BMT/13/19
ORIGINAL: English
DATE: November 8, 2011

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

WORKING GROUP ON BIOCHEMICAL AND MOLECULAR TECHNIQUES, AND DNA-PROFILING IN PARTICULAR

Thirteenth Session
Brasilia, November 22 to 24, 2011

USE OF MOLECULAR MARKERS FOR INFRINGEMENT DETECTION IN HYBRID CROPS

Document prepared by an expert from the Monsanto Company

1. There are 3 main types of germplasm infringement in hybrid crops:

   (a) Direct use of proprietary germplasm,
   (b) Predominant derivation (resulting in EDV),
   (c) Derivation from illegally accessed proprietary germplasm.

2. For the first two types, it is relatively simple to check the hybrid fingerprint profile and test the probability that one parent is a direct use or a close derivation (suspected EDV) of a hybrid parental line. Seed companies can use thousands of SNP molecular markers to fingerprint all their inbred parental lines, as well as any competitor hybrids they wish to check for suspected infringement activity. Based on fingerprint information, it is possible to compare the hybrid profile with all inbred parents in the database and at each marker locus. It is possible to calculate the probability that a particular inbred is one of the hybrid parents by using an algorithm to test hundreds of inbred parents at thousands of marker loci.

3. For the third type of infringement, analysis of the hybrid profile is more complex. The owner of a proprietary inbred can use Line-Specific-Recombination (LSR) haplotypes as tags (or encrypted signatures of the inventor) to prove derivation from that particular inbred. About 20-25 unique LSR haplotypes can be identified per inbred line. By experience, a set of

15-20 LSR haplotypes, well distributed across the genome, would be enough for very accurate tracking of parental derivation. A probability of fit between the hybrid and the proprietary inbred profiles is estimated at each of the referenced proprietary LSR windows. For hybrids fitting multiple LSR haplotypes from a same inbred parent, a derivation probability is then estimated.

4. Today, high-density fingerprinting coupled with algorithm-based data mining is offering a dependable tool with capability to accurately detect suspected misappropriation of hybrid parents.

Pierre SEHABIAGUE _ Monsanto Company

[End of document]