CYTO-MOLECULAR CHARACTERIZATION OF CHINESE CHESTNUT LINKAGE GROUP-SPECIFIC CHROMOSOMES

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Recent advances in molecular cytogenetics have made it possible to unequivocally identify individual chromosomes and to visualize the location of specific genes and/or molecular markers (of specific traits). We used molecular cytogenetics to validate the genome assembly using genetically mapped BAC clones. One to four BACs from each of the upper and lower end of each of the 12 linkage groups (LGs) were used in fluorescent in situ hybridization (FISH), to delineate the centromeric positions and identify the short and long arms of each LG-specific chromosome. In addition, ribosomal rDNA (45S and 5S rDNA) probes were used to identify their locations and LG-specific chromosomes. The chestnut chromosomes were found to be metacentric and sub-metacentric and individual LGs were assigned to each chromosome. The centromeric positions enabled to designate six of the 12 Chinese chestnut LG specific chromosomes (LG_A, LG_B, LG_C, LG_F, LG_G and LG_I) as metacentric and/or near metacentric, four (LG_E, LG_H, LG_J and LG_K) as near sub-metacentric and two (LG_D and LG_L) as clearly sub-metacentric chromosomes. The origination (zero cM) of each LG map was found to be associated with the short arm of nine LG specific chromosomes and the long arm of three chromosomes (LG_C, LG_G and LG_L). Since LG_C and LG_G re metacentric, we are only recommending that LG_L be corrected. The major 45S rDNA locus, was assigned to LG_H chromosome, and that part LG_H is missing from the linkage map. The 5S rDNA locus was found to be localized interstitially in the short arm of LG_E chromosome. The cytological positions (i.e., orientations) of all but three of the 54 BAC clones three were found to be concordant with their expected linkage map positions.