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ANALYSIS OF PVPD INBREDS WITH PUBLIC SNP MARKERS TO ESTIMATE EQUIVALENT EDV THRESHOLDS COMPARED WITH SSR MARKERS

Document prepared by experts from Pioneer Hi-Bred International

ANALYSIS OF PVPD INBREDS WITH PUBLIC SNP MARKERS TO ESTIMATE EQUIVALENT EDV THRESHOLDS COMPARED WITH SSR MARKERS

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1. Single Nucleotide Polymorphisms are rapidly becoming the marker of choice for many major crops, including maize. SNPs offer improved accuracy and decreased costs compared with SSRs. Most importantly, SNPs are 'platform independent'; irrespective of laboratory, chemistry or platform utilized, the resulting nucleotide allele call will be consistent. Therefore, data collected on different varieties in different laboratories and over time can be directly compared in a database system. This contrasts with SSRs where varying platforms can result in different allele calls. For example, a genetic distance calculation for EDV collected on an agarose gel system could be different to that collected on a polyacrylamide sequencing gel system using the same set of SSRs.

2. A database and resource for SNP discovery and trait dissection has been established for maize where genotype, phenotype and polymorphism data can be accessed for a wide range of maize inbreds and populations (Zhao *et al.* 2006. Nucleic Acids Res 34: 752-757: http://www.panzea.org). This database contains information for over 7,000 SNPs of which over 3,000 have successfully been used in assays. Pioneer has contributed sequences and locus information for 640 validated SNPs.

3. Pioneer outsourced marker design for a 768 public marker plex to Illumina®. These SNPs were selected to suit a wide variety of purposes and therefore to have distinguishing power across different heterotic groups, including Flints and tropicals. We selected a sub-set of these markers to characterize Pioneer's PVPd inbreds based on having expected heterozygosity values > 0.3 and good map distribution. We used this marker set to compare genetic distances of SNPs to SSRs in order to estimate equivalent EDV thresholds. Detailed information will be presented at the second session of the *Ad Hoc* Crop Subgroup on Molecular Techniques for Maize.

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