

**Genetic and Environmental Control of Yellow  
Pigment in Durum Wheat (*Triticum turgidum*  
*Durum*) in Australia**

Submitted by

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## Acronyms Used in this Thesis

AACC = American Association of Cereal Chemists

ABA = Abscisic acid

AGT = Australian Grain Technologies

ANOVA = Analysis of Variance

BLUE = Best linear unbiased prediction

BSA = Bulk segregant analysis

CIELAB= Commission Internationale de l'Eclairage L\* (brightness) a\* (red colour)

b\* (yellow colour)

HPLC = High pressure liquid chromatography

MAS = Marker assisted selection

MEP = 2-C-methyl-D-erythritol 4-phosphate

MRT = Multiplex ready technology

NIR = Near infra-red reflectance spectroscopy

NSW = New South Wales

NVT = National Variety Trials

PPO = Polyphenol oxidase

QTL = Quantitative trait loci

ReML = Restricted Maximum likelihood Ratio

SA = South Australia

SARDI = South Australian Research and Development Institute

SSD = Single seed descent

SSR = Simple sequence repeat

TGW = One thousand grain weight

UA = University of Adelaide

YP = Yellow pigment

YP/grain = Yellow pigment content per grain

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# Abstract

Environmental and genetic control of grain yellow pigment (YP) content of Australian durum cultivars has been investigated using large genotype x environment (including controlled environments) data sets and 2 large bi-parental recombinant inbred line durum wheat populations respectively.

Non-genetic variation in YP concentration was shown to be highly complex. This complexity was simplified by showing that final YP concentration is a function of the negative relationship between YP concentration and thousand grain weight (TGW), possibly due to starch dilution, and the total YP content synthesised per grain (YP/grain). Non-genetic variation in YP/grain was, not surprisingly, shown to be dependent on final TGW; however, it was also shown to be independent of TGW. Limited plant available water during grain filling resulted in both lower YP/grain and lower TGW; the net result was a modestly higher grain YP concentration. An hypothesis based on endosperm cell number that attempts to explain the observations is proposed and the implications of non-genetic control of YP for breeding programs discussed.

YP concentration and YP/grain were shown to be multi-genic traits and in both populations examined there was evidence of transgressive segregation. QTL on chromosomes 7AL, 7BL, 7BS, 6B, 1A and 3B in Wollaroi/Tamaroi and 7AL, 7BL, 7BS, 6BL, 6BS, 1A and 3B in WID22221/Tamaroi were additive and together explained >50% and >40% of the phenotypic variation respectively with 7AL and 7BS being the most important. Allelic variation at *Psy1-A1*, encoding phytoene synthase, was identified in both populations but contrary to expectation was not

associated with significant differences in YP phenotype. Rather the effect of chromosome arm 7AL appeared to be contributed by a QLT located proximal to *Psy1-A1*. In contrast, association between YP concentration and allelic variation at *Psy1-B1*, which has been identified in international germplasm, was confirmed in Australian durum wheat.