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THE PROBABILITY OF RANDOM IDENTITY: A METHOD FOR MOLECULAR DATA
ANALYSIS IN VARIETY CHARACTERIZATION

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For variety identification, we use the concept of probability of random identity (PRI)
(Schuster et al., 2009): $PRI = \prod_{i=1}^{l} \prod_{j=1}^{n} P_{ij}$, where P_{ij} is the frequency of the ith allele in the jth
locus, *l* is the number of alleles per locus and n the number of evaluated loci. The product of
the allele frequencies is multiplied by 100 so that it can be expressed as a percentage. To be
considered the same varieties, two samples need to present PRI of at least 0.0001%, i.e.,
another variety can randomly present the same allele profile as the variety-specific markers
set in less than 0.0001% of the cases. The probability of exclusion (PE) was estimated as a
complement of the PRI: PE = 100% - PRI. Thus, if the molecular profile of a specific marker
set in a variety has a probability of random identity of 0.0001%, the probability of exclusion
will be 99.9999%. When this molecular profile is obtained in any pair of samples, it indicates
the probability that this identity is not random and that the samples are the same variety. To
use this estimator, one needs to know the frequency of all alleles in all evaluated markers, in a
reference population. We presented the frequency of alleles for Brazilian soybean and
Brazilian wheat (Vieira et al., 2009; Oliveira et al.; 2010, Schuster et al., 2009).

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