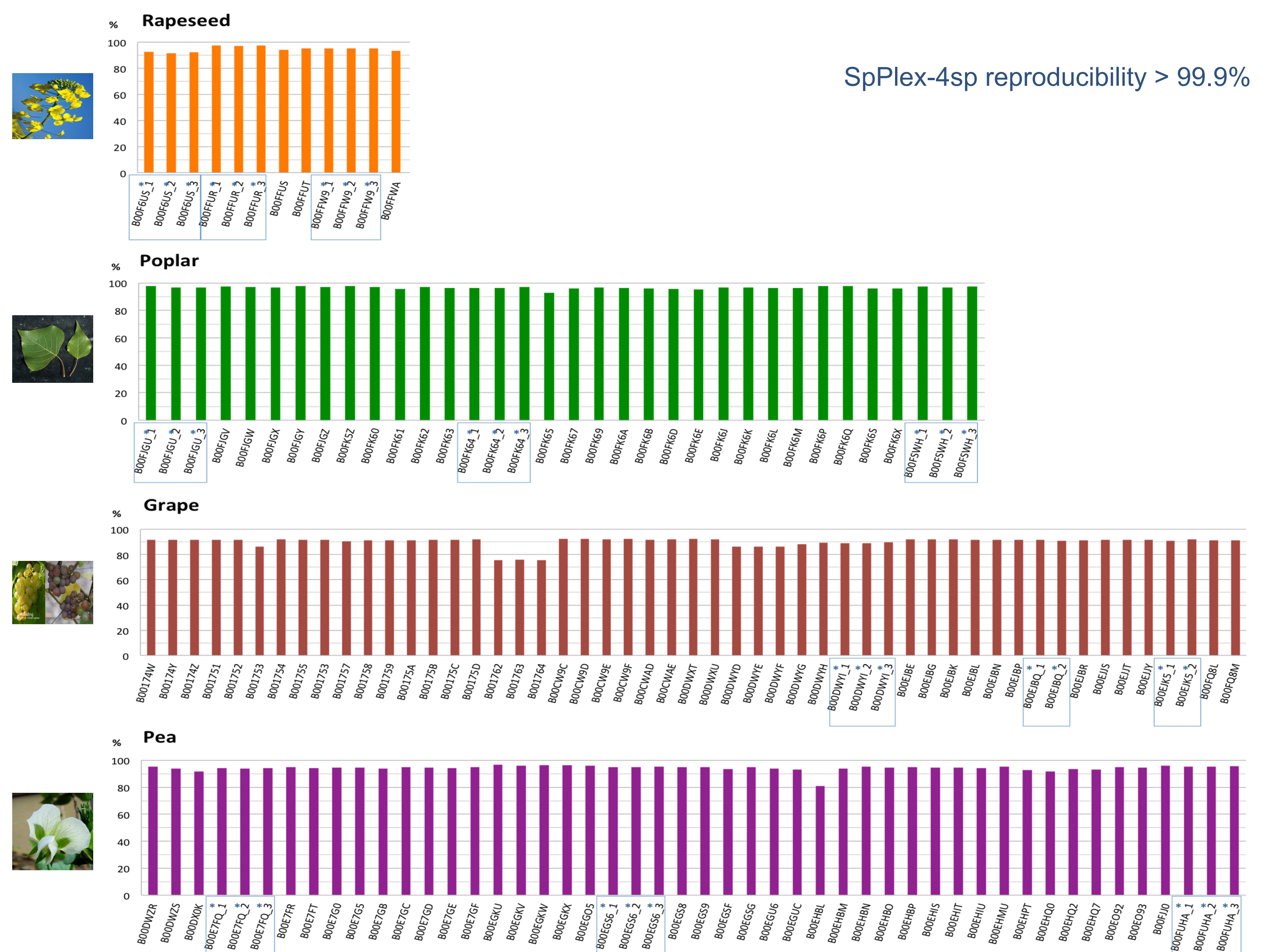
REFERENCES

- Chalhoub, B. et al.: Plant genetics. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. *Science* 2014, 345(6199):950-95
- Favre-Rampant, P. et al.: New resources for genetic studies in Populus nigra: genome wide SNP discovery and development of a 12k Infinium array. *Molecular Ecology Resources* 2015 Accepted
- Le Paslier M.-C. et al.: The GrapeReSeq 18K Vitis genotyping chip. In *Ninth International Symposium on Grapevine Physiology & Biotechnology*; La Serena, Chili. 21-26 april 2013
- Tayeh, N. et al.: Development of two major resources for pea genomics: the GenoPea 13.2K SNP Array and a high density, high resolution consensus genetic map. *Plant J.* 2015 Accepted Author Manuscript. doi:10.1111/tpj.13070

THANKS TO CEA-CNG : A. Boland-Augé group for performing DNA samples QC, M.T Bihoreau and C. Besse for providing INRA-EPGV group with access to their Infinium® platform, Y. Legros (Illumina), for helpfull advice and discussion, A. Canaguier (INRA) for design contribution, Illumina® for manufacturing and providing us this unusual Infinium® assay.

RESULTS

% of SNP allele calling consistency for each sample : 4-species vs 1-species array



CONCLUSION & PERSPECTIVES

These results indicate a high consistency of SNP allele calling between these 4-species and 1-species beadchips. For both arrays, the performances are similar : high reproducibility (group of samples indicated as * on the graphs) and high genotyping accuracy.

The data showed high sample success and genotyping calls rates, except for 3 grape and 1 pea DNA samples : manual inspection of their results indicates that refining the clusterfile will increase the genotyping accuracy of these individuals.

For rapeseed, these preliminary results will be confirmed by increasing the number of samples (ongoing).

Multi-species arrays increase efficiency, cost effectiveness in experiments and decrease the sample order constraints (minimum ordering 1152 samples).

This would be very effective for non model species, systematic identity test and segregation analysis.

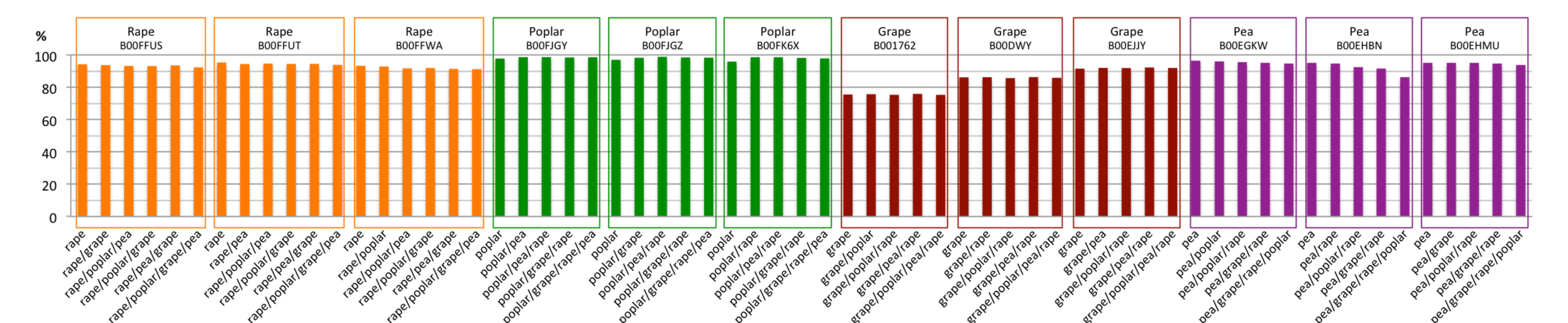
Our results strongly support the development of further multi-species beadchips.

Take home message : think to build common genomic tools beyond the needs of a single species. The multi-species chips can represent a great and cost effective resource for plant genomic applications.

MORE FOR FUN : MIX DNAs & SAVE MONEY !

We performed also genotyping of DNA mix : 2 → 4 different DNA species.

Consistency of SNP allele calling for DNAs mix vs singleton on the 4-species array



Results show a very high consistency of SNP allele calling for both high and lower quality samples (grape B001762).

SpPlex-4sp reproducibility > 99.8% for DNAs mix

Manage a such DNAs mix genotyping project could be more challenging but feel free to risk !



Plant Biology and Breeding Division
F-78026 Versailles, France



EPGV group contacts
le.paslier@cng.fr
support-epgv@cng.fr

