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USE OF MOLECULAR MARKERS FOR PROTECTION AND VARIETAL IDENTIFICATION: STATE OF THE ART IN ARGENTINA

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Soybean is a very important crop in Argentina and every year breeders present in INASE about 150 new applications. The number of varieties already in the national variety list is quite large (currently 1048 registered varieties). This makes, sometimes, very difficult to examine distinctness of new varieties because the number of varieties to be compared with the new ones is large. To address this problem, a project between public and private sector was carried out, with the aims of a) reduce the list of varieties that should be compared in the field (based on the model "Combining Phenotypic and Molecular Distances in the Management of Variety Collections" in document TGP/15/1 "Guidance on the Use of biochemical and molecular markers in the examination of Distictness, Uniformity and Stability (DUS)", that combines phenotypic and molecular distances), and of b) guarantee the traceability of varieties identity (PBR enforcement). For aim a), we select a set of 4004 SNPs markers distributed in the genome that represent the genetic background and yield an efficient discrimination power (set "Y"). Also we determine the molecular distance threshold and the minimum phenotypical distance threshold, selected based on a 3 year field trials, which in combination allow to select varieties that require comparison in the field. The results presented in document BMT/17/22 "Use of SNP markers for soybean variety protection purposes in Argentina" show that with 3 of minimum phenotypical distance threshold and with 0.36 of molecular distance threshold we reduce the pairs to be evaluated in the field by 55%. Regarding the validation of both thresholds, field trials were carried out during the summer of 2019, on a set of unpublished varieties and were sent for genotyping. We are currently in the process of data analysis.

In relation to aim b), based on the 858 soybean varieties that were genotyped (see document BMT/17/22) (all of them in the National List of varieties, coming from different breeding programs and covering 20 years of soybean breeding history) a set of 56 SNPs markers composed by the smallest number of markers that generates a unique DNA profile for each variety, were selected. Those markers are the most polymorphic selected on the criteria that, for a given variety pair, the difference is at least 3 SNPs. The allelic profile of this small marker set will be available for third parties.

Currently we are working to finalize the genotyping of soybean varieties registered during 2016-2019, analyzing new data together with the original data that generated the set of 56 markers to confirm this set or define a new one and developing a software to manage genotypic data and perform data analysis. In relation to other crops, we must to analyze the genotypic data obtained for cotton and rice to select a set of markers for variety traceability, and for wheat the expert's group had its first meeting in August, 2019. We hope that in the near future experts in pea and peanut will meet to start working on these species.

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