

P176

Diversity analysis within a collection of 1191 flint maize inbred lines using genotyping-by-sequencing

(submitted by Brigitte Gouesnard <brigitte.gouesnard@inra.fr>)

Full Author List: Gouesnard, Brigitte¹; Negro, Sandra²; Laffray, Amélie²; Glaubitz, Jeff³; Melchinger, Albrecht⁴; Revilla, Pedro⁵; Moreno-Gonzalez, Jesus⁶; Madur, Delphine²; Combes, Valérie²; Tollon-Cordet, Christine¹; Laborde, Jacques⁷; Kermarrec, Dominique⁸; Bauland, Cyril²; Moreau, Laurence²; Charcosset, Alain²; Nicolas, Stéphane²

¹ AGAP, INRA, Montpellier, France

² Génétique Quantitative et Évolution - le Moulon, INRA, Gif-sur-Yvette, France

³ Buckler Lab for maize Genetics and Diversity, Cornell University, Ithaca, USA

⁴ Seed Science, and Population Genetics, University of Hohenheim, Stuttgart, Germany

⁵ Misión Biológica de Galicia, CSIC, Pontevedra, Spain

⁶ Mabegondo Agricultural Research Centre, CIAM-INGACAL, A Coruña, Spain

⁷ Unité Expérimentale du Maïs, INRA, St Martin de Hinx, France

⁸ Unité Expérimentale Ressources Génétiques Végétales en Conditions Océaniques (UERGCO), INRA, Ploudaniel, France

Genotyping-by-sequencing (GBS) is a highly cost-effective procedure that permits the analysis of large collections of inbred lines. We used it to characterize diversity in 1191 maize flint inbred lines from the INRA collection, the European Cornfed-Flint association panel, and flint lines recently derived from landraces. We analyzed the properties of GBS data obtained with different imputation methods, by comparison with a 50K SNP array. We identified 7 ancestral groups within the Flint collection (five typically flint: Northern Flint, Italy, Pyrenees-Galicia, Argentina, Lacaune, and also Dent and Pop corn) that are in agreement with breeding knowledge. This analysis highlighted that many lines are issued from crosses between different flint ancestral groups (admixture). Approximately 200 lines also appear to be issued from crosses with dent germplasm aiming at the improvement of flint germplasm. We performed association studies on different agronomic traits, revealing SNPs associated with cob color, kernel color, and male flowering time variation. We analyzed the relationship between the haplotype diversity and the trait variation at some strong association peaks.

Funding acknowledgement: French National Research Agency (Amaizing, ANR-10-BTBR-03)