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FINAL ABSTRACTS GUIDE
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A PRELIMINARY CONSENSUS GENETIC MAP FOR ROSE

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Four genetic linkage maps were constructed for tetraploid and diploid roses using amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) markers. The two maps constructed for parents of tetraploid *Rosa hybrida* family 90-69, 82-1134 and 86-7, consist of 20 and 14 linkage groups and cover 920 and 770 cM, respectively. Two additional maps constructed for parents of diploid *R. multiflora* family 977, 95/13-39 and Spaller-3, consist of 7 linkage groups each and cover 360 and 376 cM, respectively. In the diploid family, the inheritance of floral traits, other morphological traits, and resistance to two diseases were studied. Of these, three simply inherited traits and thirteen traits controlled by quantitative trait loci (QTL) were located on the diploid maps. Thirty new rose SSR markers were developed for construction of the diploid and tetraploid maps by screening a small-insert genomic library. Based on the common SSR markers among the four maps, a preliminary consensus map for the rose genome was generated. Traits mapped in individual maps were incorporated into the consensus map. This preliminary consensus rose genetic map locating several simple and complex traits will serve as the starting point to develop a saturated consensus map of rose, which could be used in marker-assisted progeny selection, comparison with other rose and Rosaceae maps, and cloning of rose genes in the future.

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GENETIC AND MOLECULAR ANALYSES OF HORTICULTURALLY IMPORTANT TRAITS IN ROSES

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Due to its importance as an ornamental crop the rose has become the object of various research projects on genetics and molecular biology of horticulturally important traits. Apart from disease resistance, ornamental characters as e.g. scent, flower morphology and flower colour are important characters. Here we present data on the molecular analysis of a locus harbouring a disease resistance gene for black spot resistance in roses which had been identified by molecular mapping and chromosome walking. Furthermore, data on the genetics and molecular mapping of flower morphology influenced by major dominant genes as well as qtl loci will be presented.

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GENETIC DISSECTION OF GROWTH VIGOR WITH MOLECULAR MARKERS IN WHEAT

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The current breeding challenge is to reduce energy consumption needed for rose production in wheat crops in Western Europe. To this end an analysis of genetic variation for vigor-related traits in a diploid *Rosa multiflora* mapping population (Debener et al. (1999) TAG 99:891-899) was conducted. Thirteen traits, i.e. number of internodes, shoot thickness, shoot length, chlorophyll content, leaf area, leaf fresh and dry weight, shoot fresh and dry weight, total dry weight, grain weight per head, specific leaf area and growth rate, were evaluated. The phenotypic data were approximately normally distributed. Broad-sense heritabilities of the traits are high, ranging from 0.75 to 0.98. Genotyping the population with AFLP, SSR and protein kinase domain markers (PK) has led to dense parental and integrated genetic maps. SSRs are mapped on seven linkage groups in the integrated map. QTL analysis of vigor-related traits is currently being performed and preliminary results are presented.

Plant Alien Introgression
(W186-W191)

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GENETIC RESOURCES : EXTENT OF DIVERSITY, ITS USAGE, AND PURPOSE FOR WHEAT IMPROVEMENT

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The major global challenge for bread wheat production is the demand imposed by the human population that is increasing annually by 1.16 percent. Consequently, conservative estimates indicate that global wheat productivity must increase from the current 570 million tons to 720 million tons in order to address population consumption needs. The goal can be swiftly realized via sound policy setting and management practices coupled with exploitation of unique genetic resources. The latter will permit a widening of the current germplasm base, allowing wheat to adapt better under our dynamic environmental changes that cause harsher biotic/abiotic stress growing conditions. Appropriate usage of the new diversity provides a potent durable system for sustainable agriculture as measured through the tons/hectare parameter. Presented here are some applied cytogenetic aspects that influence wheat genomic manipulation based upon the use of diversity of its wild relatives that reside in the three Triticeae gene pools. Our program strategies are complemented with molecular cytology/diagnostics, gene pyramiding, and targeted use of molecular markers to essentially yield end-products dictated by the prevalent productivity challenge statistics that necessitate swift yearly yield outputs via an integrated research infrastructure.