

Improving rates of genetic gain in wheat: integrating genomics



To be useful in plant breeding technology should:

- Show an advantage over phenotypic selection
- Reduce the costs in achieving the phenotype
- Increase the speed & precision in achieving the phenotype
- Ideally led to step-changes in phenotype
- Reduce or manage the impact of GE

Genomics in the wheat breeding process

Parental selection

- diversity analysis
- gene profiling
- association studies: genomic regions linked to yield

Selection strategy

- genome wide selection
- MAS/MABC/DH
- MARS using background/foreground genotype and phenotype

Multi-environment testing

- prediction of GE response
- analysis of historical data to determine site associations

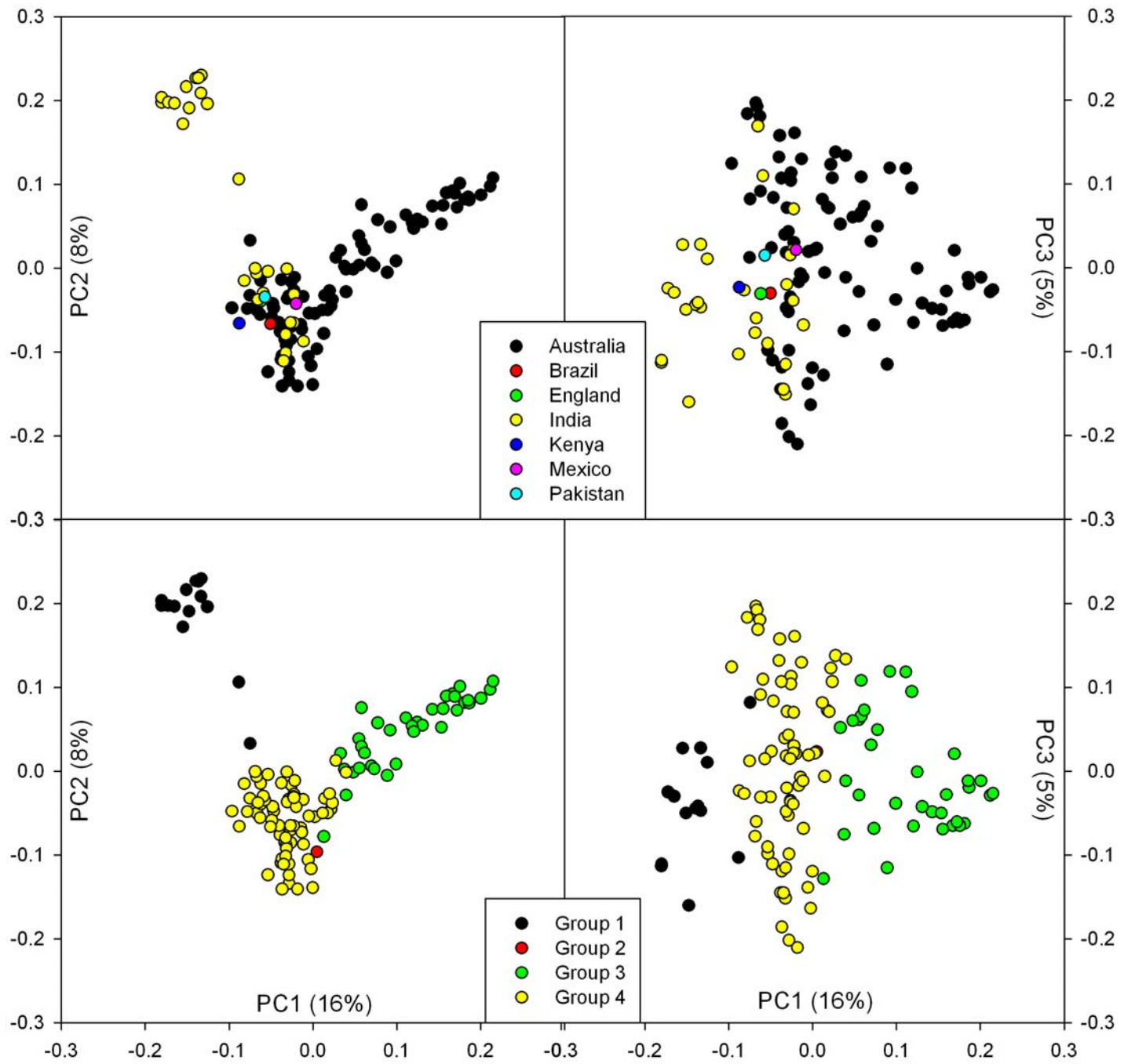
Cultivar identification & release

- genotyping & PBR requirements

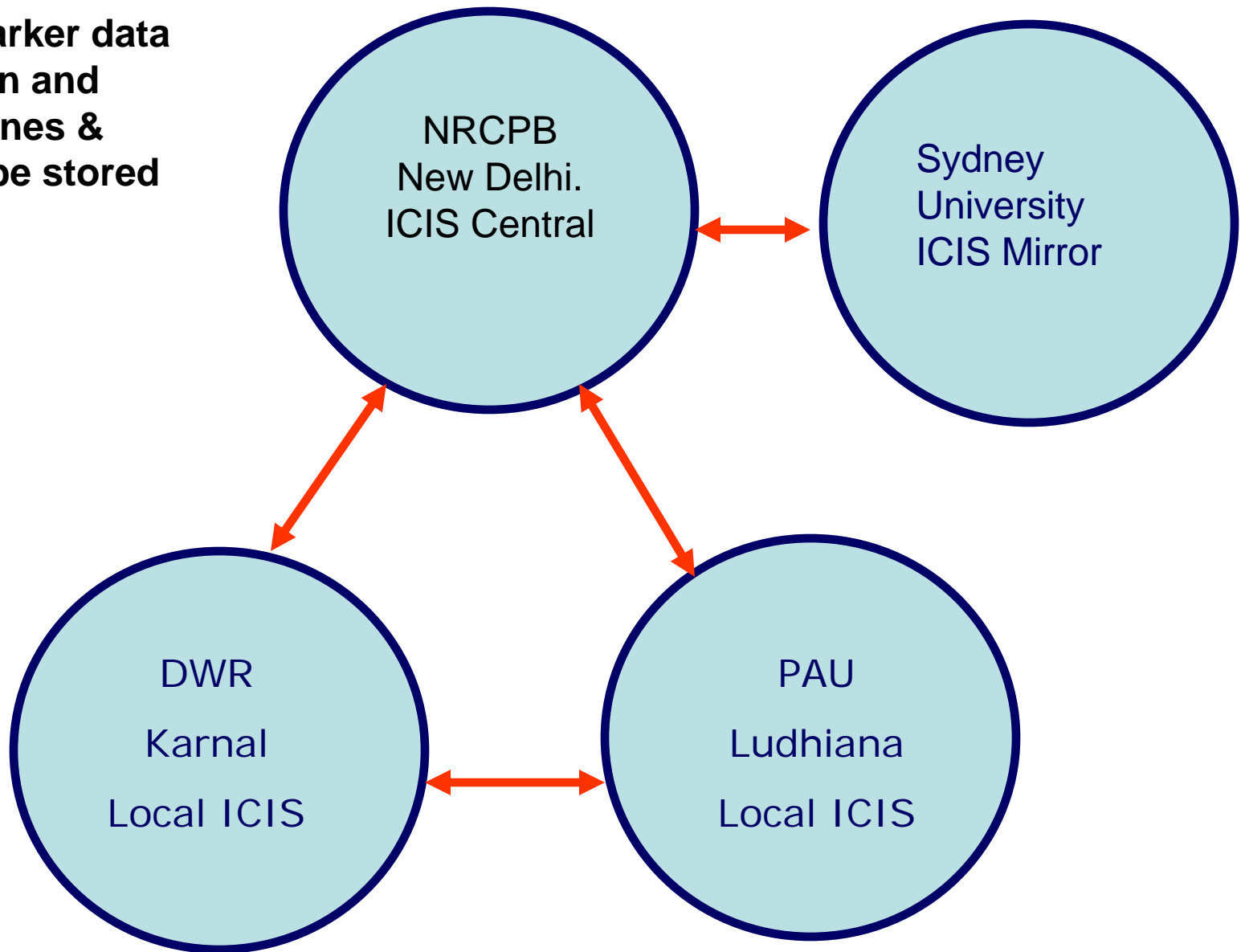
Selecting better parents: genome wide scans and foreground gene profiles

Example: the development of an Indo-Australian germplasm (*ACIAR-ICAR molecular wheat breeding program*)

- DArT profiles and known gene profiles generated on key parental materials



**DArT, marker data
for known and
target genes &
phenotype stored
in ICIS**



However: issues with combining and managing this information

DARt cluster

Rust gene profile

Phenotype

	<i>Lr34/Yr18</i>	<i>Lr24/Sr24</i>	<i>Lr37/Sr38/ Yr17</i>	<i>Sr26</i>	<i>Leaf rust</i>	<i>Stripe rust</i>	<i>Plant height</i>
ANLACE	-	+	-	-	0	20	95
Qual 2000	-	+	+	-	0	30	80
Datatine	-	+	+	-	0	10	85
<i>Yr10Yr17/ Tincurrin</i>	-	+	+	-	0	10	90
Clearfield Stl	-		-	-	20	60	85
Frame	-		-	-	30	40	90
Yitpi	-		-	-	30	40	80
Excalibur	-		+	-	40	30	95
Gladius	-	+	-	+	0	40	90
EGA Eagle Rock	-	-	+	+	10	0	90
Sunlin	+	+	-	-	0	10	90
Carinya	+	+	-	-	0	20	85
Clearfield Jnz	+	+	-	-	0	20	80
Janz	+	+	-	-	0	0	100
HSB 2398	+	-	-	+	20	0	95
HSB 2527	+	+	-	-	0	0	95
HSB 2408	-	+	-	-	15	0	90
S/K 701	+	+	-	-	30	0	95
Lang	+	+	-	-	0	30	95
Sunco	+	+	-	-	0	20	90
S/K 371	+	+	-	-	0	20	90

Types of Crosses using combined DArT and target rust gene data

Parents	Foreground target genes	DArT grouping
HD2733	<i>Lr34/Yr18; Lr28; Lr26</i>	1
C80.1/3* <i>Sr2</i> Batavia	<i>Lr34/Yr18; Lr46/Yr29; Sr2; Lr19/Sr25</i>	4
DBW14	<i>Lr34/Yr18</i>	3
PBW175	<i>Lr34/Yr18; Sr2</i>	4
FLW6	<i>Sr24/Lr24; Sr2</i>	4
HSB3176	<i>Sr2; Sr26; Yr15; Yr24</i>	4

Selecting better parents

Combining genomic regions for improved yield from association studies

An example: Association analysis of 25 years of data from CIMMYT's international nursery system (Crosa et al., 2008)

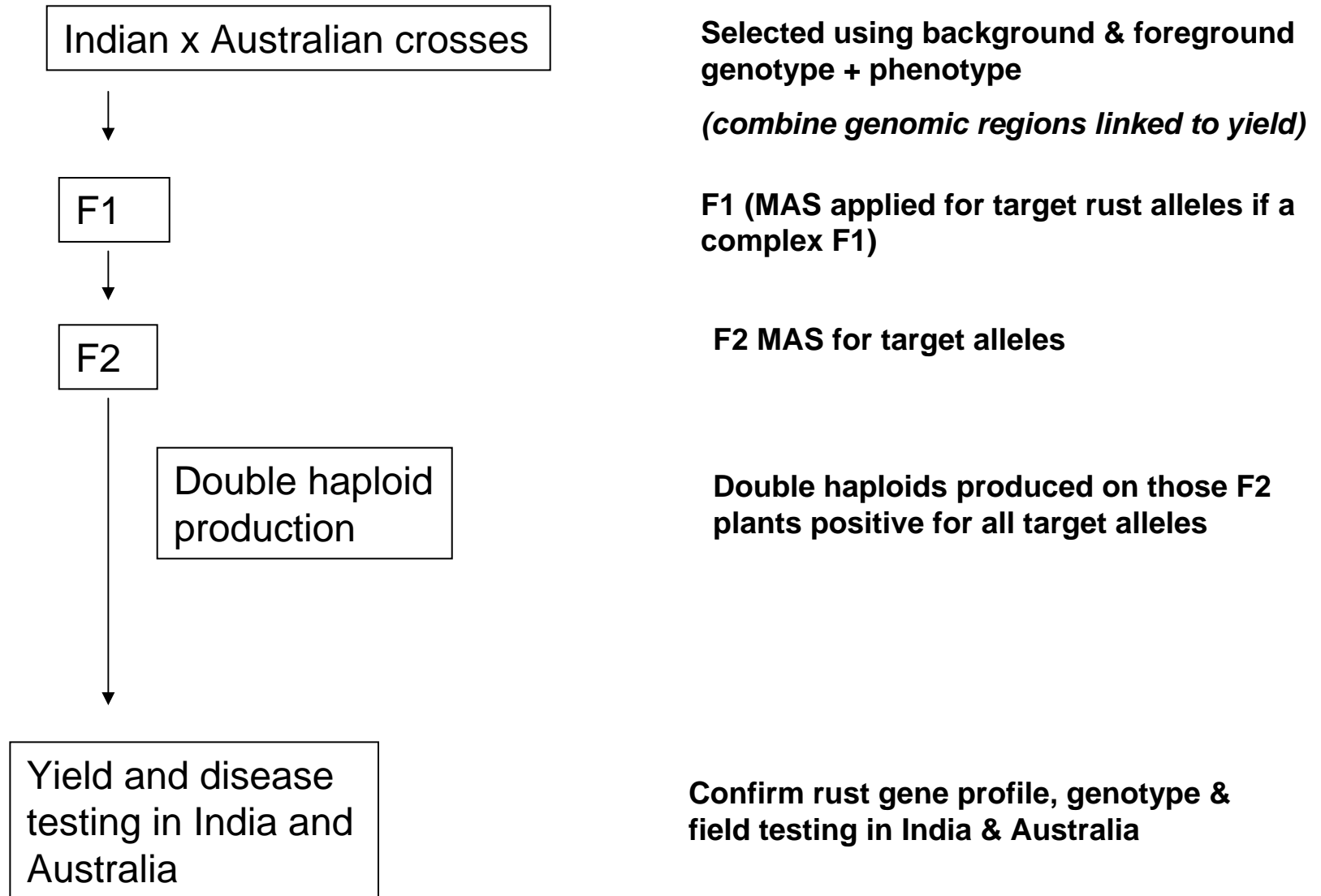
Significant DArTs associated with yield

	Short arm (S)		Long arm (L)		Unknown arm	
	DArT (wPt)	Gene and/or QTL	DArT (wPt)	Gene and/or QTL	DArT (wPt)	Gene and/or QTL
1A	5374, 4765, 2872, 9266, 2311, 7030, 4029	----	3870, 3904, 5274, 4709, 6754, 8016, 0128	QTL	9592, 1011, 6853	QTL
1B	8949, 1328, 7094, 3465, 4434, 0974, 6427, 8986, 1781, 5065, 5678, 5363, 6777, 5801, 6117, 6833, 8616	1B/1R transl.	2315, 0944, 2526, 4129	----	5316, 1139, 2019	QTL
1D	3738, 9380	----	7711, 9857, 3743, 4427, 2897, 1263, 7092	QTL	----	QTL
2A	7901, 6687, 9793, 3114	<i>Ppd3</i> QTL	5647, 2087	----	6207	QTL
2B	0100, 4916, 6706, 8326, 3983, 5672, 4125, 7757	<i>Ppd2</i>	3132, 9350, 7350, 9336, 2135, 3378, 7360, 0049	<i>Eps</i> QTL	0094, 0950, 4210	QTL
2D	4144	<i>Ppd1Rht8</i> QTL	4413	<i>Eps</i>	----	QTL
3A	9369, 1681	QTL	7756, 2698, 7992, 2938, 4725, 9268, 4407, 1688	----	----	<i>Eps</i>
3B	0365, 0995, 5716, 7015, 8352, 8983, 7142, 9310, 4209, 9510, 5390, 9170, 6047, 5105, 6802, 8886, 0280, 0384, 8238, 8096, 4412, 8845	----	----	QTL	9368, 2757	<i>Vrn</i> QTL
3D	1365, 9401	----	----	QTL	----	<i>Ppd</i> QTL

Significant DArTs associated with yield

	Short arm (S)		Long arm (L)		Unknown arm	
	DArT (wPt)	Gene and/or QTL	DArT (wPt)	Gene and/or QTL	DArT (wPt)	Gene and/or QTL
4A	2788	QTL	7280, 2084, 3795, 7807, 8271, 4620, 2533	QTL	4660, 7924	<i>Eps</i>
4B	3908, 6149	<i>Rht-1</i> , QTL	1505, 8292	QTL	3608, 5265	<i>Eps</i> QTL
4D	----	<i>Rht-2</i>	----	QTL	----	<i>Eps</i>
5A	1165, 0605	----	5231	<i>Vrn-A1</i> QTL	4249	QTL
5B	6136, 1420, 9666, 5175	----	9467, 0103, 4996, 7101, 5896, 3030, 9598	<i>Vrn-A2</i> QTL	4418, 4703, 4936	QTL
5D	1400	----	----	<i>Vrn-A3 Vrn-4</i>	----	QTL
6A	7475, 0864, 8006, 7938, 9075	----	9690, 2573, 0959, 7063, 1642, 7204	----	----	QTL
6B	9532, 1922, 3130, 9990, 6994, 8239, 4720, 1547, 6282, 3116, 3304, 1852, 7777, 4706, 3733	----	6116, 0171, 1264, 3045, 9256, 1541	----	----	<i>Eps</i> QTL1
7A	6034, 8789, 4835	QTL	3393, 6495	QTL	2266, 4553, 4748	QTL
7B	----	----	6273, 9925, 7887, 5343, 8921, 5547, 5280, 0194, 6156, 4300, 7108, 6320, 0504	QTL	1533, 9746	<i>VrnB4</i> , <i>Vrn5</i> <i>Eps</i> , QTL

Basic breeding scheme (*Indo-Australian*)



P1 x P2

Parents representing contrasting QTLs genotyped (year 1).
(Crosses may be simple, tops or doubles)

F1

Increased in the green house (year 1)

F2

Progeny selected using associated QTL markers (year 2) - greenhouse

F3

Plots representing individual plants under irrigation – all progeny genotyped (year 2)

F4

Multi-environment trials (3-4 tests) under drought pressure in the field under managed stress. Yield, rust, genotype and map-marker selection used to select lines (year 3). Gene effects estimated.



F5

Best lines enter
breeding program

Intercross selected lines based on QTL
linked markers and genotype (year 3)

Multi cross F1

Repeat
second cycle
(years 4 – 6)

**MARS for
WUE**

Conclusions

- Not yet using functional aspects of genomics in applied wheat breeding
- Need to further exploit the work of *Crossa et al* for genome wide selection in wheat
- Need to effectively *marry* genome wide scans, known gene information and phenotype to select parents in an efficient and timely way
- Need to ramp up MARS for WUE as a priority breeding strategy

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