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Mining Single Nucleotide Polymorphisms from Silkworm EST Data

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We made use of 81,635 expressed sequence tags (ESTs) derived from 12 different cDNA libraries of *Bombyx mori* to identify high-quality candidate single nucleotide polymorphisms (SNPs). By PHRAP assembling, we obtained 12,980 contigs containing 11,537 contigs assembled by more than one reads. From 117 contig sequences, which were assembled by 1,576 high-quality reads base-called with PHRED, we identified 101 candidate SNPs and 27 single base insertions/deletions based on a neighborhood quality standard (NQS) of SNP. Simultaneous, we predicted that 40 SNPs in coding region (cSNPs), 26 of which were predicted to lead to amino acid non-synonymous substitutions and 14 synonymous changes. This analysis shows that expressed sequences from multiple libraries may provide an abundant source of comparative reads to dig cSNPs from silkworm genome.

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