A.C.G.M. and S.N.P

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Genomes evolve through changes in DNA sequences as a result of nucleotide modifications (substitution and in/del) and through changes in DNA organization because of chromosome rearrangements. Beyond the knowledge of plant genetic evolution, comparative maps of related species should ease future localization and cloning of genes controlling quantitative and qualitative traits of economic interest for plant breeding purposes. The development of Amplified Consensus Genetic Markers (ACGM) between species of the same taxonomic family uses PCR technology and is based on the conservation of peptide sequences and on the potential polymorphism within genic sequences. This simple methodology is effective for "sequencing without cloning" the homologous genes in the *Brassica* tribe starting from an *Arabidopsis* sequence. The presence of single nucleotide polymorphisms (SNP) within gene sequences from different rapeseed cultivars is another important point as any candidate gene could be potentially mapped, eventually using of high throughput technology. 102 couples of consensus primers *Arabidopsis thaliana* / *B. napus* / *B.oleracea* / *B.rapa* have been validated. 119 ACGM corresponding to 373 *B. napus* sequences, 166 *B. oleracea* and 173 *B. rapa* will be available on the Genoplante web site. For 93 ACGM (274 rapeseed sequences), 168 « gene specific » primers were validated by the sequencing of one genotype. Sequencing was performed on 20-24 genotypes for 90 rapeseed genes. 47 sequences (52%) present SNPs. With a mean sequence length of 448 bps, 301 SNPs and 139 haplotypes were found. This approach provides a valuable set of non-anonymous genetic markers for comparative mapping studies, comparative mapping of QTLs and search for candidate genes. Further it contributes to a better understanding of the conservation of peptide sequences and the synteny between species that are complicated by diverse genome amphidiploidisation.