An Australian perspective on the early days of ITMI.

Rudi Appels. Centre for Comparative Genomics, Murdoch University, Perth WA 6150, Auatralia.

In the late 1970s and 1980s the cloning and sequencing of DNA segments of the wheat and rye genomes was initiated in several countries around the world. This activity focused on repetitive DNA sequences because they were more accessible for establishing the technologies required for using these sequences as molecular markers in genetic mapping and characterizing breeding lines. Early studies in Australia showed the value of the repetitive DNA sequences for characterizing chromosome arms through visualizing their distribution by *in situ* hybridization to root-tip squashes (Appels et al 1978). In view of the geographic location of Australia and the fact that it was only in the mid 1980s that FAX and email facilities became available, the discussions to start a loosely structured group of collaborators under the International Triticeae Mapping Initiative was a most welcome development. The Grains Research Development Corporation (GRDC) funded the formation of the Australian Triticeae Mapping Initiative in 1990 to complement ITMI and provide a focus for understanding the use and value of molecular markers in breeding and prebreeding. The ITMI network was the source of molecular markers to argue the case for major national molecular marker programs in wheat and barley that ran for ten years and formed the foundation (Marshall et al. 2001; Langridge and Barr 2003) of the prebreeding laboratories around Australia that are still active to this day. The genome sequencing and sequence-based genetic maps activities in wheat and barley trace their inspiration to the ITMI cooperative interactions.

Appels R, Driscoll C, and Peacock WJ. 1978. Heterochromatin and highly repeated DNA sequences in rye (*Secale cereale*). Chromosoma (Berl) 70:67-89.

Langridge P and Barr AR. 2003. Better barley faster: the role of marker assisted selection. Austr J Agric Res 54:1065-1408 (31 papers).

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SESSION III: UTILIZING TRITICEAE RESOURCES AND DIVERSITY

DNA marker-assisted chromosome engineering for efficient alien gene introgression of stem rust resistance in wheat.

Steven S. Xu [1], Zhixia Niu [1], Daryl L. Klindworth [1], Qijun Zhang [2], Shiaoman Chao [1], Timothy L. Friesen [1], Justin D. Faris [1], Yue Jin [3], and Xiwen Cai [2].

[1] USDA–ARS, Northern Crop Science Laboratory, Fargo, ND 58102, USA; [2] Department of Plant Sciences, North Dakota State University, Fargo, ND 58108, USA; and [3] USDA–ARS, Cereal Disease Laboratory, St. Paul, MN 55108, USA.

Cultivated wheat has a large number of related species that represent a valuable gene pool for wheat improvement. In the past 50 years, a number of effective stem rust resistance (*Sr*) genes identified from wild relatives of wheat have been transferred into wheat through genetic manipulation in the form of chromosome translocations and additions. In an effort to enhance the utility of the alien-derived *Sr* genes that are effective against Ug99 stem rust races, we developed an optimal scheme of chromosome engineering for efficient elimination of large amounts of alien chromatin surrounding the *Sr* genes. In this procedure, we first developed a large backcross population of homoeologous recombinants using the *ph1b* mutant in hexaploid wheat or *Ph1*-deficient aneuploid in tetraploid wheat. We then identified the recombinants carrying the gene of interest on small interstitial segments using robust DNA markers and high-throughput phenotyping and genotyping. By using this procedure, we developed wheat germplasm carrying four Ug99-resistant genes (*Sr37*, *Sr39*, *Sr43*, and *Sr47*) on minimal alien chromatin in a short period of time. We are currently applying this procedure to transfer more genes for resistance to stem rust and leaf rust from wild relative species into the wheat genome. This study demonstrated that integration of modern genomic and marker technology with classical chromosome engineering and breeding greatly improved the efficiency of transferring resistance genes from wild relatives into modern crops.