

Distinct patterns of additive and non-additive effect as revealed by MET FA models incorporated with pedigree and fgen in hybrid oilseed rape trials among Australia, China and India

Sheng Chen^{1,2,3}, Cameron Beeck², Aanandini Ganesalingam¹, Desheng Mei⁴, Neil Wratten⁵, Wayne Burton⁶, Surinder Banga⁷, Chaozhi Ma⁸, Dhiraj Singh⁹, Phillip Salisbury^{6,10}, Brian Cullis¹¹ and Wallace A. Cowling^{2,3}

¹ School of Plant Biology (M084), University of Western Australia, Crawley, WA 6009, Australia;

² Canola Breeders Western Australia Pty Ltd., Locked Bag 888, Como, WA 6952, Australia

³ UWA Institute of Agriculture, University of Western Australia, Crawley, WA 6009, Australia

⁴ Oilseed Crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan, China

⁵ Wagga Wagga Agriculture Institute, NSW DPI, Wagga Wagga, Australia

⁶ Victorian Department of Primary Industries, Horsham, Australia

⁷ Department of Plant Breeding, Punjab Agricultural University, Ludhiana, India

⁸ National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China

⁹ Department of Plant Breeding, Haryana Agricultural University, Hisar, India

¹⁰ Faculty of Land and Food Resources, The University of Melbourne, Melbourne, Australia

¹¹ School of Mathematics and Applied Statistics, University of Wollongong, Wollongong, Australia

Email: sheng.chen@uwa.edu.au

ABSTRACT

As part of the project “Oilseed Brassica Improvement in China, India & Australia” (CIM/1999/072) funded by ACIAR & GRDC, a set of 12 hybrid oilseed rape trials were performed in Australia, China and India. These trials were designed with *p*-rep using DiGGeR and analysed using multi-environmental trial factor analytic (MET/FA) model with pedigree and fgen information. Distinct patterns of additive and non-additive effects for seed yield were found over trials reflecting the GxE interactions. No significant association between genetic distance and hybrid vigour was observed for seed yield, though, in general, the inter-group hybrids were much better than the intra-group hybrids. Heterosis was as great for intra-region crosses as inter-region crosses, and the highest yielding hybrid was an F1 combination with both parents from China. There was a strong correlation between area of the largest leaf before flowering and seed yield at most sites and leaf area was a good predictor of hybrid vigour for seed yield.

Key words: Canola – heterosis – multi-environment trial

INTRODUCTION

Oilseed *Brassica napus* is a predominant oilseed crop in China and Australia, and it is also very important in India, thus the evaluation of *B. napus* germplasm from these three countries will be of great importance to oilseed *Brassica* breeding and production. New factor analytic models permit interpretation of patterns of additive and non-additive genetic variance in multi-environment trials (MET) (Beeck et al., 2010; Cullis et al., 2010). Tools are available to test the relative value of pedigree in the MET model, to observe and interpret patterns of genotype x environment interaction for additive and non-additive genetic effects, and to evaluate quantitative trait loci (QTL) for heterosis in the MET model.

The aims of this paper are (1) to test the hypothesis that F1 hybrid vigour for grain yield would be greatest in inter-group hybrids, and least in intra-group hybrids, in F1 hybrids between pure lines of oilseed *B. napus* from China, India, Australia and Europe; (2) to evaluate patterns of genotype x environment interaction for inter- and intra-group hybrids; and (3) to test whether these patterns were distinct for additive and non-additive genetic effects.

MATERIALS AND METHODS

Based on previous study (Chen et al., 2008), 13 representative pure lines of oilseed *B. napus* from genetically distinct groups in China, India, Australia and Europe were chosen and 78 F1 hybrids were made between these pure lines in a half-diallel mating design, plus 6 reciprocal hybrids. Molecular genotype of the 13 parental lines was characterized by simple sequence repeat (SSR) and diversity arrays technology (DArT) markers spanning the entire *B. napus* genome. The F1 hybrid lines and their parental inbred lines were tested in field trials set up with a spatial randomisation design using DiGger (<http://www.austatgen.org/>) (Cullis et al., 2006). The trials were conducted in Australia, China and India over 2 canola growing seasons, for a total of 12 trials. Methods for assessment and record of yield and all other traits were standardised across sites. Base model DIAG for spatial analysis was applied within trial to account for spatial trends and to remove outliers. MET/FA modelling with pedigree information was used to improve genetic variation using correlation among trials and to partition the total genetic variance into additive and non-additive effect (Beeck et al., 2010; Oakey et al., 2007). In order to distinguish the hybrids from the inbreds, fgen was also incorporated into the FA model in this study.

RESULTS AND DISCUSSION

Patterns of genotype x environment interaction differed across sites for genetic effect for seed yield (Fig. 1). In terms of additive effect for seed yield (Fig. 1A), 6 trials were clustered together, including 3 from China, 2 from IN and 1 from AU. This well reflects that fact that irrigation was applied in these trials. The trial 08IN2 was the most distant, most likely because the p-rep design was not strictly followed as in other trials. The pattern of the non-additive effect was quite different from the additive effect (Fig. 1B). This is very normal as GxE interaction differs the additive and non-additive effects for the same trait. Taken additive and non-additive effect together, the total effect for seed yield showed a different correlation pattern among trials as expected (Fig. 1C). 3 trials in China (07CN1, 08CN1 & 07CN2) were the most correlated. 2 trials in India (07IN1 & 08IN1) and 2 trials in AU (07AU2 & 08AU3) were also highly correlated. These well reflected the GxE interactions. Therefore, we concluded that the additive, non-additive and total effect for seed yield had different patterns over trials.

There was wide range of hybrid vigour for grain yield but there was no significant association between genetic distance and hybrid vigour. Anyway, in general, the inter-group hybrids were much better than the intra-group hybrids for seed yield (Fig. 2). Heterosis was as great for intra-region crosses as inter-region crosses, and the highest yielding hybrid was an F1 combination with both parents from China. There was a strong correlation between area of the largest leaf before flowering and seed yield at most sites and leaf area was a good predictor of hybrid vigour for seed yield.

This study is the first use of MET/FA for evaluation of heterosis in F1 hybrids and their inbred parents which separates additive and non-additive effects. F1 hybrids tended to be best adapted to their region of origin, but the highest yielding hybrid across environments was from two Chinese parents. It should be possible to associate genomic markers with heterosis with this approach.

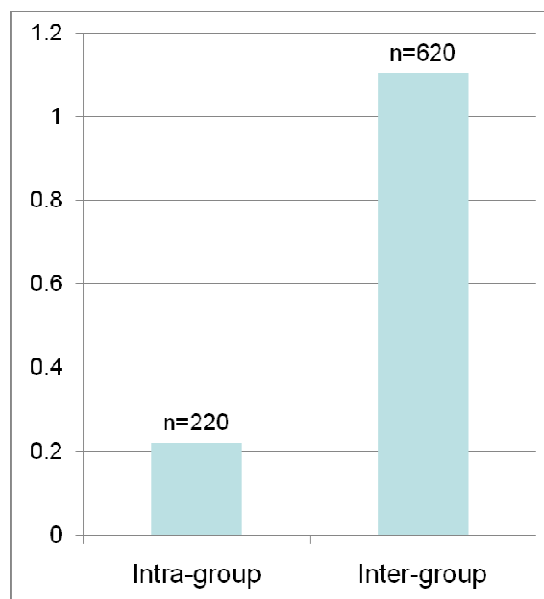


Fig. 2. The grain yield in inter-group hybrids was five times higher than in intra-group hybrids

ACKNOWLEDGEMENTS

This work was supported by the Australian Centre for International Agricultural Research (ACIAR) and Grains Research and Development Corporation (GRDC) in ACIAR project CS1/1999/072.

REFERENCES

- Beeck, C. P., Cowling, W. A., Smith, A. B., and Cullis, B. R. (2010). Analysis of yield and oil from a series of canola breeding trials. Part I. Fitting factor analytic mixed models with pedigree information. *Genome* 53, 992–1001.
- Chen, S., Nelson, M. N., Ghamkhar, K., Fu, T., and Cowling, W. A. (2008). Divergent patterns of allelic diversity from similar origins: the case of oilseed rape (*Brassica napus* L.) in China and Australia. *Genome* 51, 1-10.
- Cullis, B., Smith, A., and Coombes, N. (2006). On the design of early generation variety trials with correlated data. *J. Agric. Biol. Environ. Stat.* 11, 381-393.
- Cullis, B. R., Smith, A. B., Beeck, C. P., and Cowling, W. A. (2010). Analysis of yield and oil from a series of canola breeding trials. Part II. Exploring variety by environment interaction using factor analysis. *Genome* 53, 1002–1016.
- Oakey, H., Verbyla, A., Cullis, B., Wei, X., and Pitchford, W. (2007). Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. *Theor. Appl. Genet.* 114, 1319-1332.

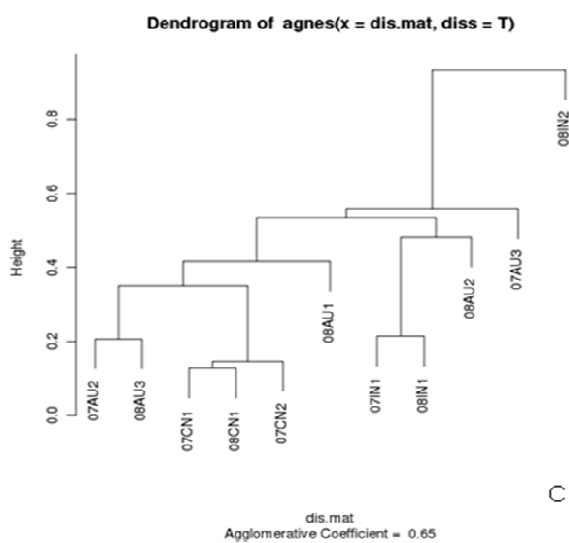
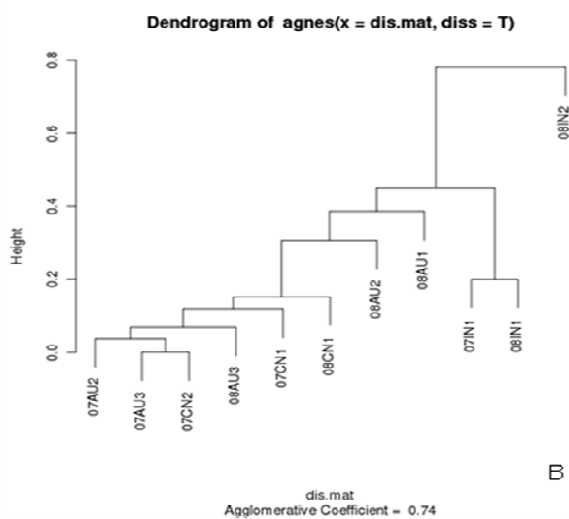
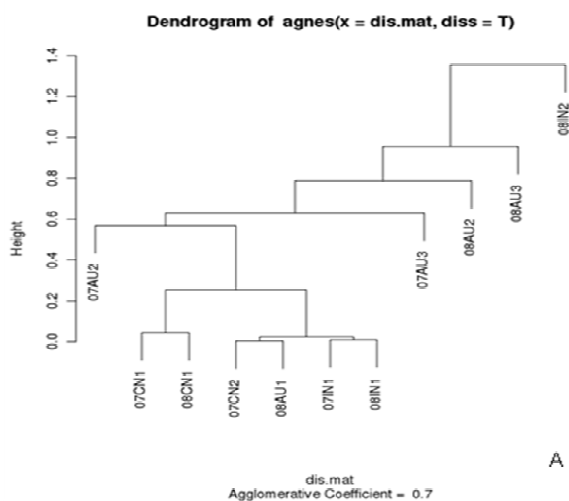


Fig. 1. Distinct patterns of additive (A), no-additive (B) and total genetic effect (C) of seed yield among trials.