ILS4
Fourth International Legume Society Conference 2023

19-22 September Granada Conference Center
Granada Spain

Enhancing abiotic stress tolerance in grain legumes: physiological and molecular approaches

Professor Kadambot H.M Siddique,
The University of Western Australia
Australia

LEGUME SOCIETY

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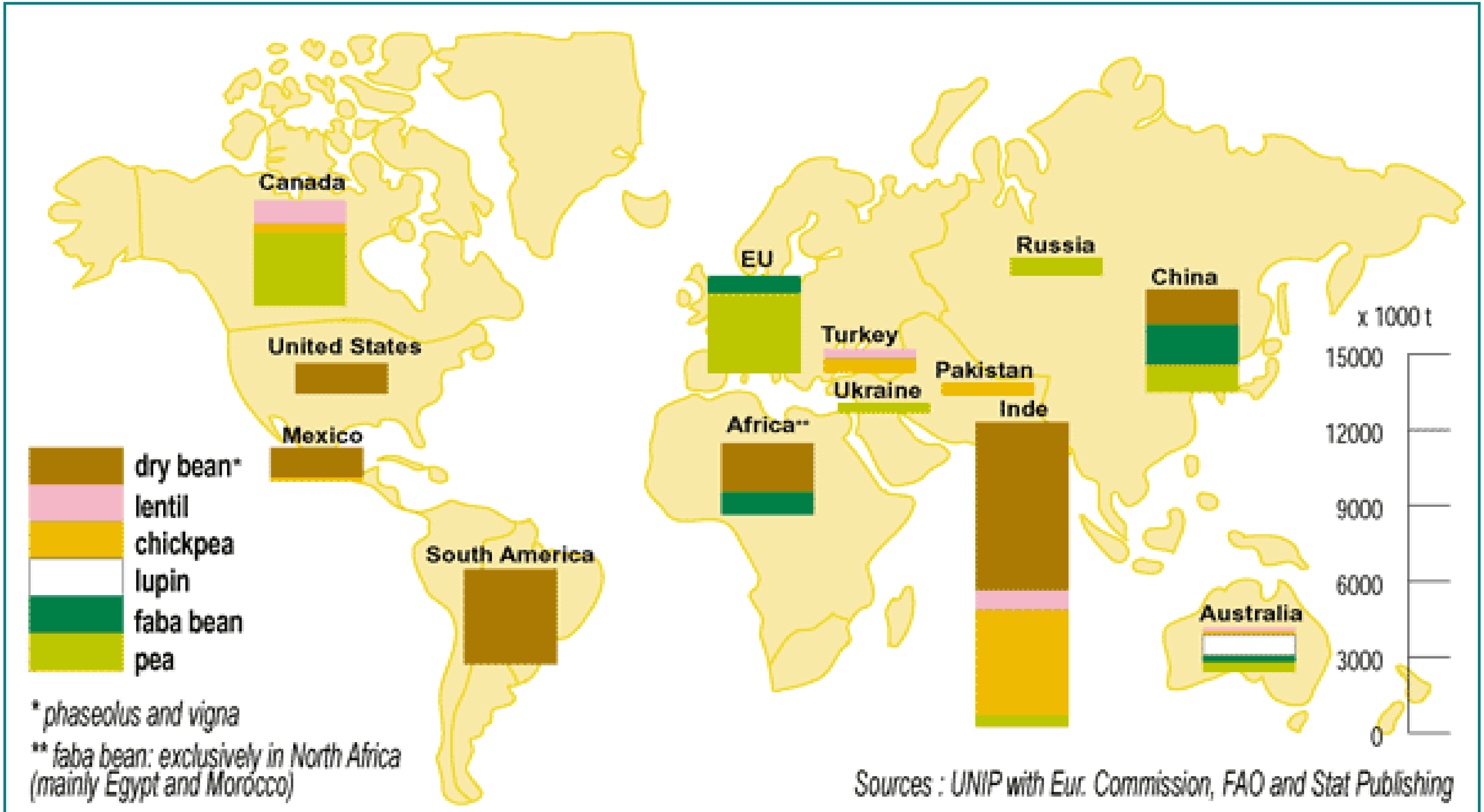
Outline

- Dryland agriculture
- Physiology of heat, chilling and salinity stresses
- Drought physiology and phenotyping
- Breeding strategies- molecular approaches
- Success stories
- Conclusions

Pulses – World Scene



Global investment in grain legume R,D&E is too low compared with cereal crops: (US $ 175 million per annum in 13 pulse crops)

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nature plants

PERSPECTIVE

PUBLISHED: 2 AUGUST 2016 | ARTICLE NUMBER: 16112 | DOI: 10.1038/NPLANTS.2016.112

Neglecting legumes has compromised human health and sustainable food production

Christine H. Foyer[1,2*], Hon-Ming Lam[3], Henry T. Nguyen[4], Kadambot H. M. Siddique[5], Rajeev Varshney[6], Timothy D. Colmer[2,5], Wallace Cowling[5], Helen Bramley[7], Trevor A. Mori[8], Jonathan M. Hodgson[8], James W. Cooper[1], Anthony J. Miller[9], Karl Kunert[10], Juan Vorster[10], Christopher Cullis[11], Jocelyn A. Ozga[12], Mark L. Wahlqvist[13,14], Yan Liang[15], Huixia Shou[16], Kai Shi[17], Jingquan Yu[17], Nandor Fodor[1], Brent N. Kaiser[18], Fuk-Ling Wong[3], Babu Valliyodan[5] and Michael J. Considine[2,5,19]

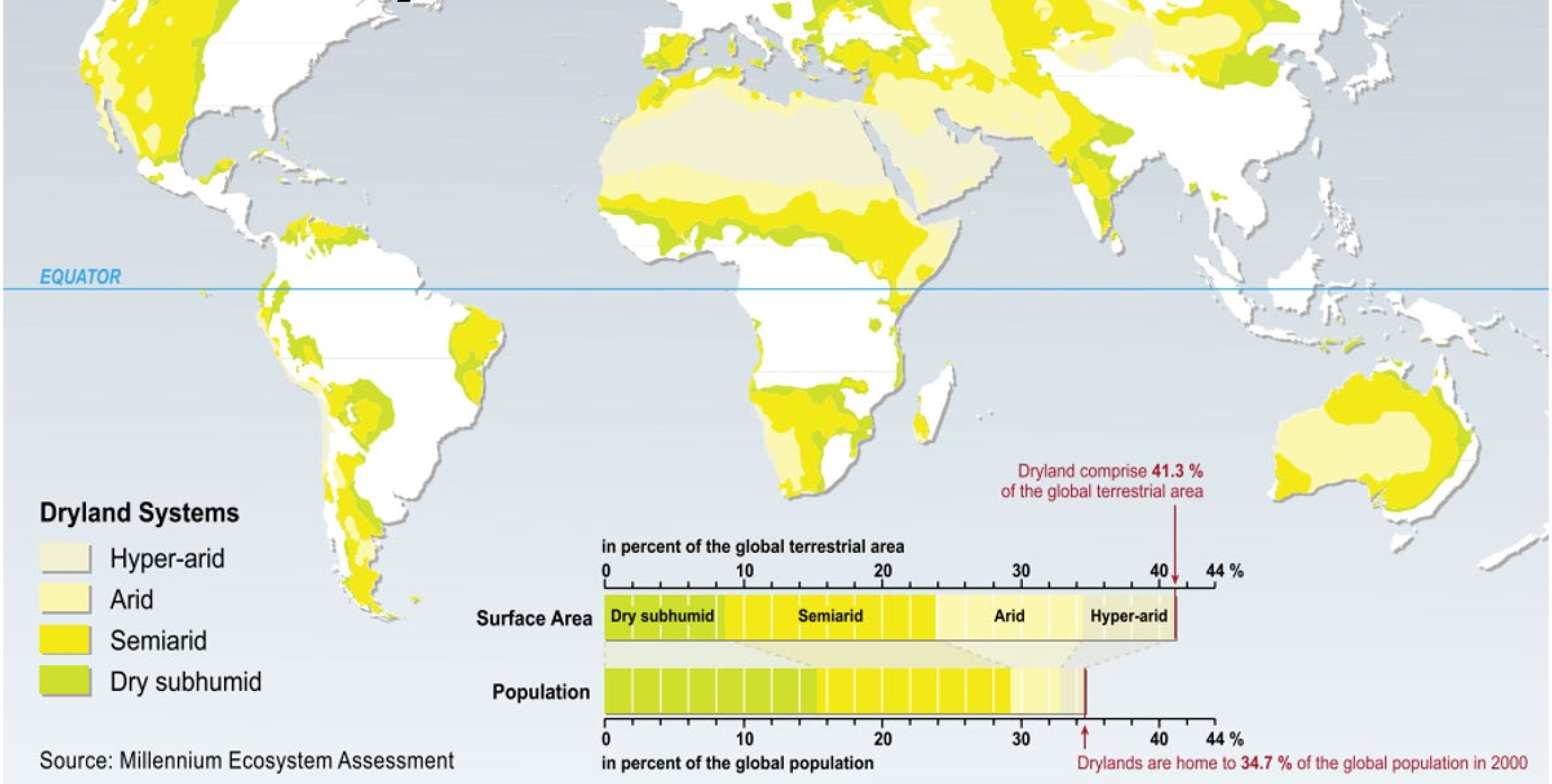
2016 INTERNATIONAL YEAR OF PULSES

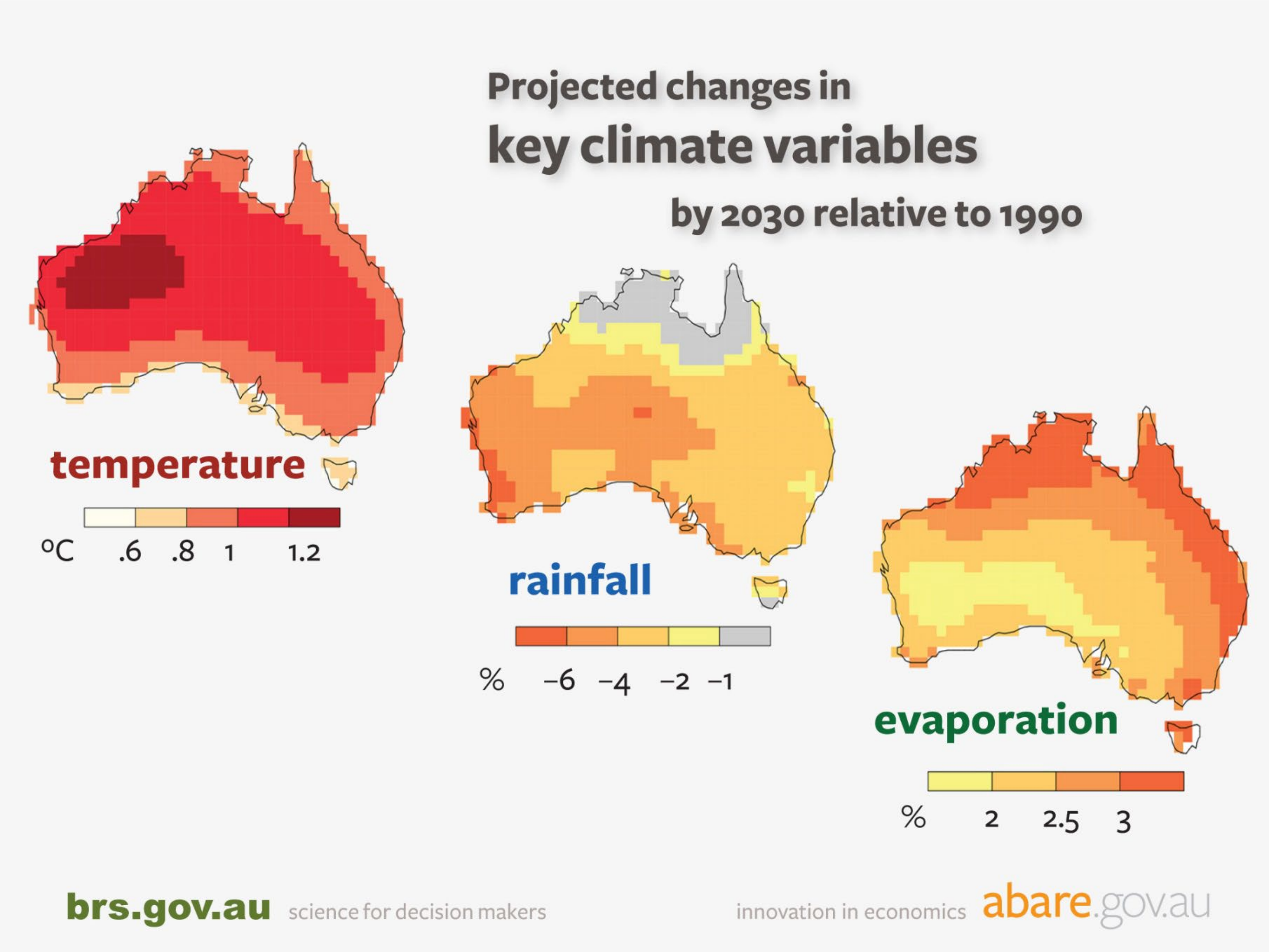
fao.org/pulses-2016 | pulses-2016@fao.org

Food and Agriculture Organization of the United Nations
Viale delle Terme di Caracalla
00153, Rome Italy

Food and Agriculture Organization of the United Nations

World drylands





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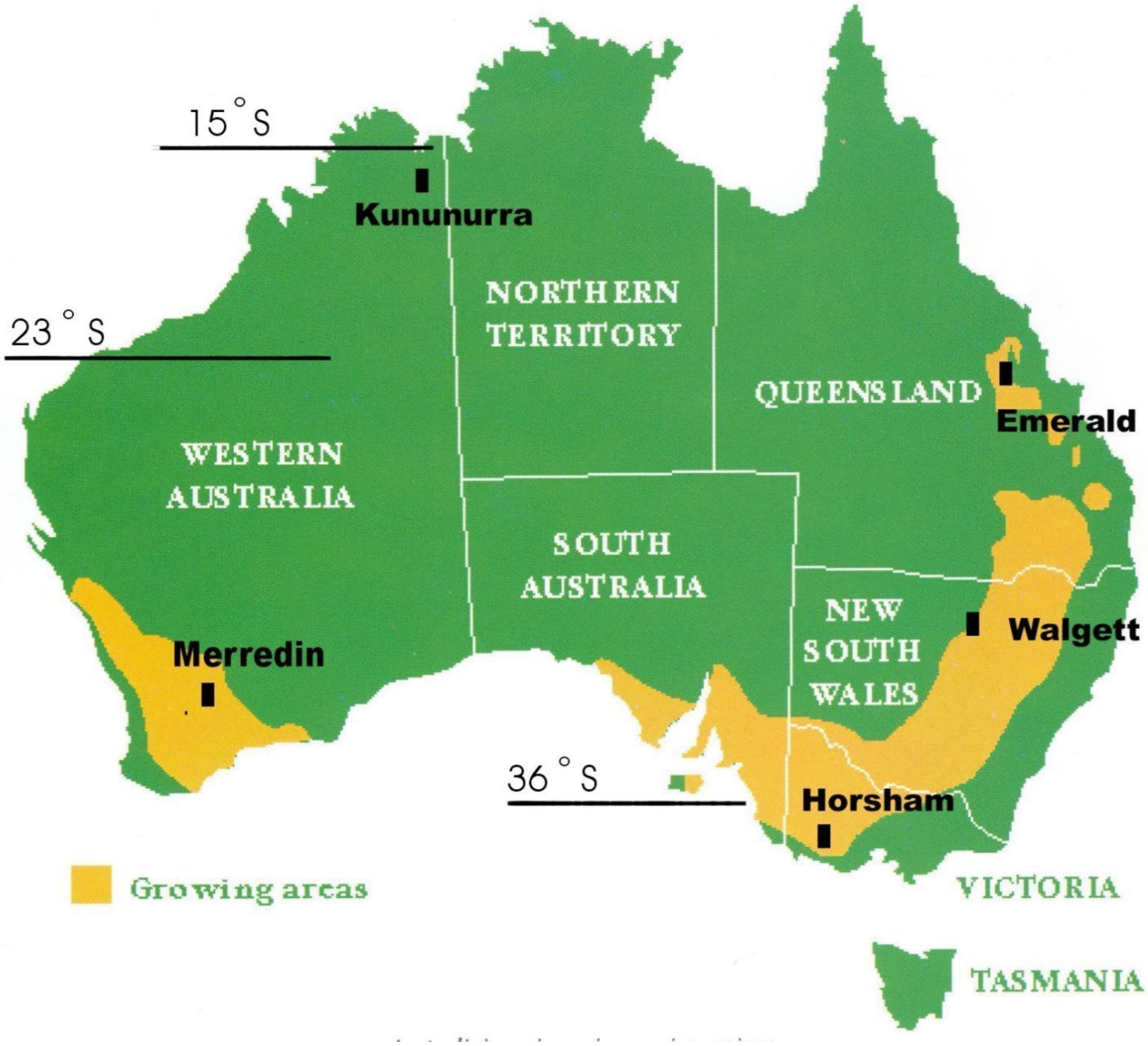
Drought alone is estimated to reduce yield by 30% annually.

This will become more severe under predicted climate change scenarios.

Targeted breeding and selection for tolerance to drought and heat are urgently required (including agronomic packages).



Grainbelt of Australia

Knights and Siddique (2003)

Mediterranean zone of Australia

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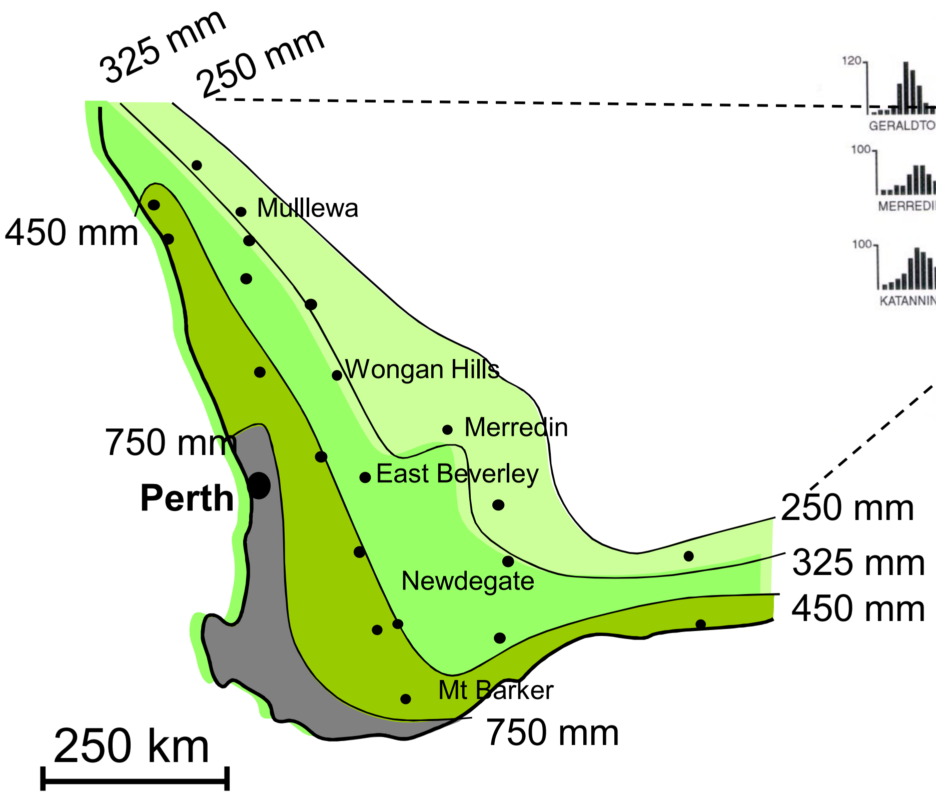
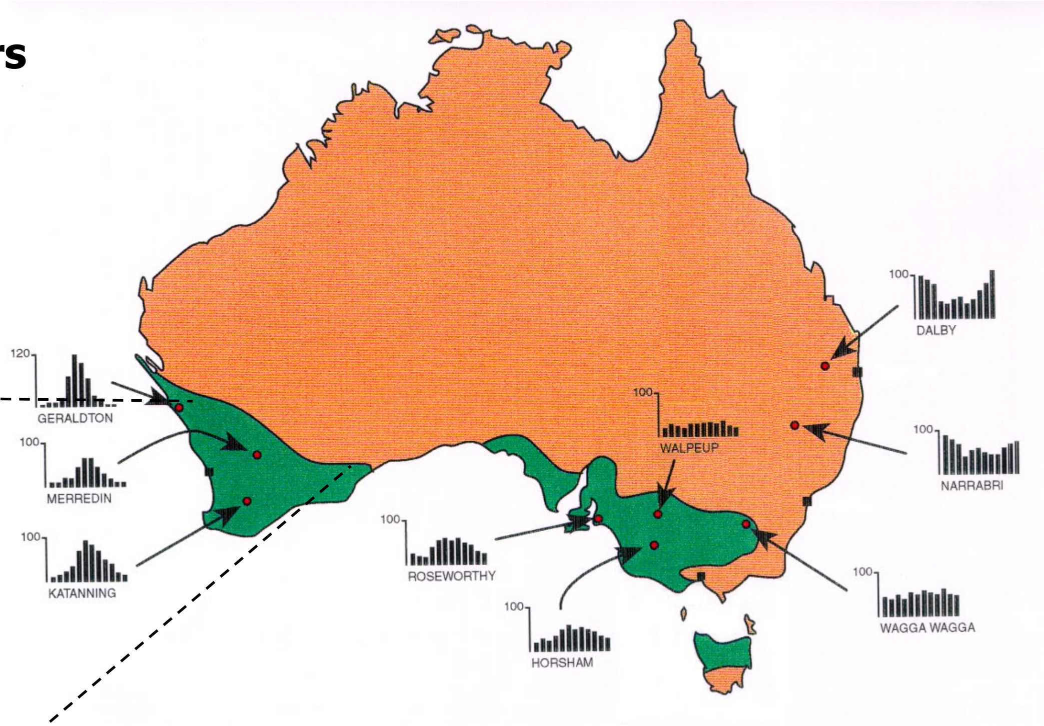
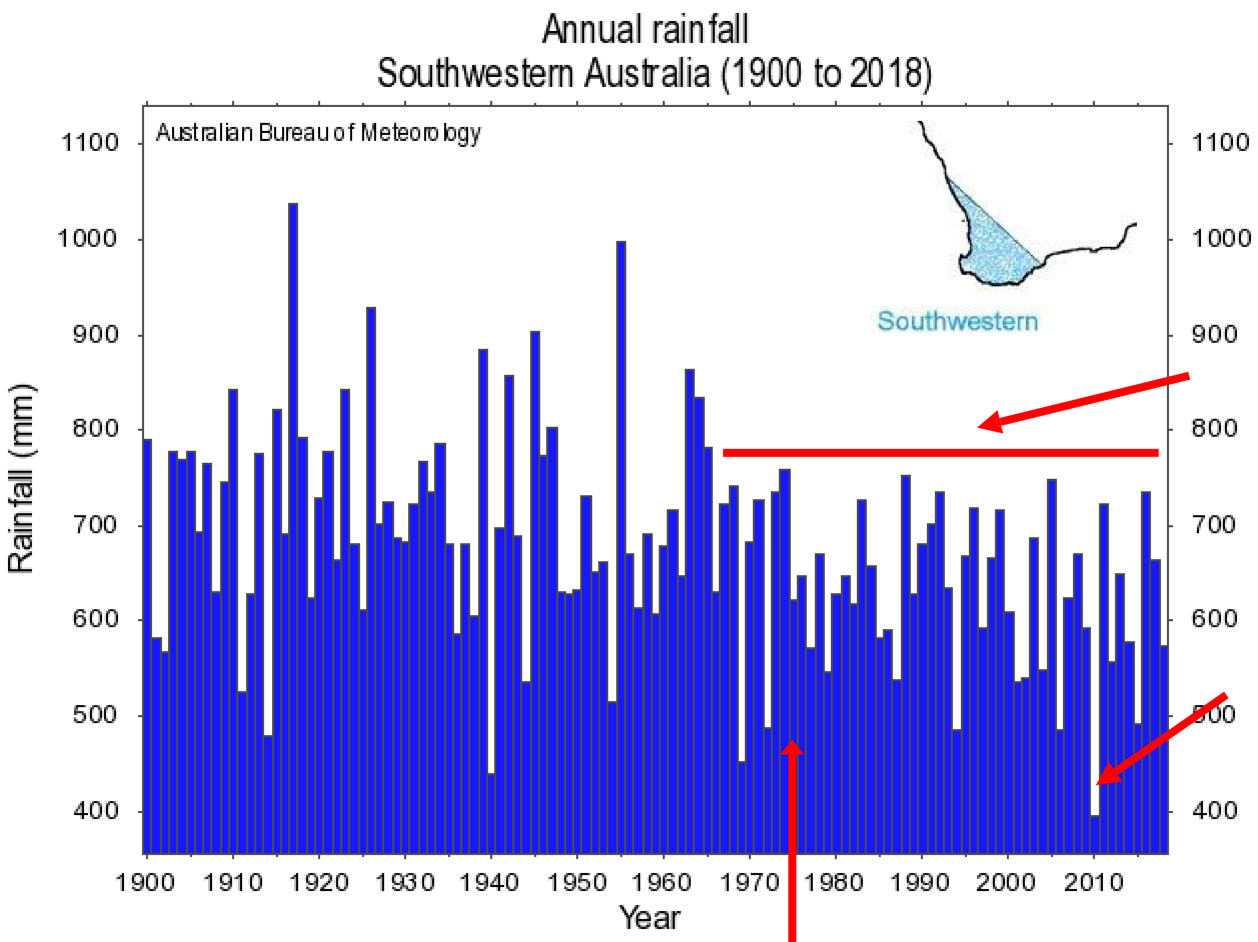
- **Climate: cold wet winters and hot dry summers**
- **12 million ha of arable land in the south west**
- **4,000 farmers, farm size 3,000 ha**





- **Rainfall focused between May-Aug**
- **Pulses are sown in autumn (Apr – Jun), often flowering from mid-Aug**

Southwestern Australia getting drier



2018

Lack of very wet years & decrease in variability

2010 - driest year on record

Significant drop in rainfall in southwest WA in the mid 1970's

Source: Bureau of Meteorology

SW WA is getting hotter

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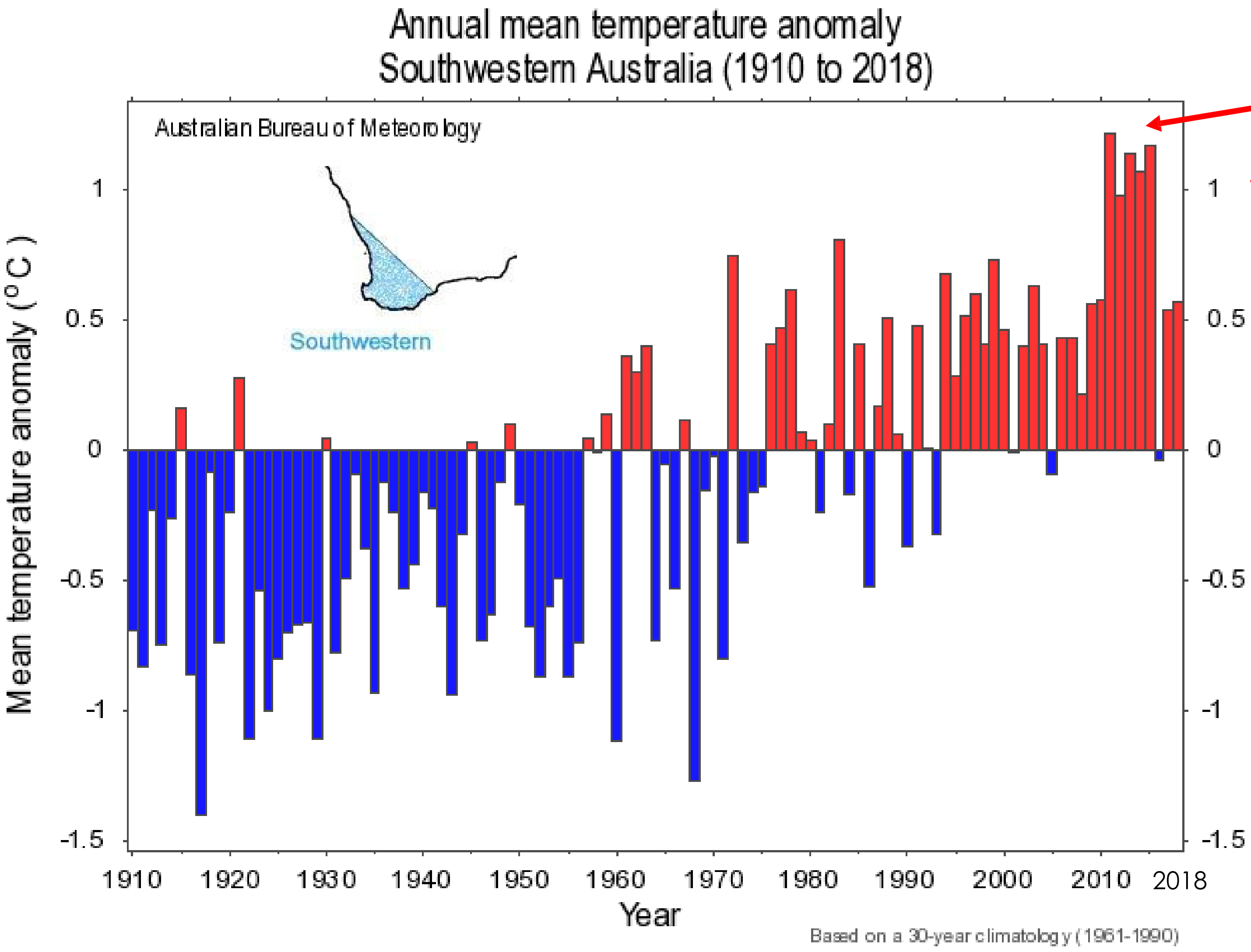
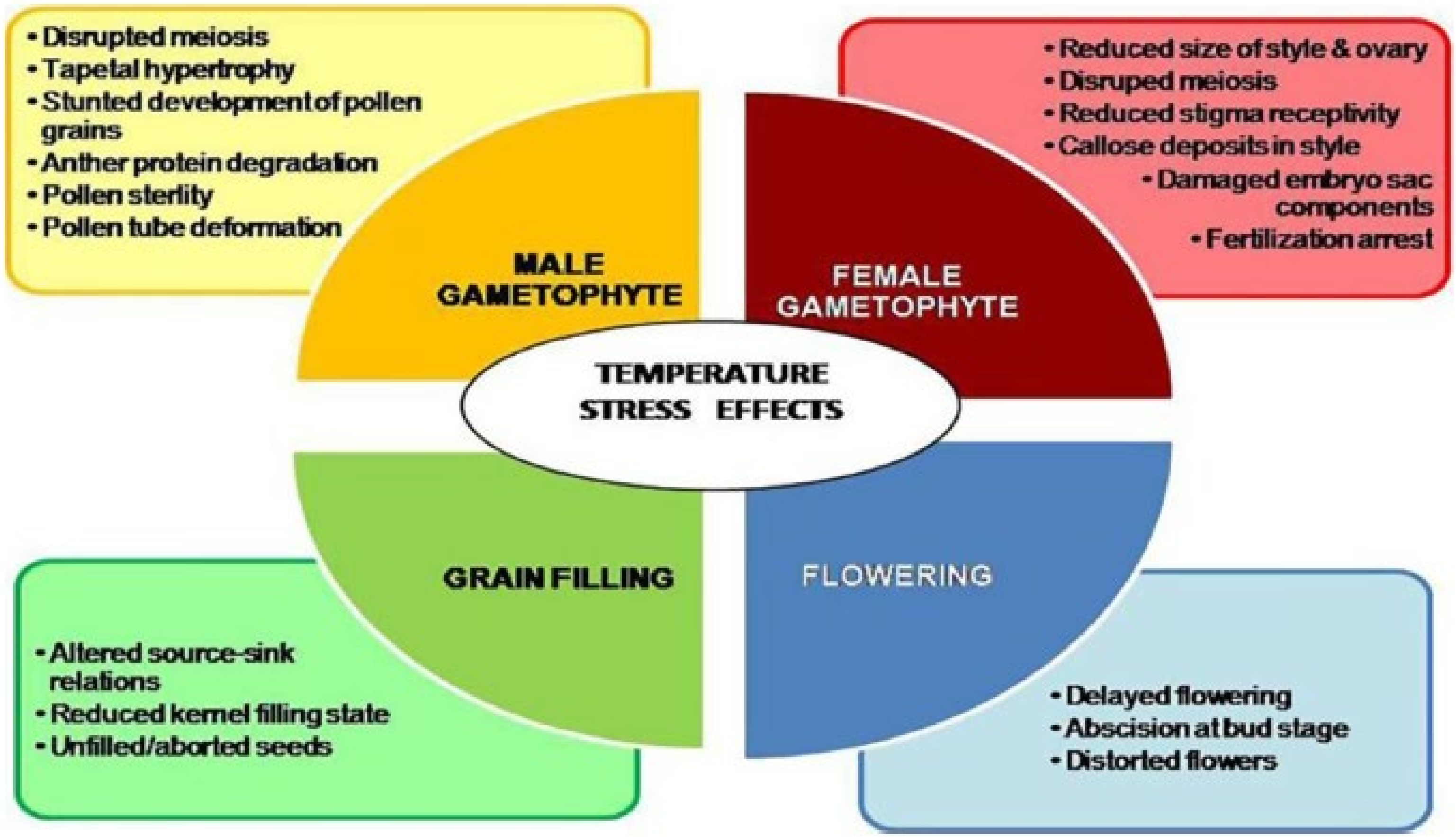


Four hottest years on record

Source: Bureau of Meteorology

http://www.bom.gov.au/cgi-bin/climate/change/timeseries.cgi?graph=tmean&area=swaus&season=0112&ave_yr=0



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Various effects of temperature stress on reproductive development stages in legumes

frontiers in Plant Science

REVIEW
published: 04 October 2017
doi: 10.3389/fpls.2017.01658

Food Legumes and Rising Temperatures: Effects, Adaptive Functional Mechanisms Specific to Reproductive Growth Stage and Strategies to Improve Heat Tolerance

Kumari Sita[1], Akanksha Sehgal[1], Bindumadhava HanumanthaRao[2], Ramakrishnan M. Nair[2], P. V. Vara Prasad[3], Shiv Kumar[4], Pooran M. Gaur[5], Muhammad Farroq[6,7,8], Kadambot H. M. Siddique[7], Rajeev K. Varshney[5,7] and Harsh Nayyar[1*]*

[1] Department of Botany, Panjab University, Chandigarh, India, [2] World Vegetable Center, South Asia, Hyderabad, India, [3] Sustainable Intensification Innovation Lab, Kansas State University, Manhattan, KS, United States, [4] International Center for Agricultural Research in the Dry Areas, Rabat, Morocco, [5] International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India, [6] Department of Agronomy, University of Agriculture Faisalabad, Faisalabad, Pakistan, [7] The UWA Institute of Agriculture, University of Western Australia, Perth, WA, Australia, [8] Department of Crop Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, Al-khod, Oman

OPEN ACCESS

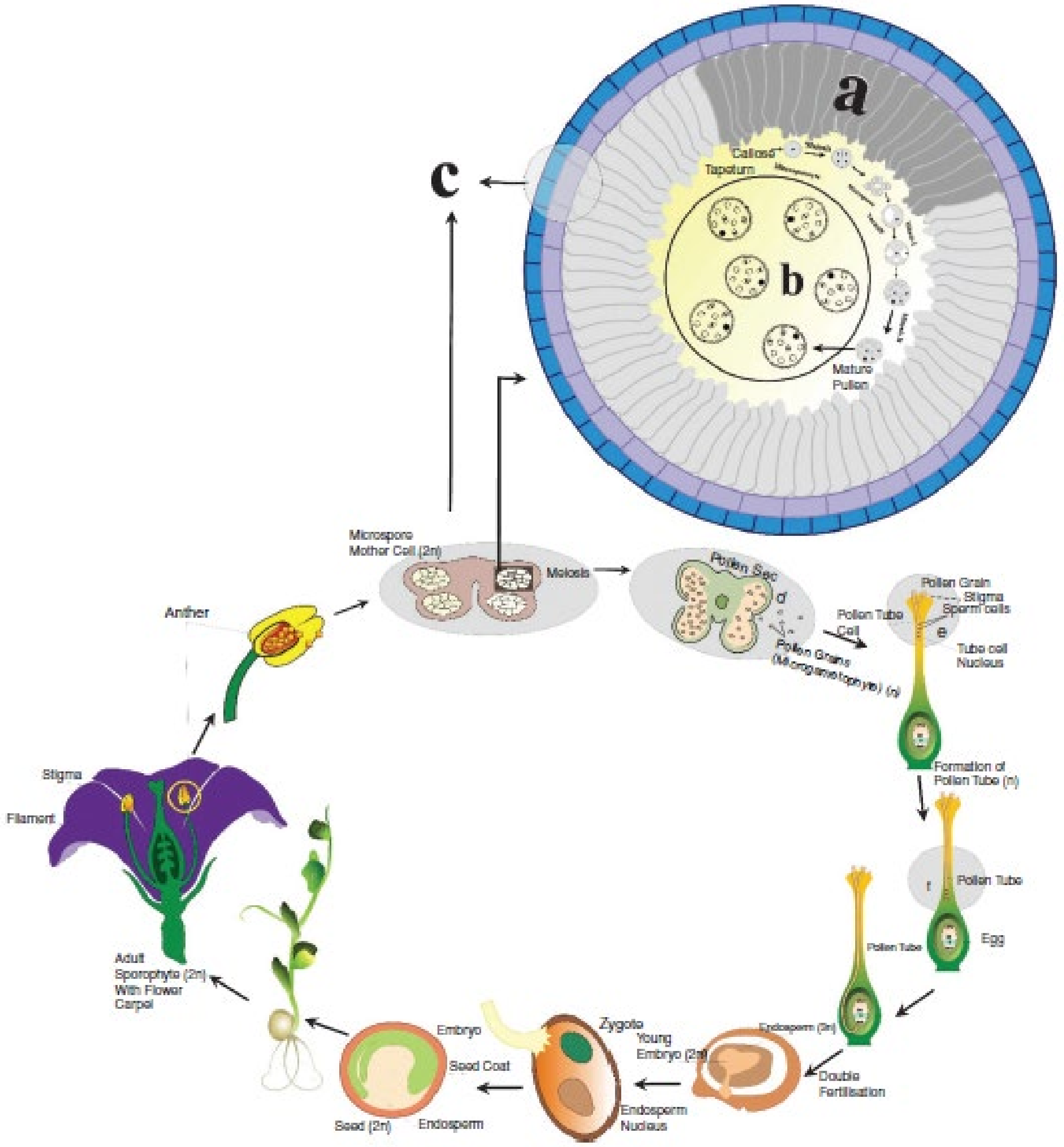
Edited by:
Oscar Vicente,
Universitat Politècnica de València,

Acta Physiol Plant (2017) 39:68
DOI 10.1007/s11738-017-2361-5

REVIEW

Temperature sensitivity of food legumes: a physiological insight

Kalpna Bhandari[1] · Kamal Dev Sharma[2] · Bindumadhava Hanumantha Rao[3] · Kadambot H. M. Siddique[4] · Pooran Gaur[5] · Shiv Kumar Agrawal[6] · Ramakrishnan M. Nair[3] · Harsh Nayyar[1]



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(a) Disintegration of tapetum layer that offers nutrients to pollen,

(b) disruption of pollen and pollen sterility,

(c) anther dehiscence due to degeneration of tapetum layer and reduced concentration and availability of soluble sugars in anther walls,

(d) pollen shattering due to meagre pollen adhesion on stigma which reduces pollen viability,

(e) reduced germination of pollen grains on pollen tube due to poor tube growth and pollen production, and less stigma receptivity

CSIRO PUBLISHING

Crop & Pasture Science, 2017, **68**, 985–1005
http://dx.doi.org/10.1071/CP17012

Review

Heat stress in grain legumes during reproductive and grain-filling phases

Muhammad Farooq[A,B,C,F], *Faisal Nadeem*[A], *Nirmali Gogoi*[D], *Aman Ullah*[A], *Salem S. Alghamdi*[C], *Harsh Nayyar*[E], *and Kadambot H. M. Siddique*[B]

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[B]The UWA Institute of Agriculture and School of Agriculture & Environment, The University of Western Australia, LB 5005, Perth, WA 6001, Australia.
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[E]Department of Botany, Panjab University, Chandigarh 160 014, India.
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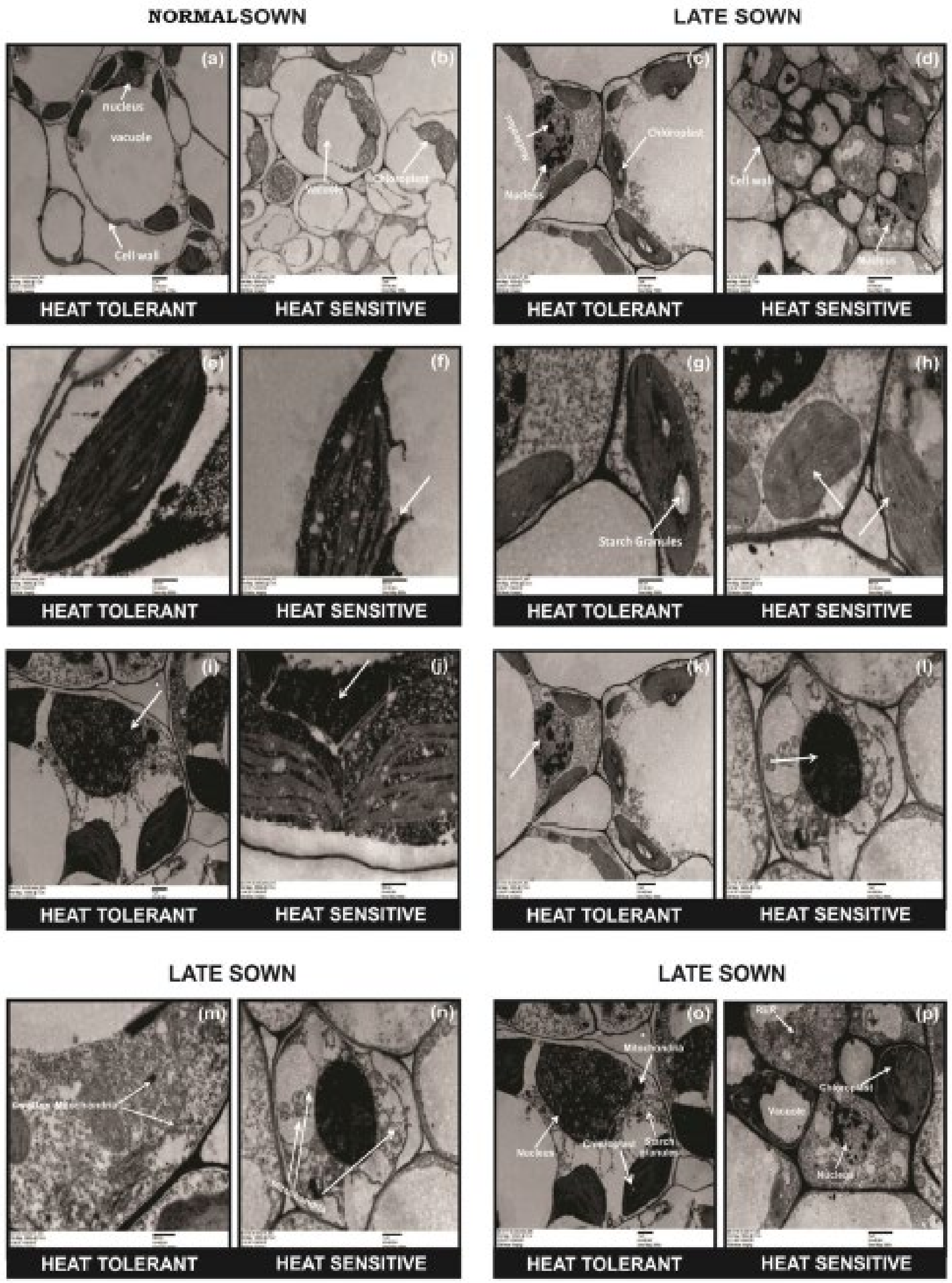

Observations of the ultra-structure of leaves in normal sown (NS) and late sown (LS) lentil plants. Heat Tolerant and Sensitive genotyeos

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Disrupted cell organelles, thickened cell wall, disrupted chloroplast, damaged and increased number of mitochondria,

dispersed chromatin in nucleus, shrinkage of vacuoles, and fewer and smaller starch granules in the chloroplast in a heat-sensitive genotype under LS conditions.

frontiers in Plant Science

ORIGINAL RESEARCH
published: 19 May 2017
doi: 10.3389/fpls.2017.00744

Identification of High-Temperature Tolerant Lentil (*Lens culinaris* Medik.) Genotypes through Leaf and Pollen Traits

Kumari Sita[1], Akanksha Sehgal[1], Jitendra Kumar[2], Shiv Kumar[3], Sarvjeet Singh[4], Kadambot H. M. Siddique[5] and Harsh Nayyar[1]*

[1] Department of Botany, Panjab University, Chandigarh, India, [2] Indian Institute of Pulses Research, Kanpur, India, [3] International Center for Agricultural Research in the Dry Areas, Rabat, Morocco, [4] Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India, [5] The UWA Institute of Agriculture, The University of Western Australia, Perth, WA, Australia

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SEM observations under normal (NS) and late-sown (LS) environment on reproductive components in heat tolerant nd sensitive lentil genotypes.

Note the (l) lack of pollen tube growth in the stylar region of LS heat sensitive genotypes compared with (k) heat-tolerant genotypes.

frontiers in Plant Science

ORIGINAL RESEARCH
published: 19 May 2017
doi: 10.3389/fpls.2017.00744

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[1] Department of Botany, Panjab University, Chandigarh, India, [2] Indian Institute of Pulses Research, Kanpur, India, [3] International Center for Agricultural Research in the Dry Areas, Rabat, Morocco, [4] Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India, [5] The UWA Institute of Agriculture, The University of Western Australia, Perth, WA, Australia

scientific reports

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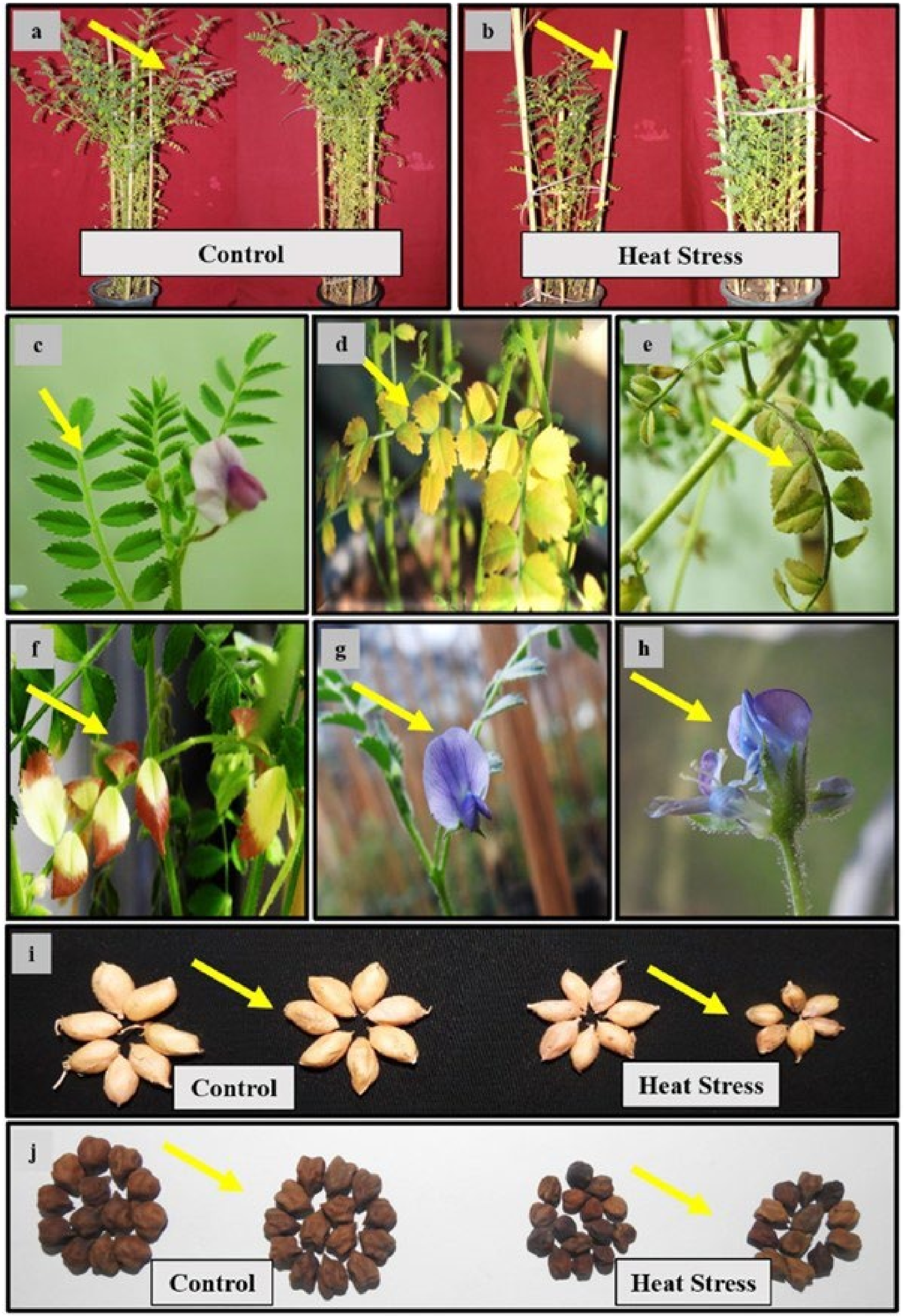
OPEN

Understanding the effect of heat stress during seed filling on nutritional composition and seed yield in chickpea (*Cicer arietinum* L.)

Poonam Devi[1], Rashmi Awasthi[1], Uday Jha[2]✉, Kamal Dev Sharma[3], P. V. Vara Prasad[4], Kadambot H. M. Siddique[5], Manish Roorkiwal[6]✉ & Harsh Nayyar[1]✉

Increasing temperature affects all food crops, thereby reducing their yield potential. Chickpea is a cool-season food legume vital for its nutritive value, but it is sensitive to high temperatures (> 32/20 °C maximum/minimum) during its reproductive and seed-filling stages. This study evaluated the effects of heat stress on yield and qualitative traits of chickpea seeds in a controlled environment. Chickpea genotypes differing in heat sensitivity [two heat-tolerant (HT) and two heat-sensitive (HS)] were raised in pots, initially in an outdoor environment (average 23.5/9.9 °C maximum/minimum), until the beginning of pod set (107–110 days after sowing). At this stage, the plants were moved to a controlled environment in the growth chamber to impose heat stress (32/20 °C) at the seed-filling stage, while maintaining a set of control plants at 25/15 °C. The leaves of heat-stressed plants of the HT and HS genotypes showed considerable membrane damage, altered stomatal conductance, and reduced leaf water content, chlorophyll content, chlorophyll fluorescence, and photosynthetic ability (RuBisCo, sucrose phosphate synthase, and sucrose activities) relative to their corresponding controls. Seed filling duration and seed rate drastically decreased in heat-stressed plants of the HT and HS genotypes, severely reducing seed weight plant^{-1} and single seed weight, especially in the HS genotypes. Yield-related traits, such as pod number, seed number, and harvest index, noticeably decreased in heat-stressed plants and more so in the HS genotypes. Seed components, such as starch, proteins, fats, minerals (Ca, P, and Fe), and storage proteins (albumin, globulins, glutelin, and prolamins), drastically declined, resulting in poor-quality seeds, particularly in the HS genotypes. These findings revealed that heat stress significantly reduced leaf sucrose production, affecting the accumulation of various seed constituents, and leading to poor nutritional quality. The HT genotypes were less affected than the HS genotypes because of the greater stability of their leaf water status and photosynthetic ability, contributing to better yield and seed quality traits in a heat-stressed environment.

Climate change is impacting global food and nutritional security[1]. As a result of the unpredictability of rising temperatures, agricultural yields have dropped sharply as the number of hot days and nights increases while the number of cold days and nights decreases[2–5]. Based on their genetic structure, plants thrive in a preferred temperature range, with exposure above this range causing heat stress (HS)[6]. Changes in the degree and duration of high temperatures affect the entire plant life cycle, including morphological, reproductive, and developmental processes, owing to considerable breakdown of the cellular machinery. Heat stress during the reproductive and



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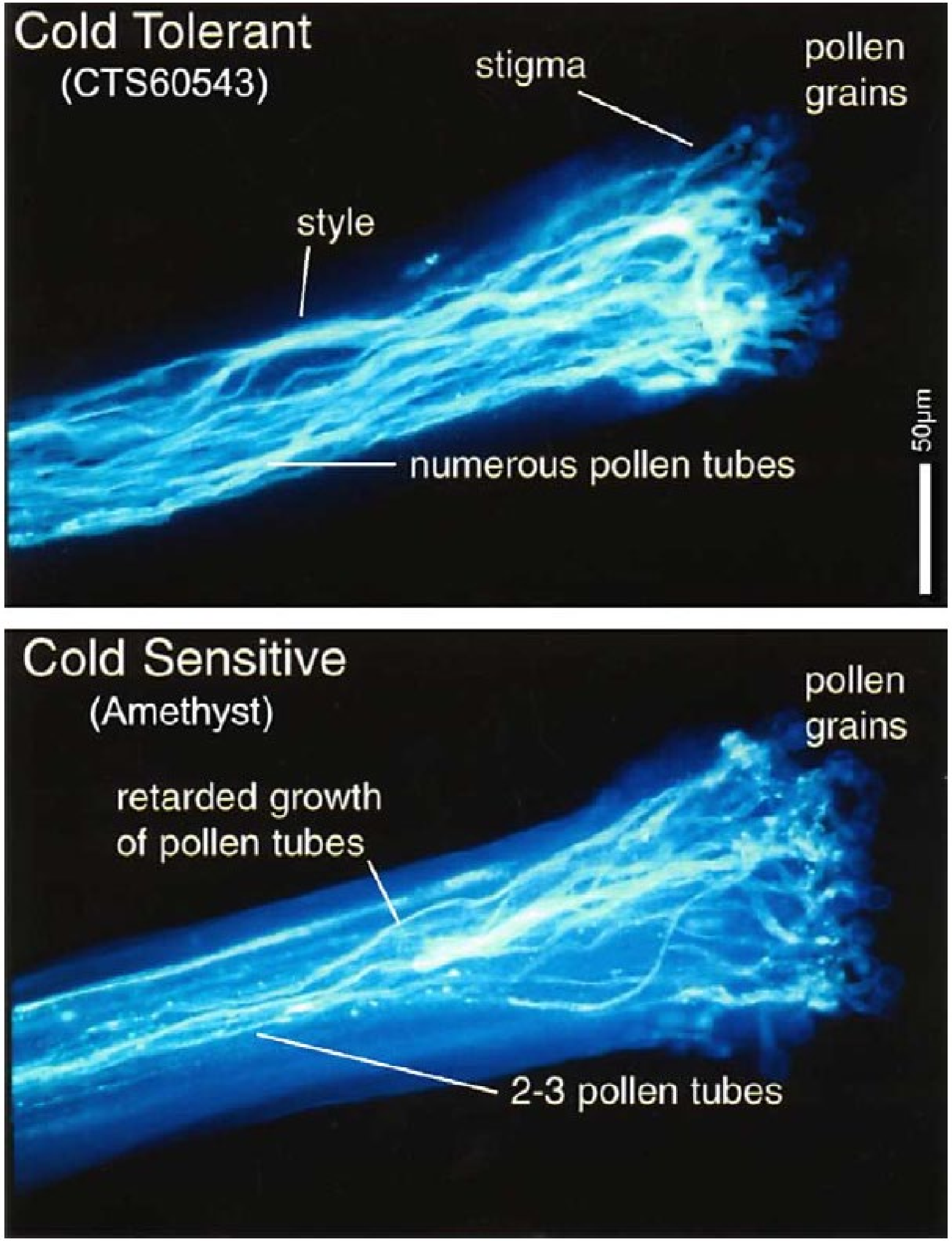
Morphological effects of heat stress (HS) observed on chickpea plants: plant height with more number of pods; under control (a), reduced plant height with lower number of pods; under HS (b),
healthy leaves; under control (c), leaf chlorosis under HS (d), leaves necrosis; under HS (e), leaf scorching/leaf bleaching of leaflets due to photooxidation under HS (f),

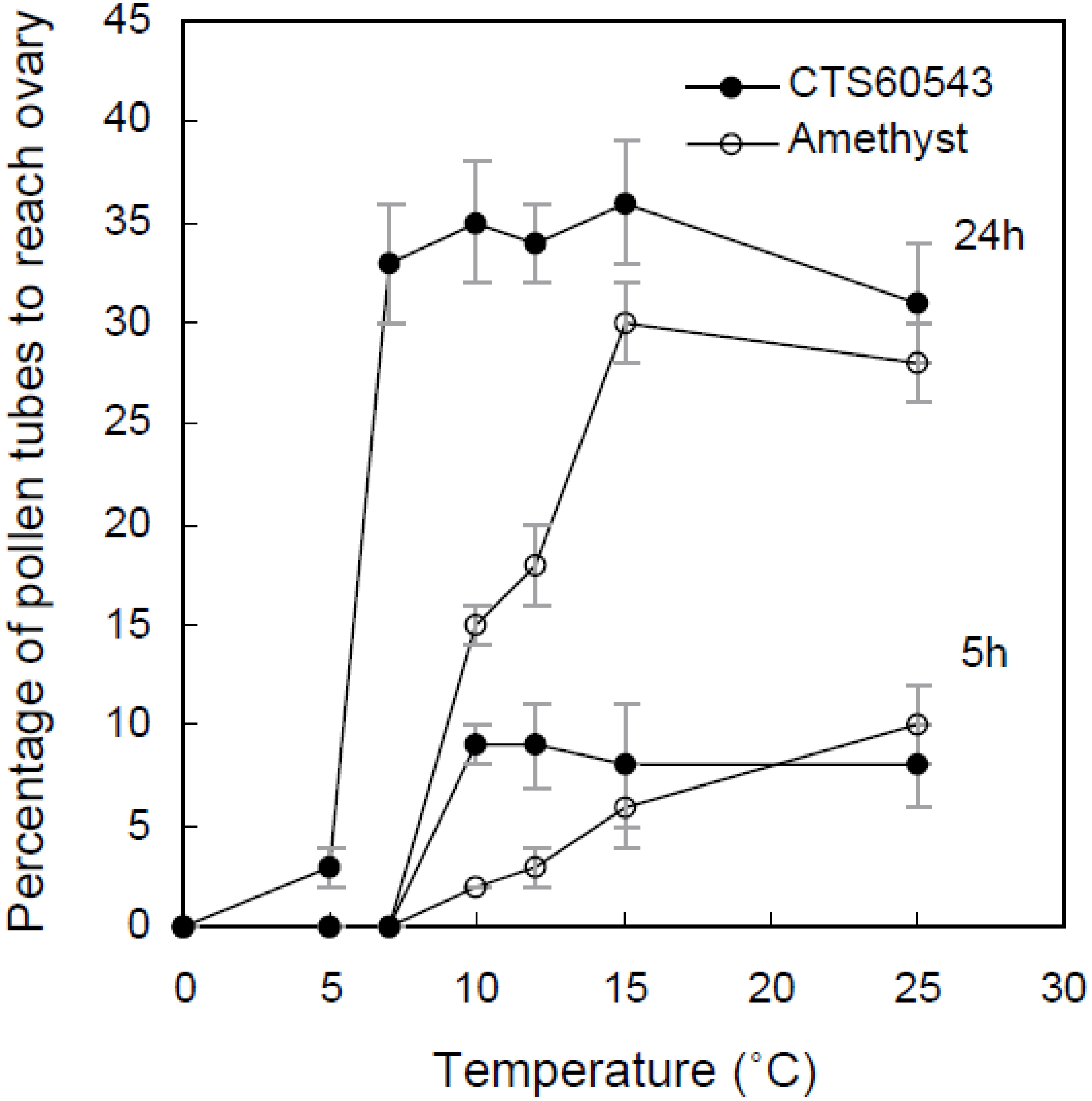
healthy flower; under the control (g), aborted flower under HS (h), comparative pod size under control and HS (i) and comparative seed size under control and HS environment (j).



Chilling Tolerance in Chickpea

More pollen tubes of CTS60543 grow down the style to the ovary at low temperature stress (7oC) compared to Amethyst.

Styles were fixed 24 h after pollination and stained with aniline blue.



The effect of temperature on the proportion of germinated pollen tubes to reach the ovary after 5 and 24 h in hand pollinated flowers in vivo in sensitive and tolerant genotypes.

Available online at www.sciencedirect.com

SCIENCE DIRECT

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Field Crops Research 90 (2004) 323–334

Field Crops Research

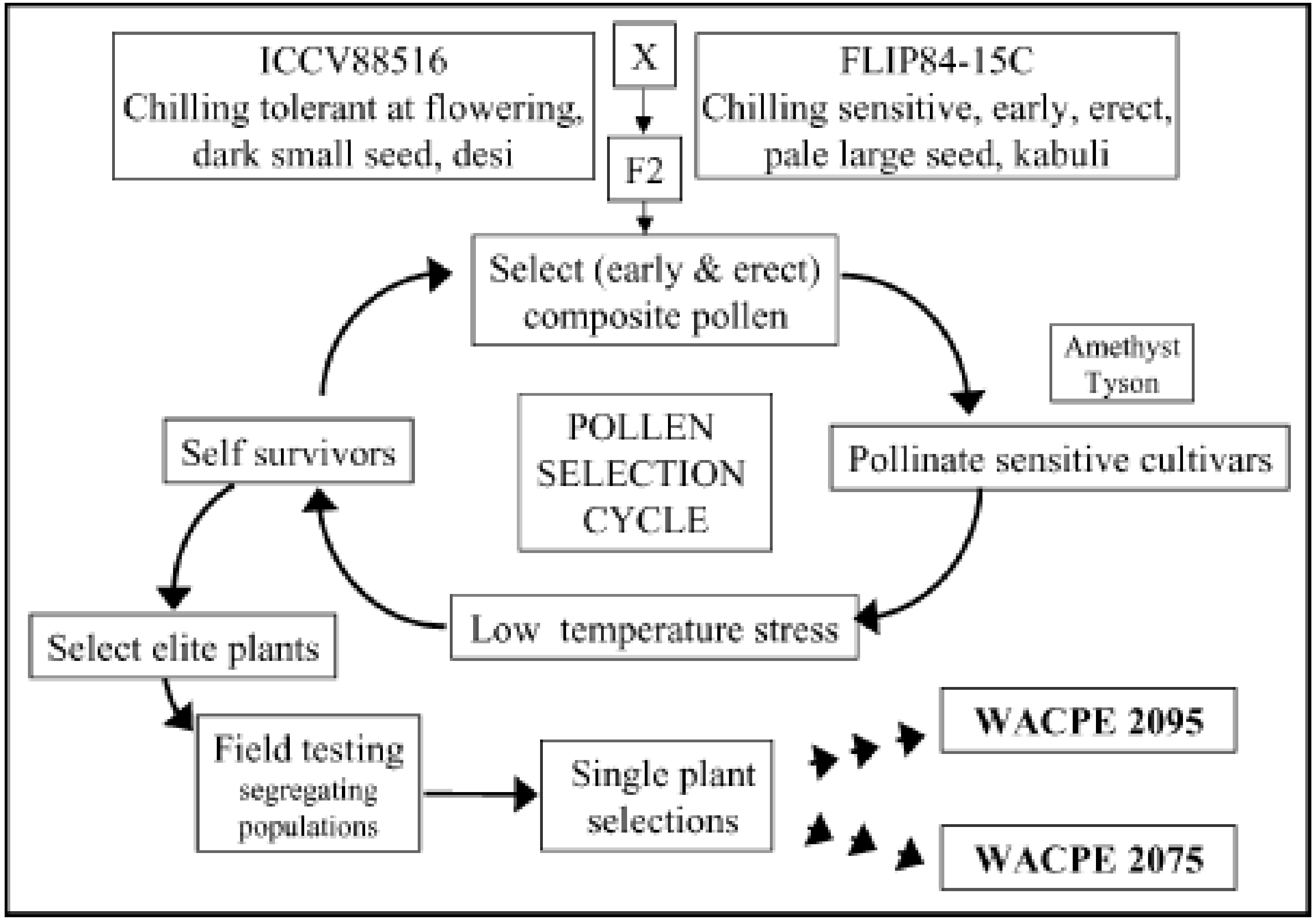
www.elsevier.com/locate/fcr

Response of chickpea genotypes to low temperature stress during reproductive development

H.J. Clarke*, K.H.M. Siddique

Centre for Legumes in Mediterranean Agriculture, Faculty of Natural and Agricultural Sciences, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia

Received 22 December 2003; received in revised form 6 April 2004; accepted 7 April 2004



Schedule for chickpea improvement, including repeat cycles of pollen selection at low temperature stress, which was used successfully to develop new cultivars for Australia

Euphytica 139: 65–74, 2004.

65

Pollen selection for chilling tolerance at hybridisation leads to improved chickpea cultivars

Heather J. Clarke[1,*], Tanveer N. Khan[1,2] & Kadambot H.M. Siddique[1]
[1]*Centre for Legumes in Mediterranean Agriculture, University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia;* [2]*Department of Agriculture Western Australia, Locked Bag 4, Bentley Delivery Centre, WA 6983, Australia; (*author for correspondence: e-mail: hclarke@cyllene.uwa.edu.au)*

Plant Physiology and Biochemistry 118 (2017) 199–217

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journal homepage: www.elsevier.com/locate/plaphy

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Review

Effects, tolerance mechanisms and management of salt stress in grain legumes

CrossMark

Muhammad Farooq [a, b, c, *], Nirmali Gogoi [d], Mubshar Hussain [e], Sharmistha Barthakur [f], Sreyashi Paul [d], Nandita Bharadwaj [d], Hussein M. Migdadi [c], Salem S. Alghamdi [c], Kadambot H.M. Siddique [b]

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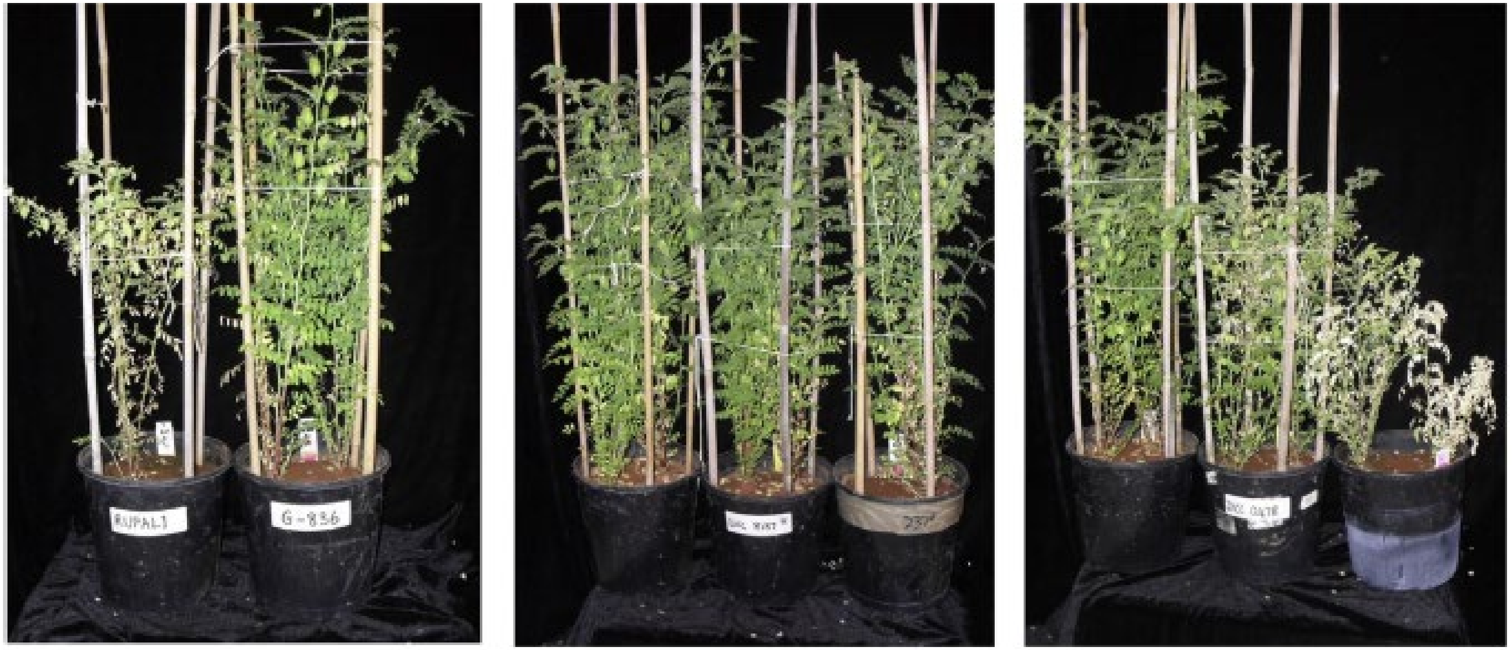
[c] College of Food and Agricultural Sciences, King Saud University, Riyadh 11451, Saudi Arabia
[d] Department of Environmental Science, Tezpur University, Tezpur 784028, Assam, India
[e] Department of Agronomy, Bahauddin Zakariya University Multan, Pakistan
[f] National Research Centre on Plant Biotechnology, Pusa Campus, New Delhi 110012, India

Influence of salt stress on the growth of different chickpea genotypes.

Genotype DICC 8187 performed better under salt stress than the other genotypes.



80 mM | 80 mM | 0 mM | 50 mM | 80 mM | 0 mM | 50 mM | 80 mM

Rupali | Genesis 836 | DICC 8187 | DICC 0478

Terminal drought

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The soil moisture stress that occurs during flowering, pod filling and seed development stage

A major constraint in >80% of global chickpea area

Breeding and selection for drought resistant genotypes are required

Overall objectives –

- Identify chickpea genotypes with resistance to drought in Mediterranean-type environments;
- Investigate the underlying physiological mechanisms.

Evaluation of germplasm from ICRISAT and Australia

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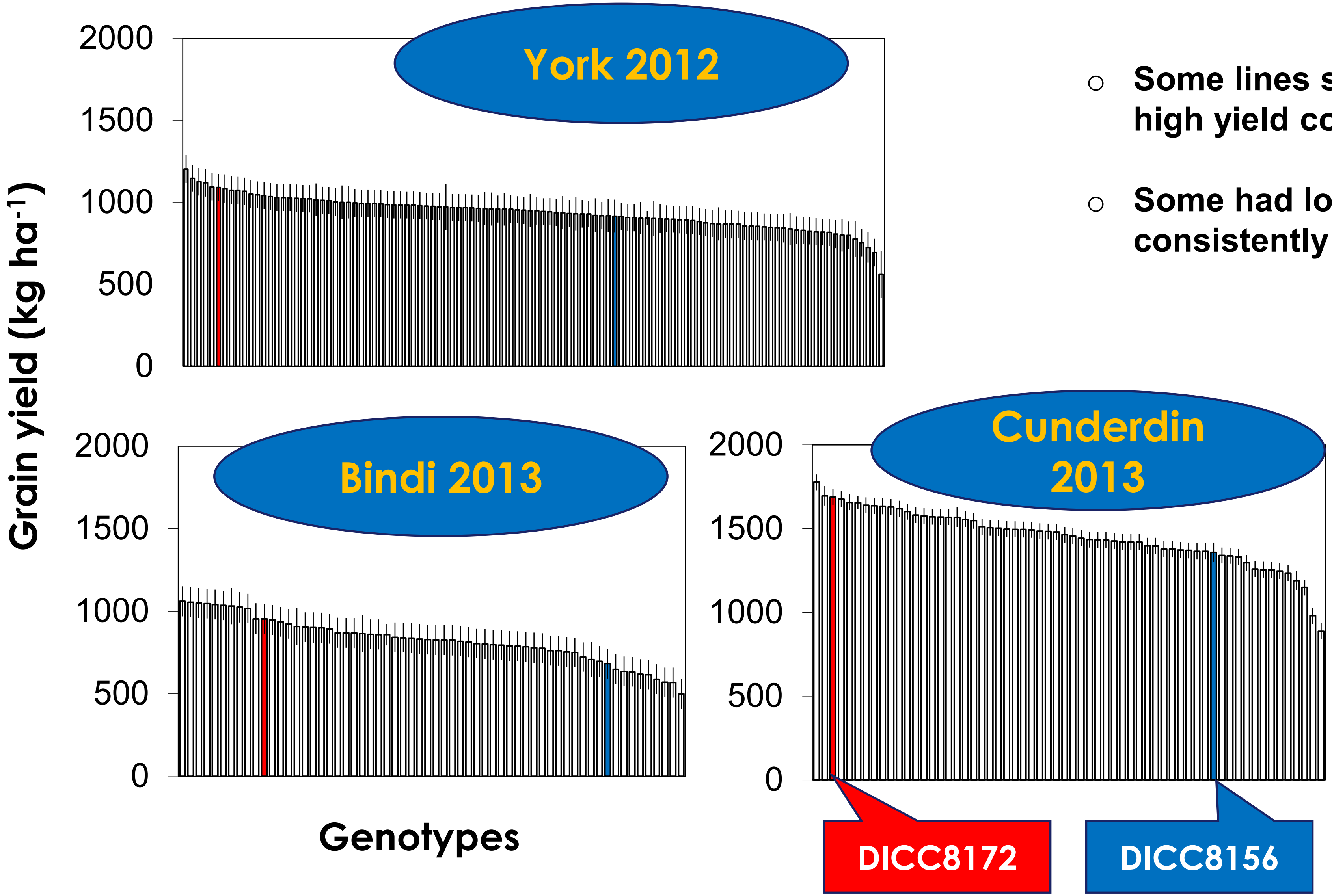
2012

York - water-limited environment, 108 lines; large plots

2013

Bindi Bindi & Cunderdin - water-limited environment, 62 lines; large plots

Glasshouse - controlled environment; Physiology of drought



- Some lines showed high yield consistently
- Some had low yield consistently

Large variation in seed yield across the field sites

Physiological responses of chickpea to drought stress

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Plants in wheelie bins (over 100kg field soil/bin) 10 times larger than in small pots

More nutrient and water resources – mimics field situation better

Water treatments

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Started at early podding

- Well-watered (WW)
- Water-stressed (WS)

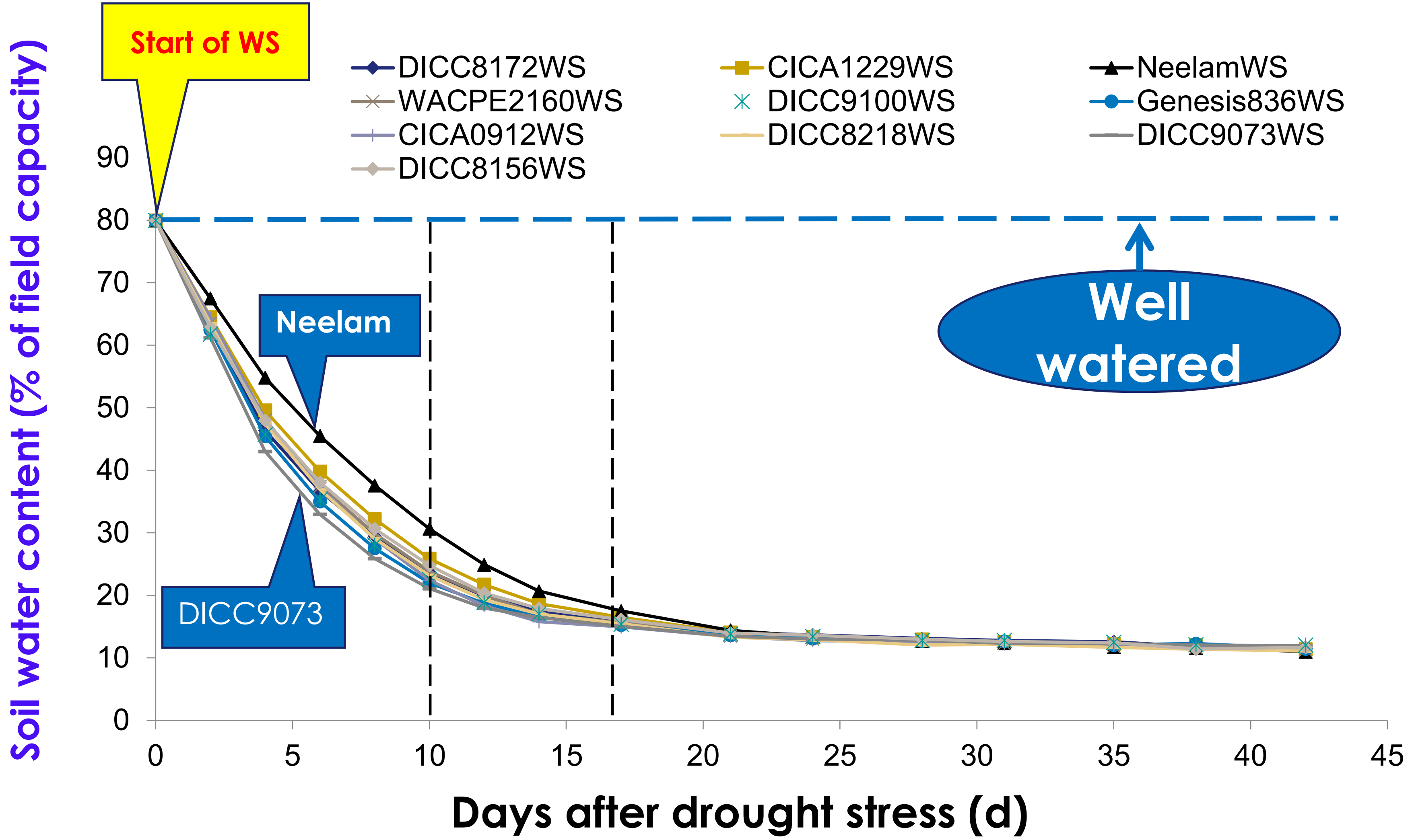


Monitor soil water content precisely is critical to drought study

80L wheelie bins

A custom-made balance to weigh bins

Change in soil water content after drought stress



Genotypic difference – 24 days after stopping water

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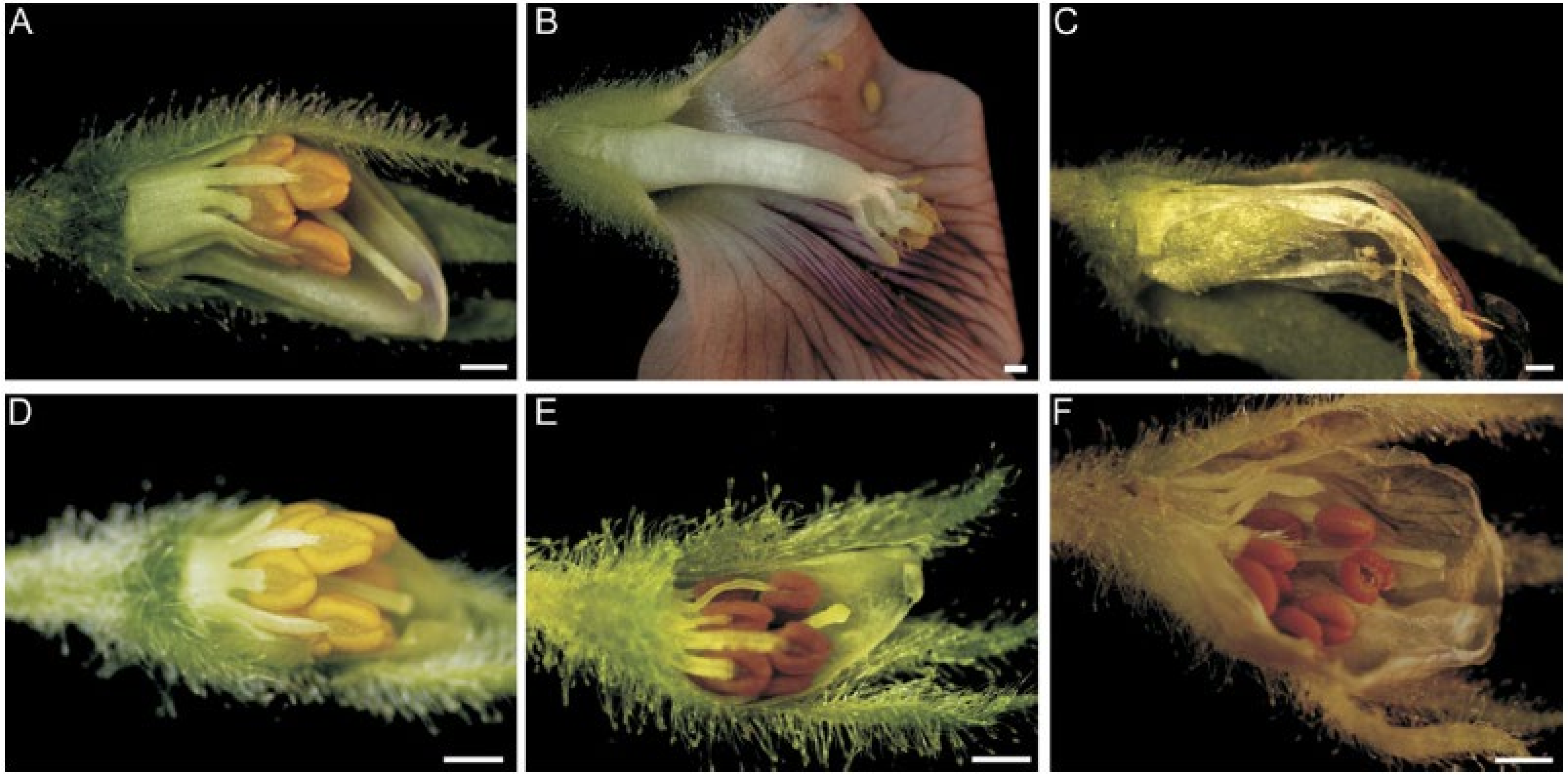
Neelam

CICA0912

The soil water content was similar among different genotypes - ~2.6% (w/w), equivalent to 13% of SFC.



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Flowers of Rupali at three stages of development in well-watered (A–C) and water-stressed plants (D–F)

Flowers in the WS plants did not burst when LWP decreased to –1.2 MPa.

Journal of Experimental Botany, Vol. 61, No. 2, pp. 335–345, 2010
doi:10.1093/jxb/erp307 Advance Access publication 23 October, 2009
This paper is available online free of all access charges (see http://jxb.oxfordjournals.org/open_access.html for further details)

Journal of Experimental Botany
www.jxb.oxfordjournals.org

RESEARCH PAPER

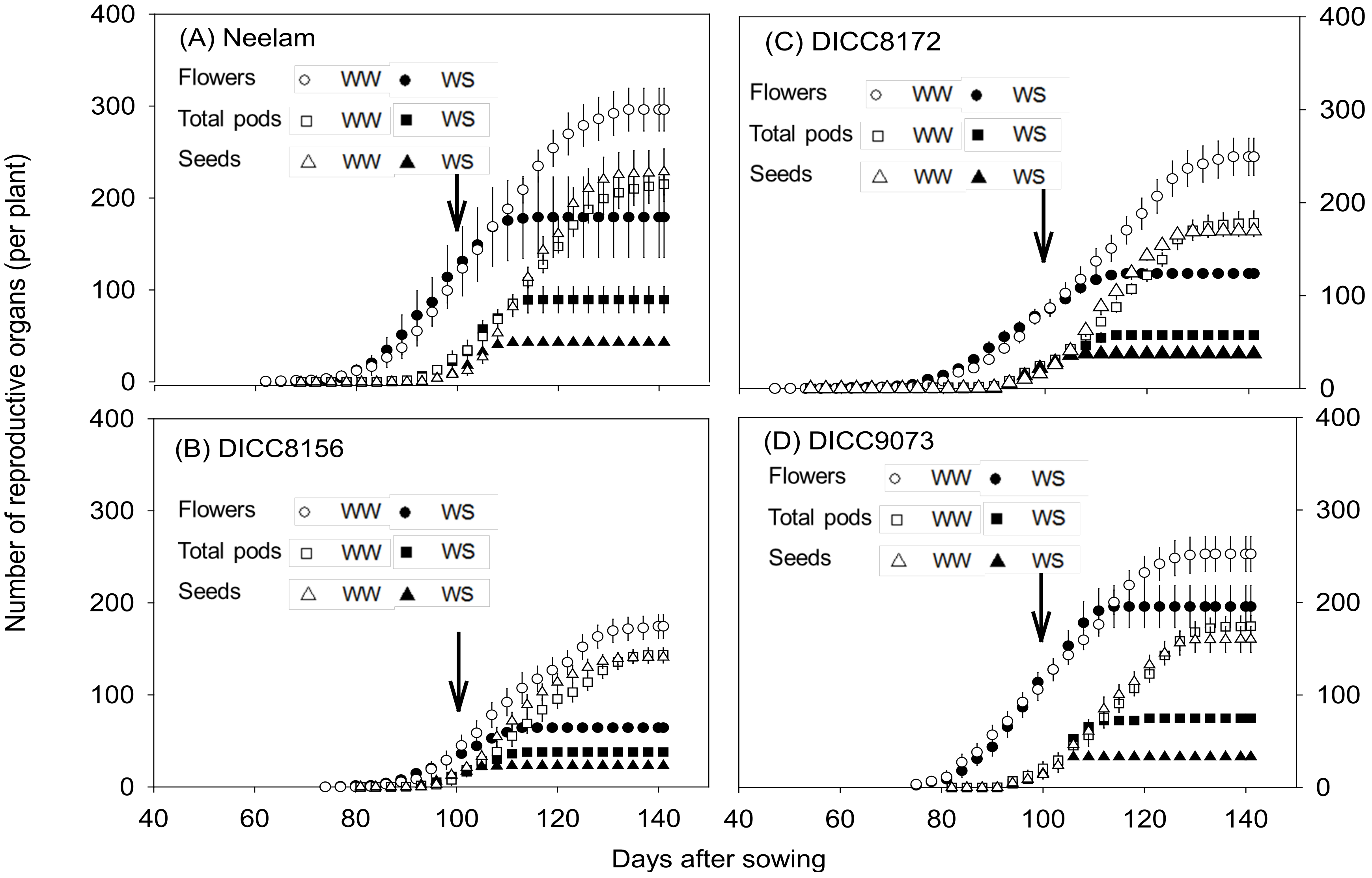
Flower numbers, pod production, pollen viability, and pistil function are reduced and flower and pod abortion increased in chickpea (*Cicer arietinum* L.) under terminal drought

Xiangwen Fang[1,2,4,*], Neil C. Turner[1,4], Guijun Yan[3,4], Fengmin Li[2] and Kadambot H. M. Siddique[1,4]

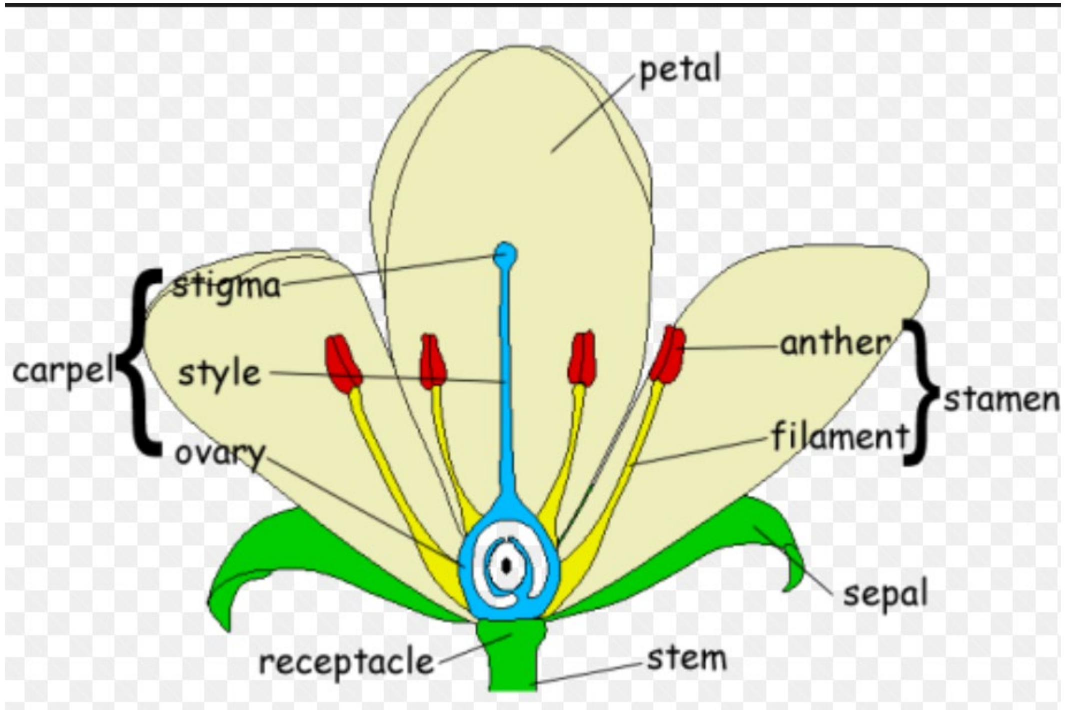
[1] Centre for Legumes in Mediterranean Agriculture, M080, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia
[2] MOE Key Laboratory of Arid and Grassland Ecology, School of Life Sciences, Lanzhou University, Lanzhou, Gansu Province 730000, PR China
[3] School of Plant Biology, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia
[4] Institute of Agriculture, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia

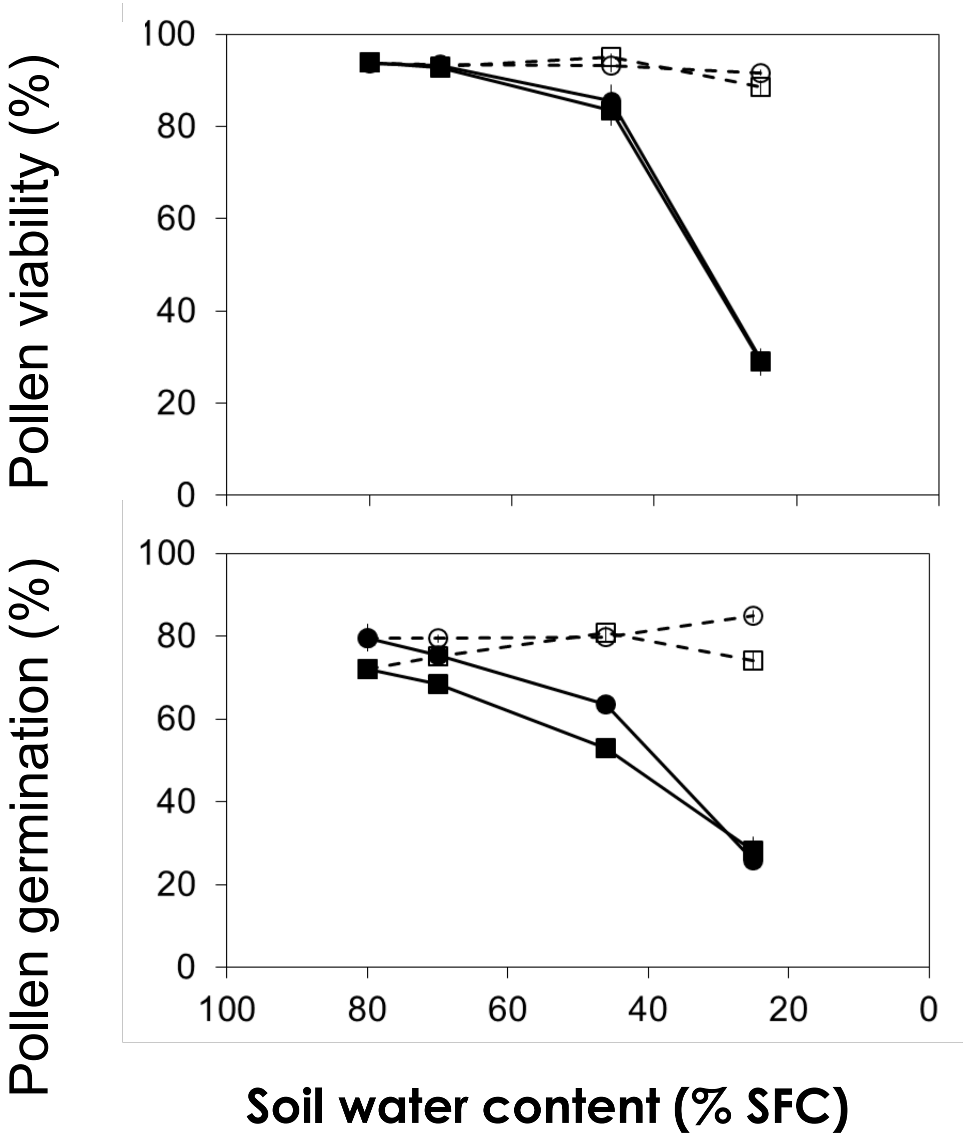
[*] To whom correspondence should be addressed. E-mail: fangxw@lzu.edu.cn

Drought reduced reproductive processes



Drought reduced pollen viability and germination





Pollen tube reached the ovary in all flowers when soil water content reduced from 80% to 25% field capacity

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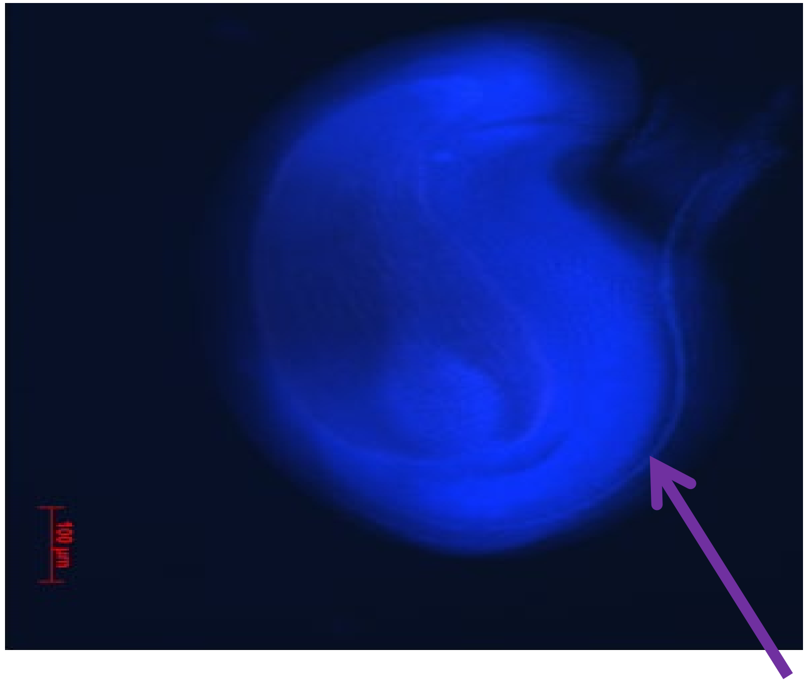

Pollen tube growing down and reaching the ovary

- Increased flower abortion –pollen tube growth into ovary could not guarantee the success of fertilisation
- Possible inhibition on ovary fertility;
- Short of carbohydrate supply, and/or hormone?

Abscisic acid was likely related to early pod abortion

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ABA in young pods at 9 days after flowering

Pods developed from flowers tagged	Abscisic acid concentration (ng g^{-1} FW)			
	DICC8156WW	DICC8156WS	DICC8172WW	DICC8172WS
80% SFC	907 ± 166	1157 ± 225	474 ± 32	620 ± 103
50% SFC	781 ± 97	5197 ± 425	622 ± 57	2907 ± 524

ABA accumulation in the seed/pod may be associate with pod/seed abortion

Pang *et al.* J Exp Bot 2016

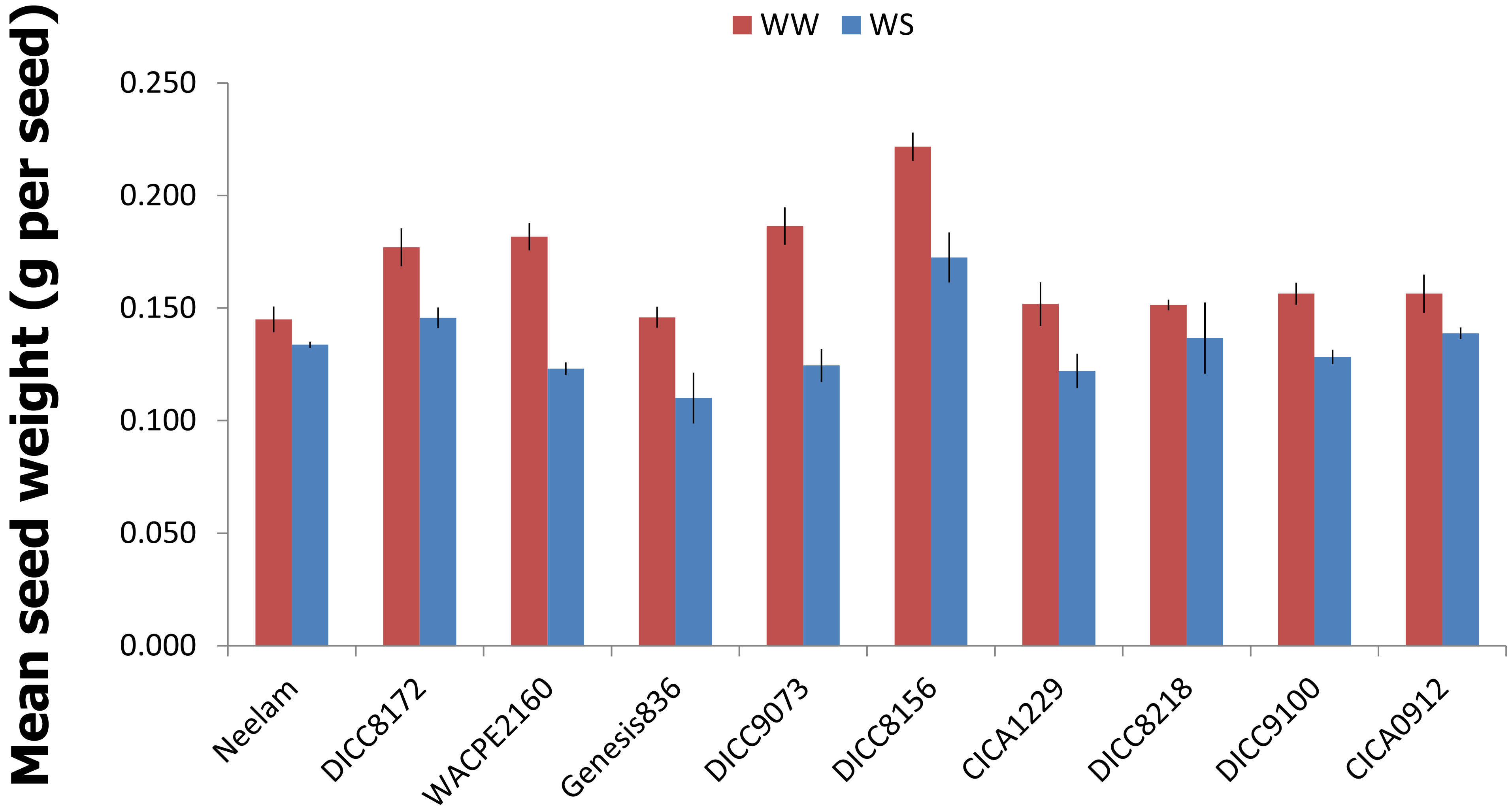
ABA concentration increased 3-5 times under WS

Seeds developed from flowers produced at 80% FC

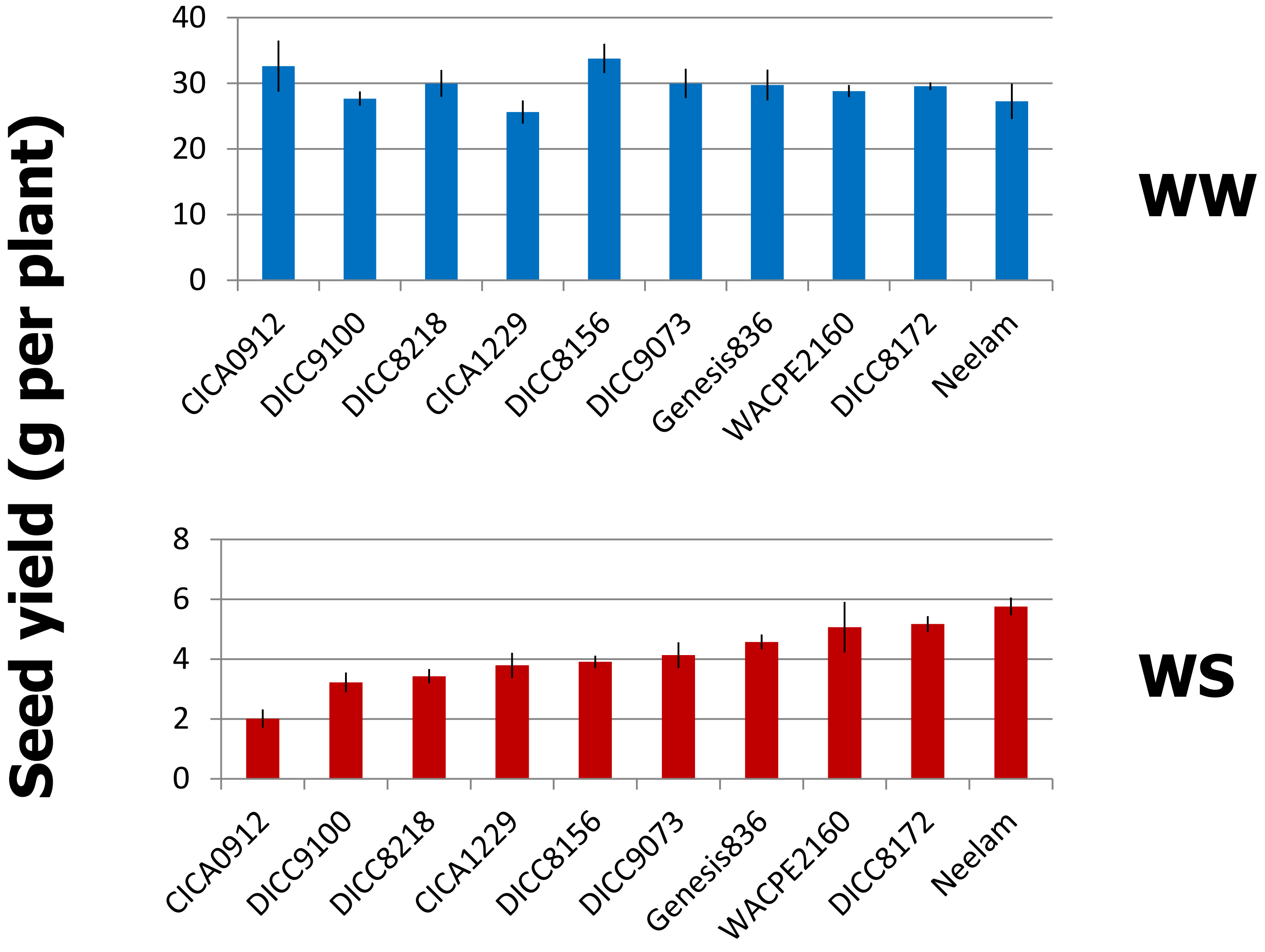
Tissue	Days after flowering	Abscisic acid concentration ($ng\ g^{-1}$ FW)			
		DICC8156WW	DICC8156WS	DICC8172WW	DICC8172WS
Pod wall	16	544 ± 22	1493 ± 155	345 ± 49	840 ± 49
	23	76 ± 18	405 ± 97	74 ± 4	322 ± 44
Seed	16	625 ± 44	1746 ± 41	637 ± 87	1451 ± 297
	23	1236 ± 68	3008 ± 461	1260 ± 178	3969 ± 69

Pang *et al.* J Exp Bot 2016

Drought reduced seed size



Drought reduced seed yield



Chickpea root system phenotyping platform

THE UNIVERSITY OF WESTERN AUSTRALIA

Journal of Experimental Botany, Vol. 68, No. 8 pp. 1987–1999, 2017
doi:10.1093/jxb/erw368 Advance Access publication 6 October 2016
This paper is available online free of all access charges (see http://jxb.oxfordjournals.org/open_access.html for further details)

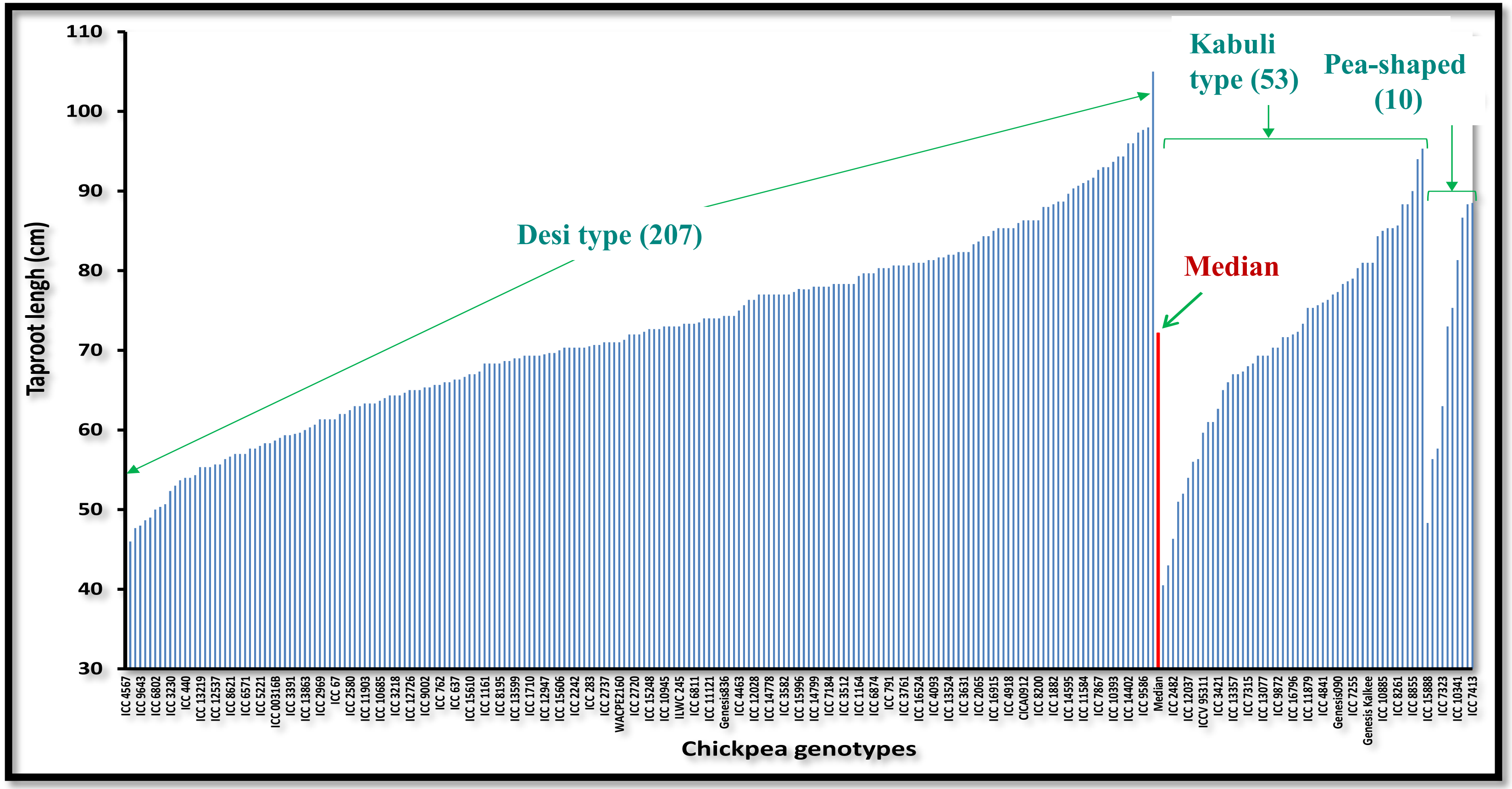
RESEARCH PAPER

Characterising root trait variability in chickpea (*Cicer arietinum* L.) germplasm

Yinglong Chen[1,2,*], Michel Edmond Ghanem[3] and Kadambot HM Siddique[1,*]

[1] The UWA Institute of Agriculture, The University of Western Australia, LB 5005, Perth WA 6001, Australia
[2] The State Key Laboratory of Soil Erosion and Dryland Farming on the Loess Plateau, Institute of Soil and Water Conservation, Northwest A&F University, and Chinese Academy of Sciences, Yangling, Shaanxi 712100, China
[3] International Centre for Agricultural Research in the Dry Areas, North-Africa Platform, Rabat, Morocco

Taproot length



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RESEARCH PAPER

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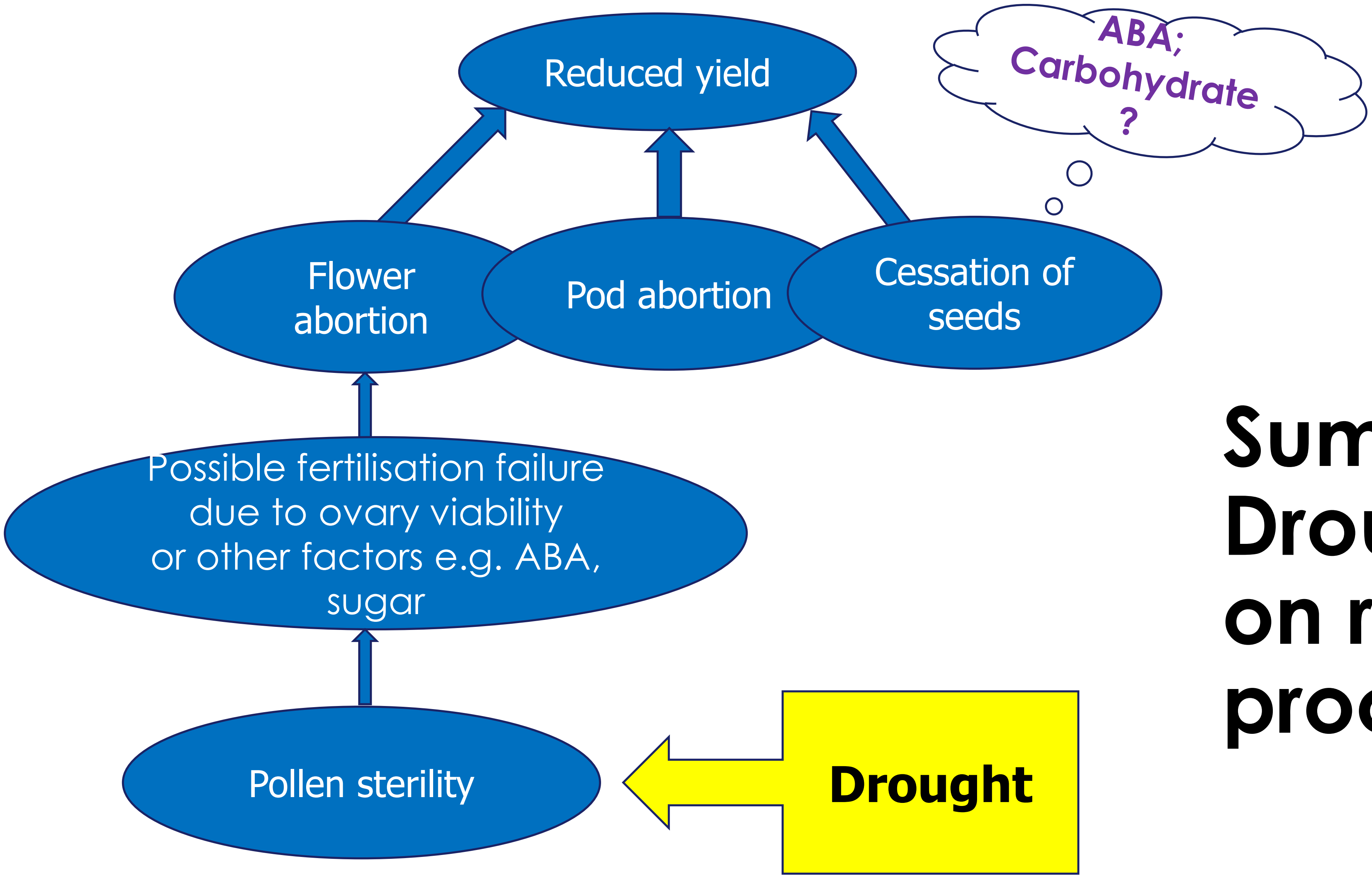
Summary: Drought impacts on reproductive process



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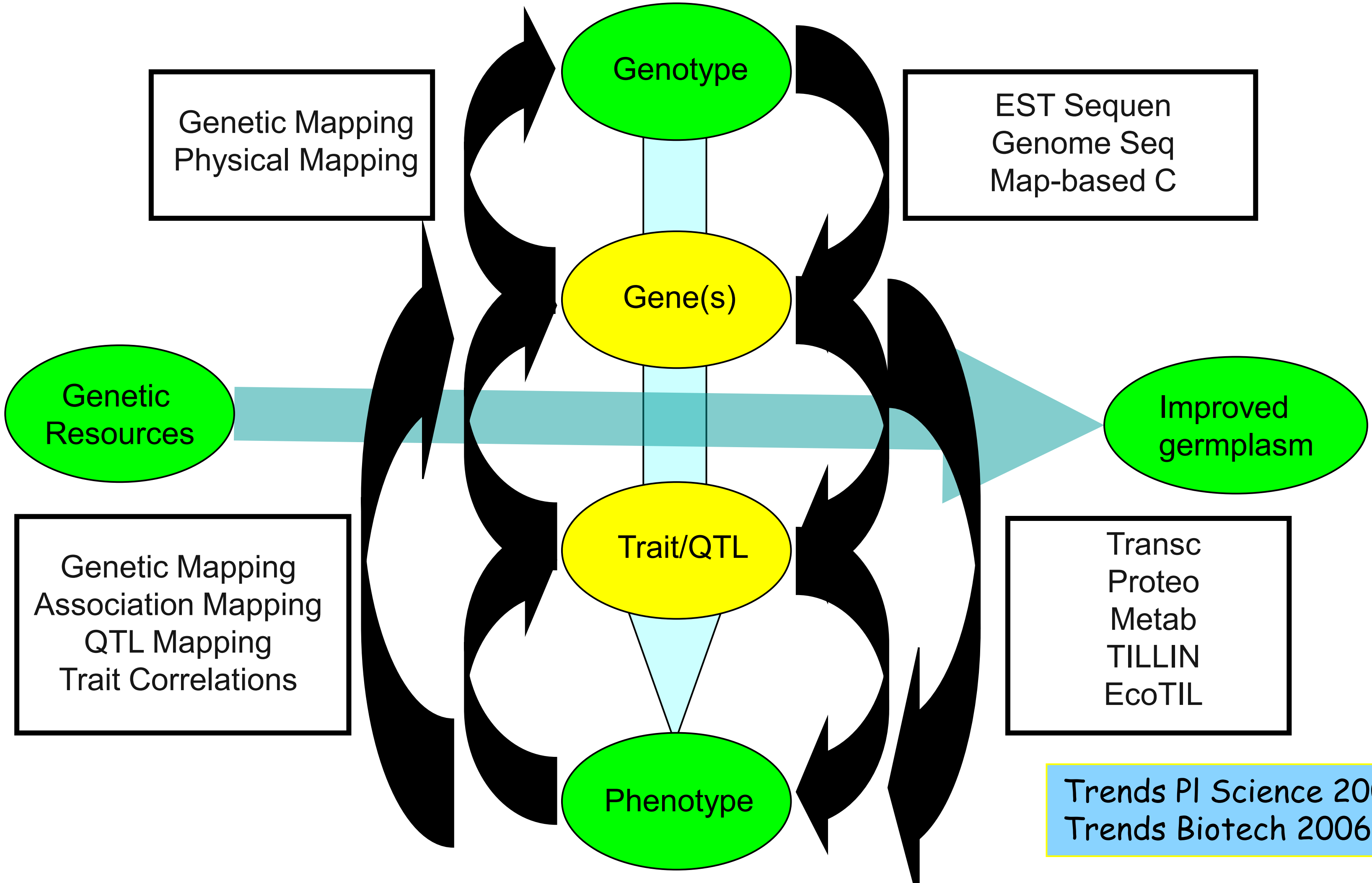
Genomics-assisted breeding: predicting the phenotypes



Trends Pl Science 2005
Trends Biotech 2006

Source: Rajeev Varshney

Functional Genomics of Chickpea to enhance drought tolerance

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Crossing the genome to phenome divide in the crop legume Chickpea (*Cicer arietinum*) to enhance its drought tolerance.

- development of pangenome and gene-linked proteomics and metabolomics focused on drought tolerance.
- use genetic resources from Indian and Australian partners
- combine expertise in the development of genome/ protein/ metabolite datasets that will define genomic variation and gene/protein expression profiles linked to drought tolerance.

2019-2023
Australia India Strategic Research Fund (AISRF):

Australian Government
Department of Industry, Innovation and Science

Department of BioTechnology, Government of India
सत्यमेव जयते

Jawaharlal Nehru University

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nature genetics
ARTICLES
https://doi.org/10.1038/s41588-019-0401-3

THE UNIVERSITY OF WESTERN AUSTRALIA

Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits

Rajeev K. Varshney[1*], Mahendar Thudi[1], Manish Roorkiwal[1], Weiming He[2], Hari D. Upadhyaya[1], Wei Yang[2], Prasad Bajaj[1], Philippe Cubry[3], Abhishek Rathore[1], Jianbo Jian[2], Dadakhalandar Doddamani[1], Aamir W. Khan[1,4], Vanika Garg[1,5], Annapurna Chitikineni[1], Dawen Xu[2], Pooran M. Gaur[1], Narendra P. Singh[6], Sushil K. Chaturvedi[6,22], Gangarao V. P. R. Nadigatla[7], Lakshmanan Krishnamurthy[1], G. P. Dixit[6], Asnake Fikre[8,23], Paul K. Kimurto[9], Sheshshayee M. Sreeman[10], Chellapilla Bharadwaj[11], Shailesh Tripathi[11], Jun Wang[2,12], Suk-Ha Lee[13], David Edwards[4], Kavi Kishor Bilhan Polavarapu[5], R. Varma Penmetsa[14], José Crossa[15], Henry T. Nguyen[16], Kadambot H. M. Siddique[4], Timothy D. Colmer[4], Tim Sutton[17,18], Eric von Wettberg[19], Yves Vigouroux[3], Xun Xu[2,20*] and Xin Liu[2,21*]

We report a map of 4.97 million single-nucleotide polymorphisms of the chickpea from whole-genome resequencing of 429 lines sampled from 45 countries. We identified 122 candidate regions with 204 genes under selection during chickpea breeding. Our data suggest the Eastern Mediterranean as the primary center of origin and migration route of chickpea from the Mediterranean/Fertile Crescent to Central Asia, and probably in parallel from Central Asia to East Africa (Ethiopia) and South Asia (India). Genome-wide association studies identified 262 markers and several candidate genes for 13 traits. Our study establishes a foundation for large-scale characterization of germplasm and population genomics, and a resource for trait dissection, accelerating genetic gains in future chickpea breeding.

Article

A chickpea genetic variation map based on the sequencing of 3,366 genomes

https://doi.org/10.1038/s41586-021-04066-1

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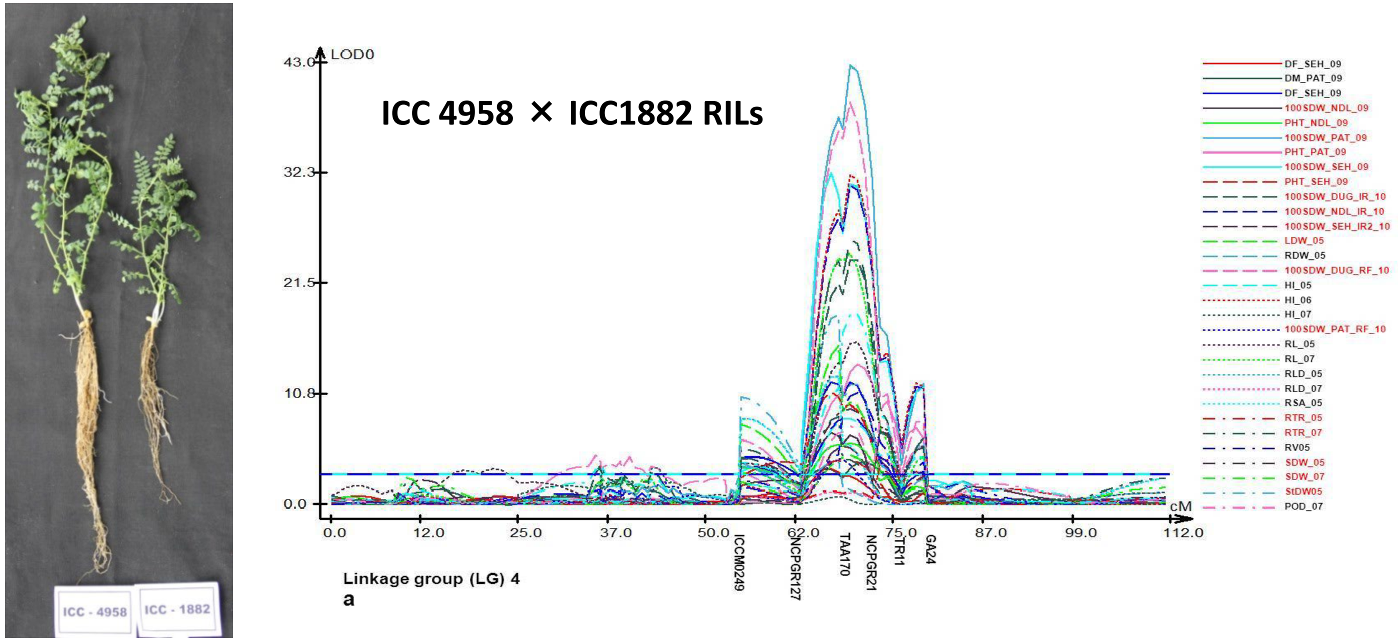
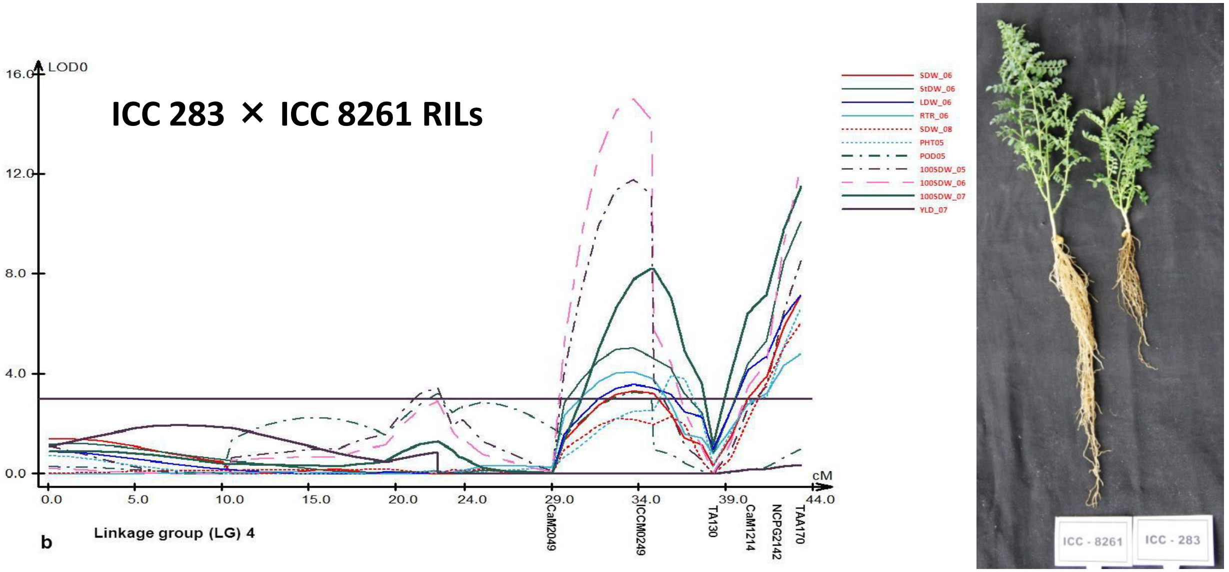
Open access

Rajeev K. Varshney[1,2,✉], Manish Roorkiwal[1], Shuai Sun[3,4,5], Prasad Bajaj[1], Annapurna Chitikineni[1], Mahendar Thudi[1,6], Narendra P. Singh[7], Xiao Du[3,4], Hari D. Upadhyaya[8,9], Aamir W. Khan[1], Yue Wang[3,4], Vanika Garg[1], Guangyi Fan[3,4,10,11], Wallace A. Cowling[12], José Crossa[13], Laurent Gentzbittel[14], Kai Peter Voss-Fels[15], Vinod Kumar Valluri[1], Pallavi Sinha[1,16], Vikas K. Singh[1,16], Cécile Ben[14,17], Abhishek Rathore[1], Ramu Punna[18], Muneendra K. Singh[1], Bunyamin Tar'an[19], Chellapilla Bharadwaj[20], Mohammad Yasin[21], Motisagar S. Pithia[22], Servejeet Singh[23], Khela Ram Soren[7], Himabindu Kudapa[1], Diego Jarquín[24], Philippe Cubry[25], Lee T. Hickey[15], Girish Prasad Dixit[7], Anne-Céline Thuillet[25], Aladdin Hamwieh[26], Shiv Kumar[27], Amit A. Deokar[19], Sushil K. Chaturvedi[28], Aleena Francis[29], Réka Howard[30], Debasis Chattopadhyay[29], David Edwards[12], Eric Lyons[31], Yves Vigouroux[25], Ben J. Hayes[15], Eric von Wettberg[32], Swapan K. Datta[33], Huanming Yang[10,11,34,35], Henry T. Nguyen[36], Jian Wang[11,35], Kadambot H. M. Siddique[12], Trilochan Mohapatra[37], Jeffrey L. Bennetzen[38], Xun Xu[10,39] & Xin Liu[10,11,40,41,✉]

Zero hunger and good health could be realized by 2030 through effective conservation, characterization and utilization of germplasm resources[1]. So far, few chickpea (*Cicer arietinum*) germplasm accessions have been characterized at the genome sequence level[2]. Here we present a detailed map of variation in 3,171 cultivated and 195 wild accessions to provide publicly available resources for chickpea genomics research and breeding. We constructed a chickpea pan-genome to describe genomic diversity across cultivated chickpea and its wild progenitor accessions. A divergence tree using genes present in around 80% of individuals in one species allowed us to estimate the divergence of *Cicer* over the last 21 million years. Our analysis found chromosomal segments and genes that show signatures of selection during domestication, migration and improvement. The chromosomal locations of deleterious mutations responsible for limited genetic diversity and decreased fitness were identified in elite germplasm. We identified superior haplotypes for improvement-related traits in landraces that can be introgressed into elite breeding lines through haplotype-based breeding, and found targets for purging deleterious alleles through genomics-assisted breeding and/or gene editing. Finally, we propose three crop breeding strategies based on genomic prediction to enhance crop productivity for 16 traits while avoiding the erosion of genetic diversity through optimal contribution selection (OCS)-based pre-breeding. The predicted performance for 100-seed weight, an important yield-related trait, increased by up to 23% and 12% with OCS- and haplotype-based genomic approaches, respectively.





A genomic region (called QTL hotspot) harbouring QTLs for root traits and various other drought tolerance related traits identified on LG 4

Source: Varshney et al. 2014.

SOCIETY FOR EXPERIMENTAL BIOLOGY

Journal of Experimental Botany
https://doi.org/10.1093/jxb/erac348 Advance Access Publication 25 August, 2022
This paper is available online free of all access charges (see https://academic.oup.com/jxb/pages/openaccess for further details)

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RESEARCH PAPER

Characterization of '*QTL-hotspot*' introgression lines reveals physiological mechanisms and candidate genes associated with drought adaptation in chickpea

Rutwik Barmukh[1,2], Manish Roorkiwal[1,3,4,*], Girish P. Dixit[5], Prasad Bajaj[1], Jana Kholova[6,7], Millicent R. Smith[1,8], Annapurna Chitikineni[1], Chellapilla Bharadwaj[3,9], Sheshshayee M. Sreeman[10], Abhishek Rathore[1], Shailesh Tripathi[9], Mohammad Yasin[11], Adiveppa G. Vijayakumar[12], Someswar Rao Sagurthi[2], Kadambot H.M. Siddique[3] and Rajeev K. Varshney[1,3,13,*]

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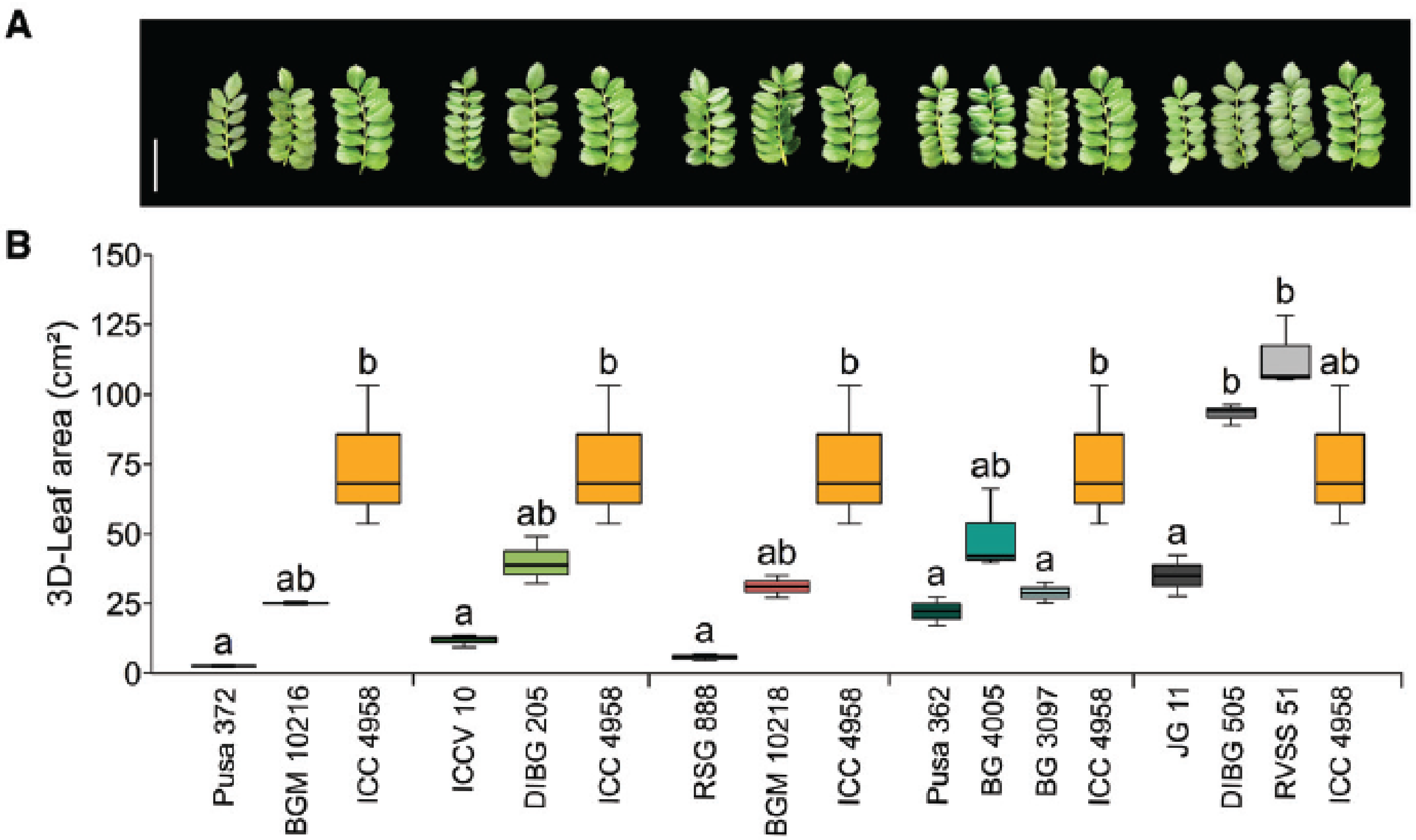
[2] Department of Genetics, Osmania University, Hyderabad, India
[3] The UWA Institute of Agriculture, The University of Western Australia, Perth, Western Australia, Australia
[4] Khalifa Center for Genetic Engineering and Biotechnology, United Arab Emirates University, Al-Ain, United Arab Emirates
[5] ICAR - Indian Institute of Pulses Research (IIPR), Kanpur, India
[6] Crops Physiology & Modeling, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[7] Department of Information Technologies, Faculty of Economics and Management, Czech University of Life Sciences Prague, Kamýcká 129, Prague, Czech Republic
[8] Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Australia
[9] ICAR - Indian Agricultural Research Institute (IARI), Delhi, India
[10] Department of Crop Physiology, University of Agricultural Sciences, Bengaluru, India
[11] RAK College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, India
[12] UAS-Dharwad Regional Agricultural Research Station, Vijayapura, India
[13] Centre for Crop and Food Innovation, State Agricultural Biotechnology Centre, Murdoch University, Murdoch, Western Australia, Australia

* Correspondence: rajeev.varshney@murdoch.edu.au or mroorkiwal@uaeu.ac.ae

To investigate the mechanisms underpinning the positive effects of '*QTL-hotspot*' on seed yield under drought, we introgressed this region from the ICC 4958 genotype into five elite chickpea cultivars.

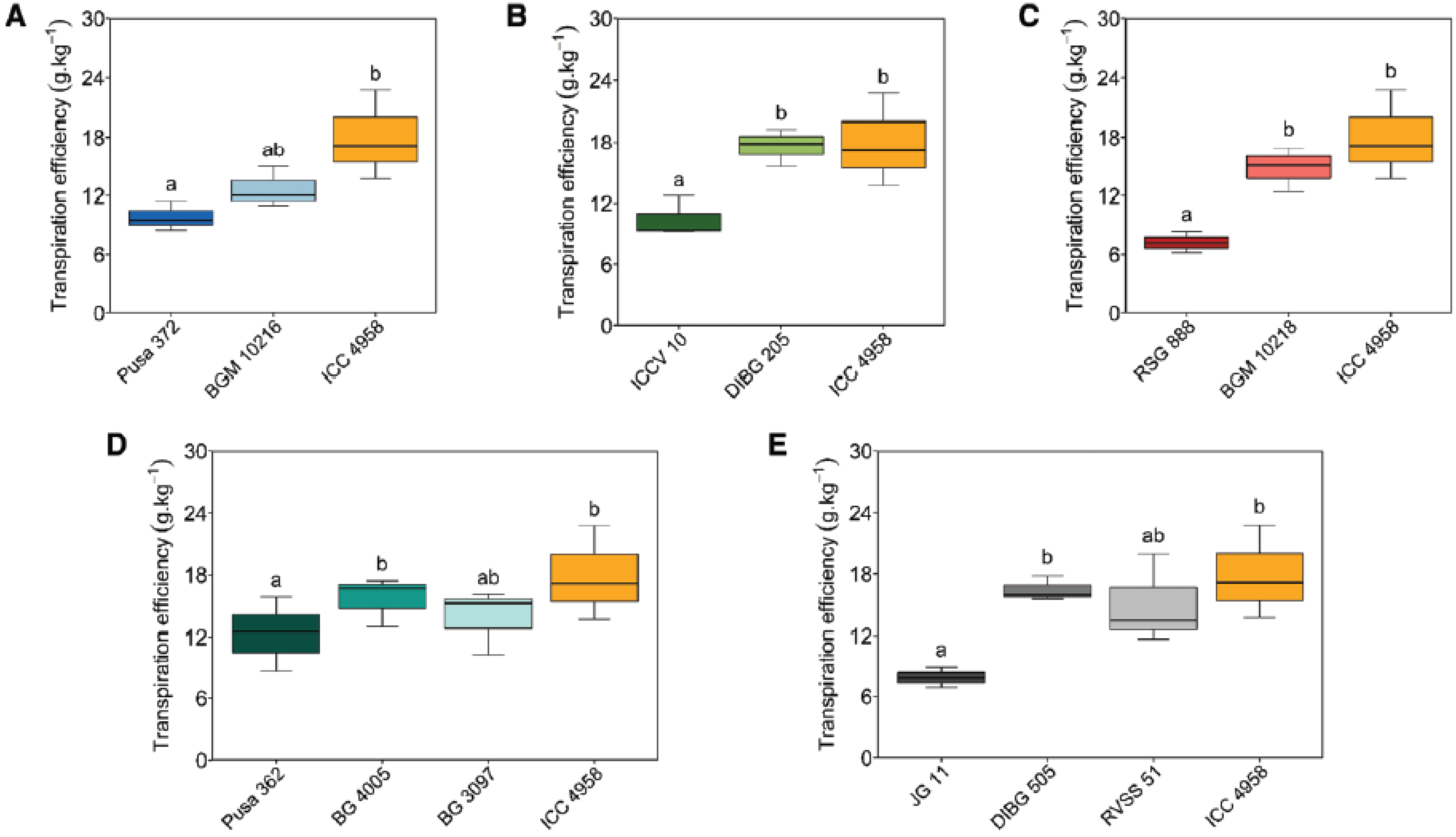
The resulting introgression lines (ILs) and their parents were evaluated in multi-location field trials and semi-controlled conditions.

The results showed that the '*QTL-hotspot*' region improved seed yield under rainfed conditions by increasing seed weight, reducing the time to flowering, regulating traits related to canopy growth and early vigour, and enhancing transpiration efficiency.



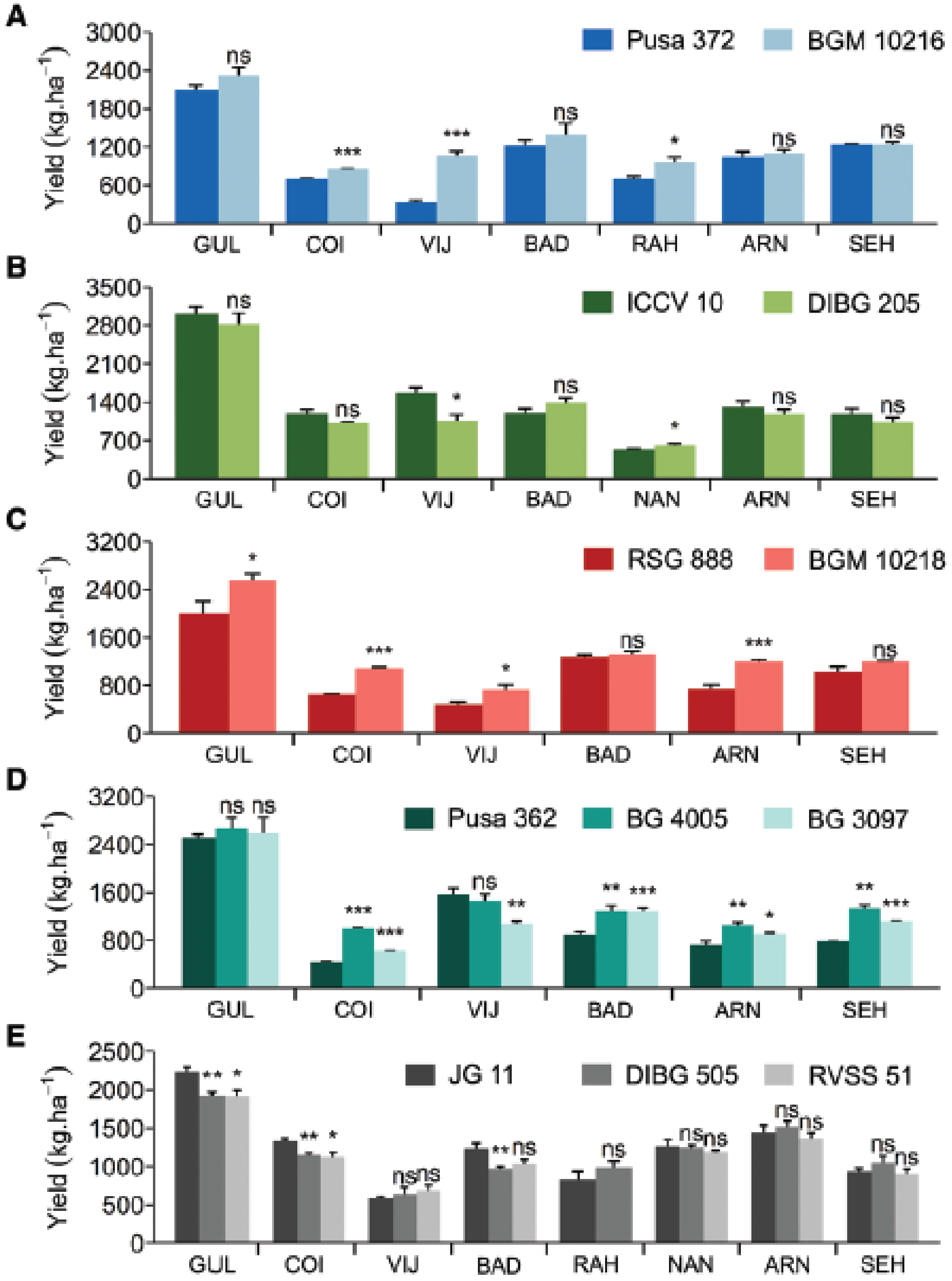
Phenotypic characterization of 3D-leaf area in chickpea introgression lines (ILs) and their parental lines using the LeasyScan platform.

Barmukh et al 2022



Effects of '*QTL-hotspot*' on transpiration efficiency in chickpea introgression lines (ILs) and their parental lines under water deficit.

Barmukh et al 2022



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Yield performance of chickpea introgression lines (ILs) and their recurrent parental lines in the rainfed multi-location field trials in 2018–2019.

The donor parent in each case was ICC 4958, which possess '*QTL-hotspot*'.

Mean plot yields are shown for (A) Pusa 372 and BGM 10216, (B) ICCV 10 and DIBG 205, (C) RSG 888 and BGM 10218, (D) Pusa 362, BG 4005, and BG 3097, (E) JG 11, DIBG 505, and RVSS 51.

The locations are as follows: GUL, Gulbarga; COI, Coimbatore; VIJ, Vijayapur; BAD, Badnapur; RAH, Rahuri; NAN, Nandyal; ARN, Arnej; SEH, Sehore.

Barmukh et al 2022

Drought tolerant chickpeas in India

Pusa JG 16
Yield potential:
2,124 kg/ha

IPC L4-14
Yield potential:
1,600 kg/ha

Pusa Chickpea
10216
Yield potential:
2,575 kg/ha

Pusa Chickpea
4005
Yield potential:
1,940 kg/ha

Drought-tolerant chickpea lines entering variety release pipeline (**EUCK-6, EUCD-P6, and EUCD-P52**) in Kenya

Girar

- Yield potential: 2,139 kg/ha
- 14.2% yield advantage over check variety in Ethiopia

Geletu

- Yield potential: 3,822 kg/ha
- 15% yield advantage over check variety in Ethiopia

Farmer-preferred MABC lines of drought tolerant chickpea in Tanzania

Drought tolerant chickpeas in Africa

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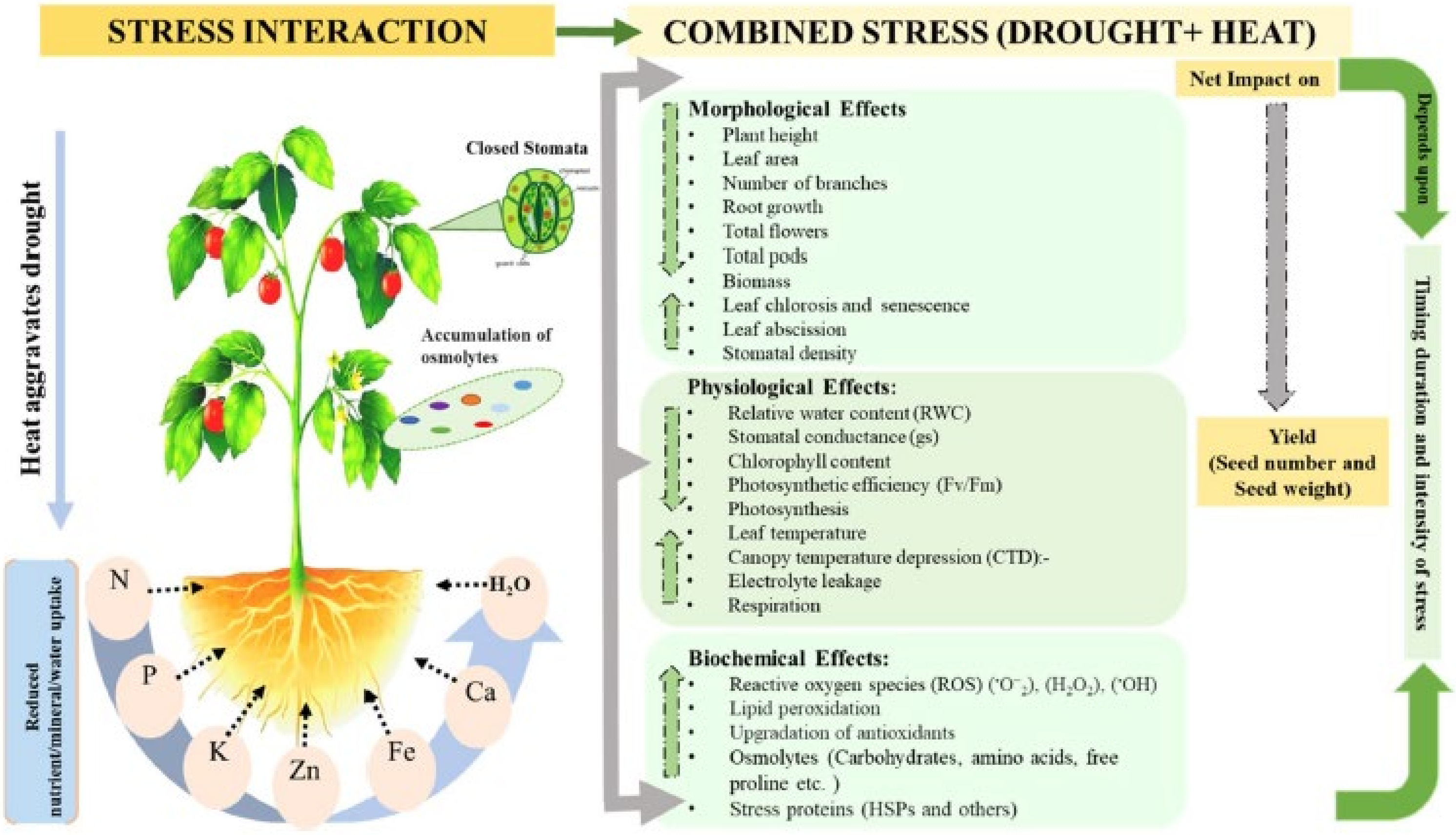

Plant Cell Reports
https://doi.org/10.1007/s00299-021-02742-0

REVIEW

Check for updates

'Omics' approaches in developing combined drought and heat tolerance in food crops

Anjali Bhardwaj[1] · Poonam Devi[1] · Shikha Chaudhary[1] · Anju Rani[1] · Uday Chand Jha[2] · Shiv Kumar[3] · H. Bindumadhava[4] · P. V. Vara Prasad[5] · Kamal Dev Sharma[6] · Kadambot H. M. Siddique[7] · Harsh Nayyar[1]

Received: 24 March 2021 / Accepted: 24 June 2021

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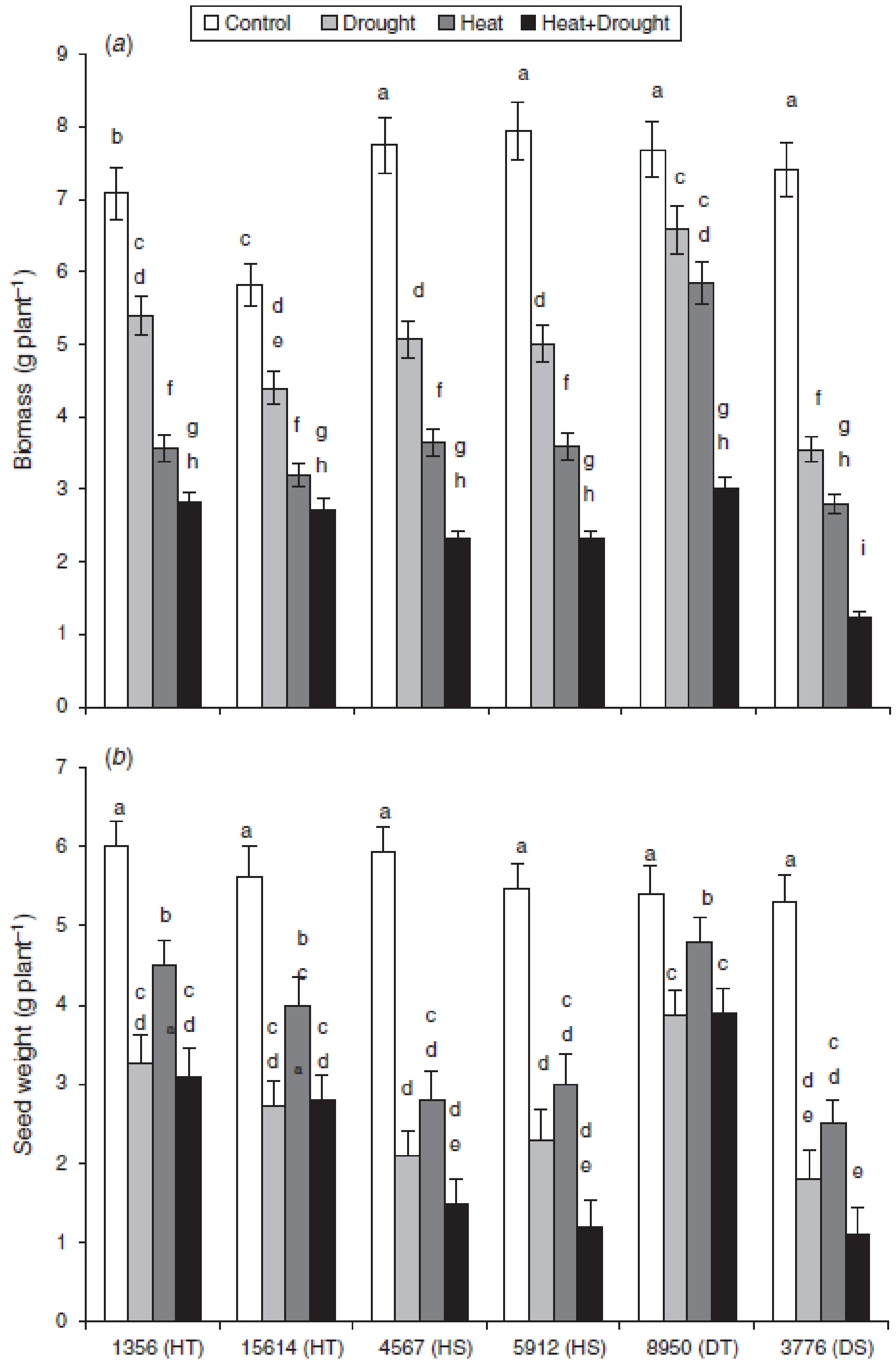
Simultaneous occurrence of drought and heat stress significantly affects the various traits (morphological, physiological, biochemical and genes) of the plants.

At physiological level, relative leaf water content, stomatal conductance, chlorophyll concentration and photosynthetic traits decrease canopy temperature depression, electrolyte leakage, respiration and oxidative stress increase.

Plants adapt themselves under such conditions by modulating the expressions of antioxidants, osmolytes, and stress proteins.

All these traits synergistically affect the yield and resulted in major agronomic .losses



(*a*) Aboveground biomass (stems, leaves and pod shells) and (*b*) seed weight per plant of six chickpea genotypes that were heat tolerant (HT), heat sensitive (HS), drought tolerant (DT) or drought sensitive (DS), in the normal-sown well-watered (Control),

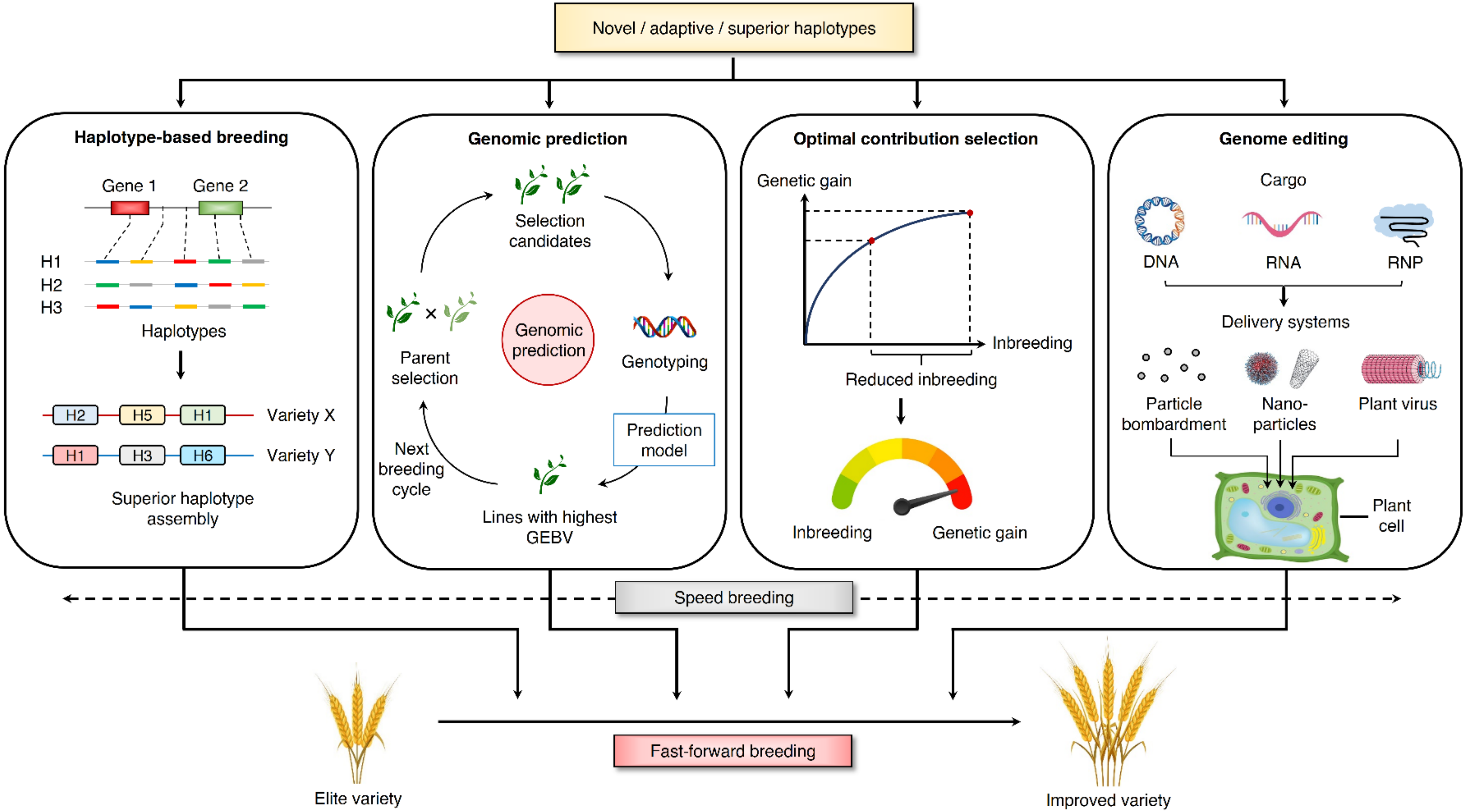
CSIRO PUBLISHING
Crop & Pasture Science, 2017, **68**, 823–841
https://doi.org/10.1071/CP17028

Effects of individual and combined heat and drought stress during seed filling on the oxidative metabolism and yield of chickpea (*Cicer arietinum*) genotypes differing in heat and drought tolerance

Rashmi Awasthi[A], *Pooran Gaur*[B], *Neil C. Turner*[C], *Vincent Vadez*[B], *Kadambot H. M. Siddique*[C], *and Harsh Nayyar*[A,D]

[A]Department of Botany, Panjab University, Chandigarh 160014, India.
[B]ICRISAT, Patancheru 502 324, Greater Hyderabad, Telengana, India.
[C]The UWA Institute of Agriculture and UWA School of Agriculture and Environment, The University of Western Australia, M082, Locked Bag 5005, Perth, WA 6001, Australia.
[D]Corresponding author. Email: harshnayyar@hotmail.com

Fast-forward breeding approaches

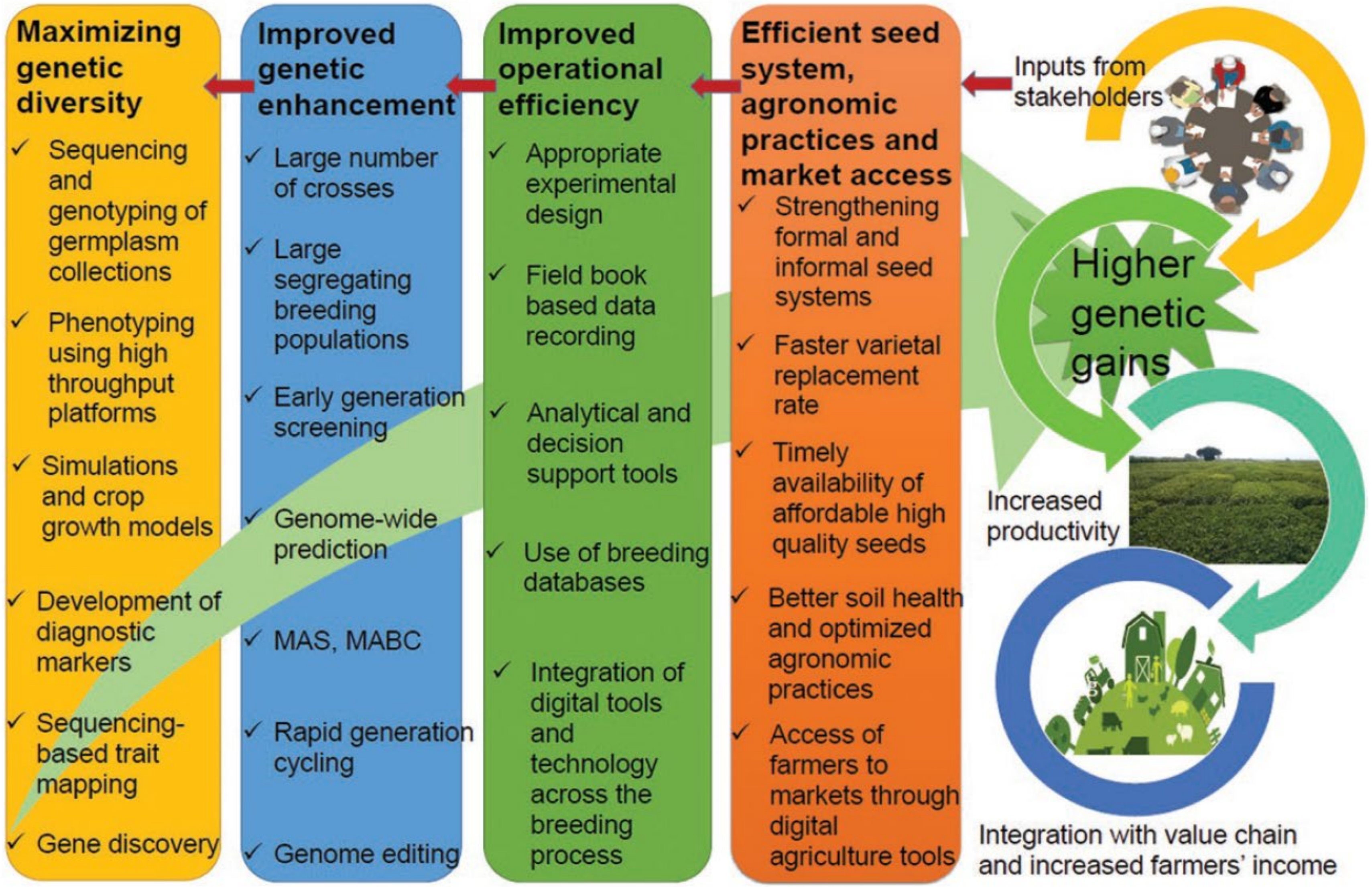


Innovative genomic breeding approaches can integrate superior haplotypes/ alleles into elite varieties to accelerate the development of superior varieties

Trends Genet. (2021)

Conclusions

Strategy for strengthening the breeding process



Journal of Experimental Botany (2018) Rajeev K. Varshney, Mahendar Thudi, Manish K. Pandey, Francois Tardieu, Chris Ojiewo, Vincent Vadez, Anthony M. Whitbread, Kadambot H. M. Siddique, Henry T. Nguyen, Peter S. Carberry and David Bergvinson