P056

Chromosome composition in an F_2 hexaploid x durum cross analyzed by DArT markers and MCFISH

Eberhard FS[1], Zhang P[2], Lehmensiek A[1], Sutherland MW[1], Hare R[3], Simpfendorfer S[3]

[1] *Centre for Systems Biology, University of Southern Queensland, Toowoomba, Qld, 4350*

[2] *University of Sydney, Plant Breeding Institute, Cobbitty, NSW 2570*

[3] *NSW Dept of Primary Industries, Tamworth NSW 2340, Australia*

A major constraint to tetraploid durum wheat production in Australia is widespread susceptibility to crown rot, due to infection by *Fusarium pseudograminearum.* Several sources of partial resistance to this disease are available in hexaploid bread wheats and genetic markers for quantitative trait loci conditioning this resistance have been identified. We are currently attempting to transfer crown rot resistance from these hexaploid sources into susceptible tetraploid wheats. However, knowledge of the fate of D-genome material in hexaploid/tetraploid crosses is incomplete, while the degree of recombination between the A- and B-genomes of the parents in these crosses is also of critical interest. Diversity Array Technology (DArT) markers and multicolour fluorescence *in situ* hybridisation (MCFISH) were employed to investigate parental inheritance in the F_2 progeny from a cross between the hexaploid bread wheat line '2-49' and the tetraploid durum variety 'Bellaroi'. Of the 83 F_2 progeny analyzed with DArT, 82 contained one or more D-genome chromosomes, either complete or partial. The marker profiles indicated that all lines possessed recombined A- and B-genome loci derived from both parents, indicating the absence of parental selfs. The majority of A- and B-genome chromosomes showed a random re-assortment of parental genes. MCFISH analysis was conducted on 28 additional **Chromosome biotechnology poster abstracts**
plants from the same F_2 population. All lines contained varying numbers of D-genome chromosomes, while two plants carried A-D translocations. Investigations of F_3 plants from an independent 2-49/Bellaroi cross indicated that only 16 out of 33 plants still contained D genome material.