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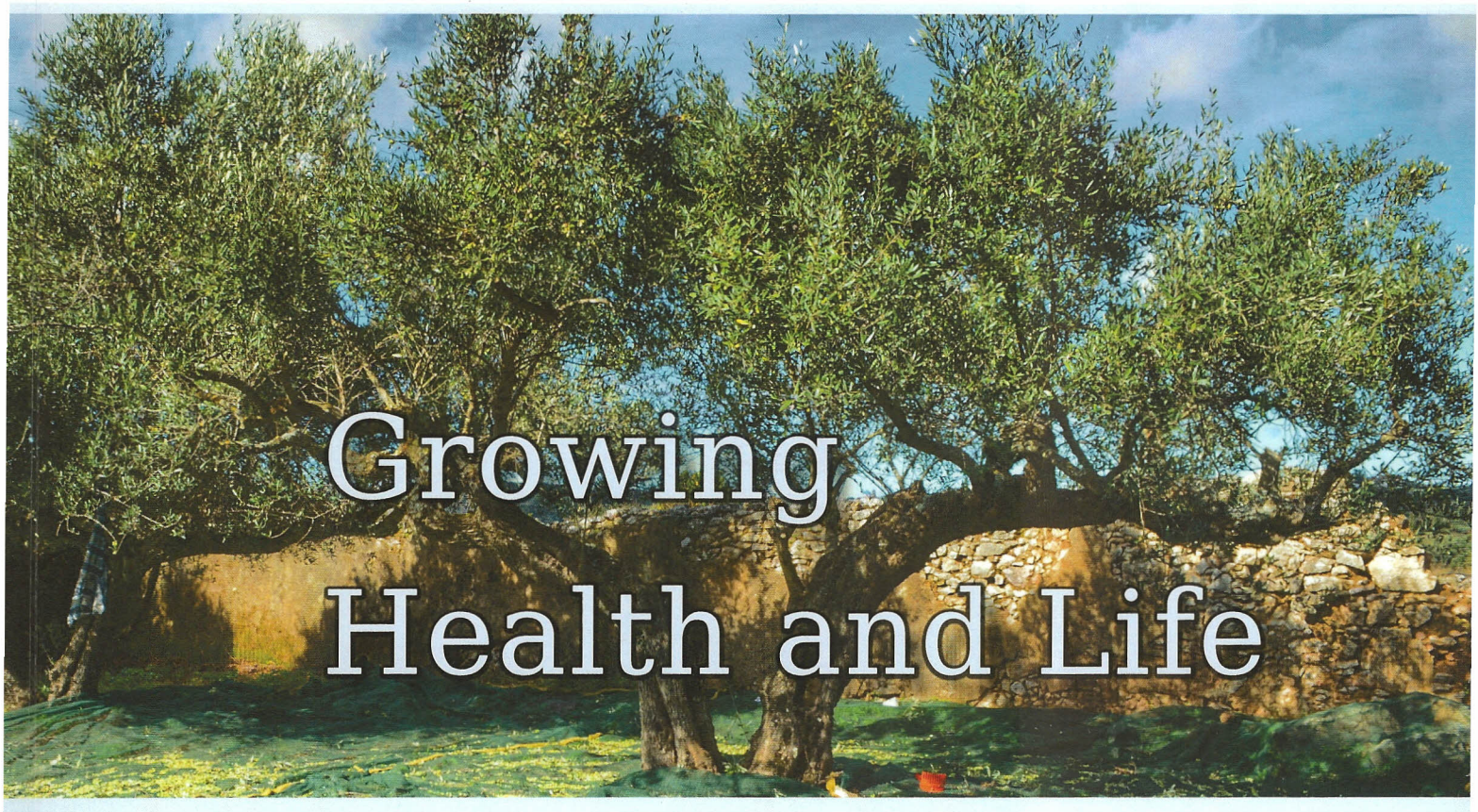

Programme

& Book of Abstracts

CHANIA, CRETE, GREECE, OCTOBER 17-21, 2016

III International Symposium on Horticulture in Europe SHE2016

Programme and Book of Abstracts

Chania, Greece
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GENETIC DISSECTION OF TOMATO FRUIT QUALITY IN THE GENOME ERA: NEW TOOLS FOR IN DEPTH QTL CHARACTERIZATION

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Tomato fruit quality is characterized by a large number of components influenced by the genotypes and the environment. To better understand the genetic control of these components, quantitative trait loci (QTL) have been mapped for years. Today the genome sequence availability changes the paradigm of genetic approaches. QTL have been first identified using linkage mapping populations and positional cloning identified a few QTLs. However linkage mapping is limited to the analysis of traits differing between two parental lines. Genome-wide association (GWA) has then been proposed to assess a large range of variability. In tomato, we have shown that GWA study is possible, using the admixed nature of cherry tomato genomes that reduces the impact of population structure. Nevertheless, GWA success is limited in some regions due to the low decay of linkage disequilibrium, which varies along the genome. Rare alleles are also difficult to detect with GWA studies. Multi-parent advanced generation intercross (MAGIC) populations offer an alternative to traditional linkage and GWAs by increasing the precision of QTL mapping but with equilibrated allelic frequencies. We have developed a MAGIC population by crossing eight tomato lines whose genomes were resequenced. We showed the potential of the MAGIC population when coupled with whole genome sequencing to detect candidate single nucleotide polymorphisms (SNP) underlying the QTLs. QTLs for fruit quality traits were mapped and related to the variations detected at the genome sequence and expression levels. The advantages and limitations of the three types of population, in the context of the available genome sequence and resequencing facilities, will be discussed.