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Phylogeographic Evidence Of Crop Neo-Diversity In Sorghum

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We report here a study on sorghum, using a well characterized sample of diverse cultivars that we resequenced for portions of six genes possibly involved in grain quality variation. Our study was based on 1.7 Mbp sequence data enabling a comparison between 129 to 184 accessions of sorghum for six genes and 1008 to 3771 bp per gene. A total of 170 polymorphisms, including 141 SNPs and 29 Insertion/Deletion Polymorphisms, were recorded within a total of 11279 bp scored. We analysed the distribution of polymorphisms by comparing the area of origin of sorghum and areas where sorghum migrated in the course of domestication and subsequent human migrations. We observed an array of situations. On one hand we have polymorphisms which are distributed in agreement with a neutral hypothesis, on the other extreme we have Opaque2, for which new polymorphisms have appeared in areas outside the area of origin. This, we argue, is novel diversity which was selected by man in the course of domestication: crop neo-diversity. Documentation of the extent of crop neo-diversity is very important. In breeding it might explain how narrow-based populations can be improved in the long term; in germplasm management it implies reformatting concepts and approaches, whereby diversity is not just reduced from wild to landraces and to improved materials; it may stimulate studies which investigate patterns of diversity in regions where crops were 'adapted' by man, in the search for adaptive neo-diversity.