Genomic Designing of Climate-Smart Oilseed Crops

Chittaranjan Kole
Editor

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Where I worked with him on the Brassicaceae system and learnt how to develop novel concepts of plant molecular genetics and side-by-side generate genetic resources for crop improvement.

Preface

The last 120 years have witnessed a remarkable evolution in the science and art of plant breeding culminating in quite a revolution in the second decade of the twenty-first century! A number of novel concepts, strategies, techniques, and tools have emerged from time to time over this period, and some of them deserve to be termed as milestones. Traditional plant breeding, immediately following the rediscovery of the laws of inheritance, has been playing a spectacular role in the development of innumerable varieties in almost all crops during this entire period. Mention must be made on the corn hybrids, rust-resistant wheat, and obviously the high-yielding varieties in wheat and rice that ushered the so-called green revolution. However, the methods of selection, hybridization, mutation, and polyploidy employed in traditional breeding during this period relied solely on the perceivable phenotypic characters. But most, if not all, of the economic characters in crops are governed by polygenes which are highly influenced by environment fluctuations, and hence, phenotype-based breeding for these traits has hardly been effective.

Historical discovery of DNA structure and replication in 1953 was followed by a series of discoveries in the 1960s and 1970s that paved the way for recombinant DNA technology in 1973 facilitating the detection of a number of DNA markers in 1980 onwards and their utilization in construction of genetic linkage maps and mapping of genes governing the simply inherited traits and quantitative trait loci controlling the polygenic characters in a series of crop plants starting with tomato, maize, and rice. Thus, new crop improvement technique called as molecular breeding started in later part of the twentieth century. On the other hand, genetic engineering made modification of crops for target traits by transferring alien genes, for example, the *Bt* gene from the bacteria *Bacillus thuringiensis*. A large number of genetically modified crop varieties have thus been developed starting with the commercialization of "flavr Savr" tomato in 1994.

Meantime, the manual DNA sequencing methodology of 1977 was being improved with regard to speed, cost-effectiveness, and automation. The first-generation sequencing technology led to the whole genome sequencing of Arabidopsis in 2000 and followed by rice in 2002. The next-generation sequencing technologies were available over time and used for sequencing of genomes of many

other model and crop plants. Genomes, both nuclear and organellar, of more than 100 plants have already been sequenced by now, and the information thus generated are available in public database for most of them. It must be mentioned here that bioinformatics played a remarkable role in handling the enormous data being produced in each and every minute. It can be safely told that the "genomics" era started in the beginning of the twenty-first century itself accompanying also proteomics, metabolomics, transcriptomics, and several other "omics" technologies.

Structural genomics has thus facilitated annotation of genes, enumeration of gene families and repetitive elements, and comparative genomics studies across taxa. On the other hand, functional genomics paved the way for deciphering the precise biochemistry of gene function through transcription and translation pathways. Today, genotyping-by-sequencing of primary, secondary, and even tertiary gene pools; genome-wide association studies; and genomics-aided breeding are almost routine techniques for crop improvement. Genomic selection in crops is another reality today. Elucidation of the chemical nature of crop chromosomes has now opened up a new frontier for genome editing that is expected to lead the crop improvement approaches in near future.

At the same time, we will look forward to replacement of genetically modified crops by cisgenic crops through transfer of useful plant genes and atomically modified crops by employing nanotechnology that will hopefully be universally accepted for commercialization owing to their human-friendly and environment-friendly nature.

I wish to emphatically mention here that none of the technologies and tools of plant breeding are too obsolete or too independent. They will always remain pertinent individually or as complementary to each other, and will be employed depending on the evolutionary status of the crop genomes, the genetic resources and genomics resources available, and above all the cost-benefit ratios for adopting one or more technologies or tools. In brief, utilization of these crop improvement techniques would vary over time, space, and economy scales! However, as we stand today, we have all the concepts, strategies, techniques, and tools in our arsenal to practice 'genome designing', as I would prefer to term it, of crop plants not just genetic improvement to address simultaneously 'food, nutrition, energy, and environment security, briefly the FNEE security', as I introduced the concept in 2013 and have been talking about for the last 5 years at different platforms.

Addressing FNEE security has become more relevant today in the changing scenario of climate change and global warming. Climate change will lead to greenhouse gas emissions and extreme temperatures leading to different abiotic stresses including drought or waterlogging, on the one hand, and severe winter and freezing, on the other hand. It will also severely affect uptake and bioavailability of water and plant nutrients and will adversely cause damage to physical, chemical, and biological properties of soil and water in cropping fields and around. It is also highly likely that there will be emergence of new insects and their biotypes and of new plant pathogens and their pathotypes. The most serious concerns are, however, the unpredictable crop growth conditions and the unexpected complex interactions among all the above stress factors leading to drastic reduction in crop yield and

quality in an adverse ecosystem and environment. Climate change is predicted to significantly reduce productivity in almost all crops. For example, in cereal crops, the decline of yield is projected at 12–15%. On the other hand, crop production has to be increased at least by 70% to feed the alarmingly growing world population, projected at over 9.0 billion by 2050 by even a moderate estimate.

Hence, the unpredictability of crop growing conditions and thereby the complexity of biotic and abiotic stresses warrant completely different strategies of crop production from those practiced over a century aiming mostly at one or the few breeding objectives at a time such as yield, quality, resistance to biotic tresses due to disease–pests, tolerance to abiotic stresses due to drought, heat, cold, flood, salinity, acidity, improved water and nutrient use efficiency, etc. In the changing scenario of climate change, for sustainable crop production, precise prediction of the above limiting factors by long-term survey and timely sensing through biotic agents and engineering devices and regular soil and water remediation will play a big role in agriculture. We have been discussing on "mitigation" and "adaptation" strategies for the last few years to reduce the chances of reduction of crop productivity and improve the genome plasticity of crop plants that could thrive and perform considerably well in a wide range of growing conditions over time and space. This is the precise reason for adopting genomic designing of crop plants to improve their adaptability by developing climate-smart or climate-resilient genotypes.

Keeping all these in mind, I planned to present deliberations on the problems, priorities, potentials, and prospects of genome designing for development of climate-smart crops in about 50 chapters, each devoted to a major crop or a crop group, allocated under five volumes on cereal, oilseed, pulse, fruit, and vegetable crops. These chapters have been authored by more than 250 of eminent scientists from over 30 countries including Argentina, Australia, Bangladesh, Belgium, Brazil, Canada, China, Egypt, Ethiopia, France, Germany, Greece, India, Ireland, Japan, Malaysia, Mexico, New Zealand, Kenya, Pakistan, Philippines, Portugal, Puerto Rico, Serbia, Spain, Sri Lanka, Sweden, Taiwan, Tanzania, Tunisia, Uganda, UK, USA, and Zimbabwe.

There are a huge number of books and reviews on traditional breeding, molecular breeding, genetic engineering, nanotechnology, genomics-aided breeding, and gene editing with crop-wise and trait-wise deliberations on crop genetic improvement including over 100 books edited by me since 2006. However, I believe the present five book volumes will hopefully provide a comprehensive enumeration on the requirement, achievements, and future prospects of genome designing for climate-smart crops and will be useful to students, teaching faculties, and scientists in the academia and also to the related industries. Besides, public and private funding agencies, policy-making bodies, and the social activists will also get a clear idea on the road traveled so far and the future roadmap of crop improvement.

I must confess that it has been quite a difficult task for me to study critically the different concepts, strategies, techniques, and tools of plant breeding practiced over the last 12 decades that also on a diverse crop plants to gain confidence to edit the chapters authored by the scientists with expertise on the particular crops or crop groups and present them in a lucid manner with more or less uniform outline of contents and formats. However, my experience gained over the last 7 years in the capacity of the Founding Principal Coordinator of the International Climate Resilient Crop Genomics Consortium (ICRCGC) was highly useful while editing these books. I have the opportunity to interact with a number of leading scientists from all over the world almost on regular basis. Organizing and chairing the annual workshops of ICRCGC since 2012 and representing ICRCGC in many other scientific meetings on climate change agriculture offered me a scope to learn from a large number of people from different backgrounds including academia, industries, policy-making bodies, funding agencies, and social workers. I must acknowledge here the assistance I received from all of them to keep me as a sincere student of agriculture specifically plant breeding.

This volume entitled Genomic Designing of Climate-Smart Oilseed Crops includes eight major crops including Soybean, Oilseed Rape, Groundnut, Sunflower, Flax, Rape and Mustard, Sesame, and Castor Bean. These chapters have been authored by 54 scientists from six countries including Australia, Canada, China, India, Serbia, and USA. I place on record my thanks for these scientists for their contributions and cooperation.

My own working experience on oilseed crops dates back to early 90s in the laboratory of Prof. Thomas C. Osborn in the Department of Agronomy of the University of Wisconsin-Madison. I must confess that this period of about 4 years through working on the Brassicaceae system in his lab and other two labs of his collaborating faculties including Prof. Paul H. Williams in the Department of Plant Pathology and Prof. Jiwan P. Palta in the Department of Horticulture had tailored my mind-set and enriched my expertise and helped me to grow as a science worker. Hence, I have dedicated this book to Prof. Osborn as a token of my respect, thanks, and gratitude.

New Delhi, India Chittaranjan Kole

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Abbreviations

^{13}C	Isotope carbon 13
$\Delta^{13}C$	Carbon isotope discrimination
ABA	Abscisic acid
AC	Ash content
ADH	Alcohol dehydrogenase
AFLP	Amplified fragment length polymorphism
ALA	α-linolenic acid
ALS	Acetolactate synthase
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
APX	Ascorbate peroxidase
AQP	Aquaporin
ARF	Auxin-response factor
ATP	Adenosine triphosphate
ATR	Atrazine
ATT	Acquired thermotolerance
BABA	β-Aminobutyric acid
BAC	Bacterial artificial chromosome
Bar	Bialaphos resistance gene
BC	Back cross
BH	Branching habit
BIM	Bayesian interval mapping
BL	Bayesian LASSO
BLAST	Basic local alignment search tool
BLUP	Best linear unbiased prediction
BPMV	Bean pod mottle virus
BRR	Bayesian ridge regression
BSA	Bulked segregant analysis
Bt	*Bacillus thuringiensis*
C1O	C+1 alleles with capsule open at tip

CaMV	Cauliflower mosaic virus
Cas9	CRISPR-associated 9 protein
CAT	Catalase
CC	Climate change
CDS	Coding DNA sequence
CEG	Core eukaryotic genes
CGMCP	Centre for Genetic Manipulation of Crop Plants
CGRIS	Chinese Genetic Resources Information System
CID	Carbon isotope discrimination
CIM	Common Information Model
CIM	Composite interval mapping
CL	Capsule length
cM	CentiMorgan
CNV	Copy number variant
CO_2	Carbon dioxide
CMS	Cytoplasmic male sterility
CN	Capsule number per plant
CNN	Capsule node number
CNPA	Centro Nacional de Pesquisa de Algodao
CNS	Capsule number per stem
CNV	Copy number variant
CR	Clubroot resistance gene
CRISPR	Clustered regularly interspaced short palindromic repeats
CRP	Coordinated research project
CRR	Charcoal rot resistance
cry1AcF	Delta-endotoxin of *Bacillus thuringiensis* gene (1AcF)
cry1EC	Delta-endotoxin of *Bacillus thuringiensis* gene (1EC)
CS	Climate smart
CTD	Canopy temperature depression
CWR	Crop wild relative
CZL	Capsule zone length
DAG	Diacylglycerols
DALP	Direct amplification of length polymorphism
DAP	Days after planting
DArT	Diversity arrays technology
DAS	Days after sowing
DDBJ	DNA Databank of Japan
DEG	Differentially expressed gene
DGAT	Diacylglycerol acetyltransferase
dgatA	Acyl-CoA:diacylglycerol acyltransferase A
DH	Doubled haploid
DI	Disease index
DMO	Dicamba monooxygenase
DREB	Dehydration responsive element binding (protein)
DREB2A	Drought responsive element binding protein 2A

DS	Determinate sesame
DSB	Double-stranded break
DSF	Days from sowing to flowering
dsRNA	Double-stranded RNA
Dt	Determinate
DTF	Days to flowering
Dw	Dwarf
Dwf	Dwarfing gene
ECP/GR	European Cooperative Programme for Crop Genetic Resources Network
EDB	European Brassica Database
ELS	Early leaf spot
EMF	Embryonic flower
EMS	Ethyl methanesulphonate
EPA	Eicosapentaenoic acid
EPA	Environmental Protection Agency (USA)
EPSP	5-Enolpyruvylshikimate-3-phosphate
ESCORENA	European Co-operative Research Network on Flax and other Bast Plants
ESPS	5-Enolpyruvylshikimate-3-phosphate synthase
EST	Expressed sequence tag
ETI	Effector-triggered immunity
F_2	Second filial generation
FA	Fatty acid
FA	Flowers per leaf axil
FAO	Food and Agriculture Organization
FC	Fiber content
FCL	Length of the lateral capsule
FCT	Thickness of the lateral capsule
FCW	Width of the lateral capsule
FDA	Food and Drug Administration (USA)
FLC	Flowering Locus C
FNEE	Food, nutrition, energy and environment
FNI	Fast neutron irradiation
FOS	*Fusarium oxysporum* f.sp. *sesami*
FSD	Fresh seed dormancy
FT	Flowering locus T
G × E	Genotype × environment
GAB	Genomics-assisted breeding
GBS	Genotyping-by-sequencing
GCA	General combining ability
GE	Genetically engineered
GEAC	Genetic Engineering Appraisal Committee (India)
GEBV	Genome-estimated breeding value
GFF	General feature format

GFP	Green fluorescent protein
GM	Genetically modified
GMHRA	Glyphosate acetyltransferase and modified soybean acetolactate synthase
GN	Grain number per capsule
GO	Gene ontology
GP	Gene pool
GR	Glyphosate resistant
GRD	Groundnut rosette disease
GRDC	Grains Research and Development Corporation
GRIN	Germplasm Resources Information Network (USA)
GRU	Germplasm Resources Unit
GS	Genomic selection
GSO	Seamless capsule open at tip
GSS	Genome survey sequence
GUS	β-glucuronidase gene
GWAS	Genome-wide association study
H	Index of genetic diversity
HAAS	Henan Academy of Agricultural Sciences
HDR	Homology-directed repair
He	Average expected heterozygosity per locus
HFC	Height to the first capsule
Hi-C	Chromosome conformation capture
HOA	High OA
HPPD	4-Hydroxyphenylpyruvate dioxygenase
HR	Highly resistant
HS	Highly susceptible
Hsfs	Heat shock transcription factors
HSP	Heat shock protein
HSRC	Henan Sesame Research Center
I	Shannon's information index
IAEA	International Atomic Energy Agency
IBC	Institute of Biodiversity Conservation
IBPGR	International Bureau of Plant Genetic Resources
ICGR-CAAS	Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ID	Indehiscent
IFDB	International Flax Database
IFVCNS	Institute of Field and Vegetable Crops
IL	Internode length
ILs	Interspecific lines
IND	Improved nondehiscent
InDel	Insertion/Deletion
INTA	Instituto Nacional de Tecnología Agropecuaria

IOD	Iodine value
IP	Intellectual property
IPCC	Intergovernmental Panel on Climate Change
ISSR	Inter-simple sequence repeat
ITPGRFA	The International Treaty for Plant Genetic Resources for Food and Agriculture
KASP	Kompetitive allele-specific polymerase chain reaction
KEGG	Kyoto Encyclopedia of Genes and Genomes
LD	Linkage disequilibrium
LD	Long day
LEA	Late embryogenesis abundant
LG	Linkage group
LIN	Linolenic acid
LIO	Linoleic acid
LIS-1	Linum insertion sequence 1
LLS	Late leaf spot
LN	Leaf number per plant
LncRNA	Long noncoding RNA
LOA	Low OA
LOD	Logarithm of odds
LRR	Leucine-rich repeat
MABC	Marker-assisted backcrossing
MAGIC	Multiparent advanced generation intercross
MAPKK	Mitogen-activated protein kinase kinase
MARS	Marker-assisted recurrent selection
MAS	Marker-assisted selection
MBB	Mexican bean beetle
MBPG	Multinational Brassica Genome Sequencing Project
MCL	Length of the central capsule
MCT	Thickness of the central capsule
MCW	Width of the central capsule
MDA	Malondialdehyde
MG	Maturity group
MIM	Multiple interval mapping
MLS	Multilateral System
MoEF&CC	Ministry of Environment, Forest and Climate Change (India)
MR	Moderately resistant
MSD	Main stem diameter
MSIL	Length of main stem internode
MSNN	Node number of main stem
MTA	Marker-trait association
MTA	Material Transfer Agreement
Na	Number of alleles
NAM	Nested association mapping
NARS	National Agricultural Research System (India)

NBPGR	National Bureau of Plant Genetic Resources (India)
NBS	Nucleotide-binding site
NCBI	National Center for Biotechnology Information
NDVI	Normalized difference vegetation index
Ne	Effective number of alleles
NGS	Next-generation sequencing
NHEJ	Non-homologous end joining
NIL	Near-isogenic lines
NN	Node number
*npt*II	Neomycin phosphotransferase II gene
NTG	N-methyl-N′-nitro-N-nitrosoguanidine
NUE	Nutrient use efficiency
OA	Osmotic adjustment
OA	Oxalic acid
OC	Oil content
OLE	Oleic acid
OLP	Osmotin-like protein gene
PAGE	Parametric analysis of gene set enrichment
PAL	Palmitic acid
PAT	Phosphinothricin acetyltransferase
PAV	Presence/absence variants
PCR	Polymerase chain reaction
PE	Paired end
PEG	Polyethylene glycol
PGR	Pod growth rate
PH	Plant height
PHB	Polyhydroxybutyrate
PIABS	Photosynthetic efficacy index
PIC	Polymorphic information content
PiHS	Population-based integrated haplotype score
Pl	Downy mildew resistance gene
PLCP	Papain-like cysteine protease
PLH	Potato leafhopper
PO	Protein content
POX	Peroxidase
PPO	Polyphenol oxidase
PR	Pathogenesis-related
PRH	Bearing height of primar raceme
PUFA	Polyunsaturated fatty acids
PVE	Phenotypic variation explained
QTL	Quantitative trait locus
QTLs	Quantitative trait loci
R	Resistance gene
RAD	Restriction site-associated DNA
RAPD	Random amplified polymorphic DNA

RCA	*R. communis* agglutinin
RcPAL	*Ricinus communis* phenylalanine ammonialyase gene
RcPEPC	*Ricinus communis* phosphoenolpyruvate carboxylase gene
Rf	Fertility restoration gene
RFLP	Restriction fragment length polymorphism
RGB	Red, green and blue
RGC	Resistance gene candidate
RHL	Residual heterozygous line
RIL	Recombinant inbred line
RNAi	RNA interference
ROD	Reduction of density
RR-BLUP	Ridge regression best linear unbiased prediction
RRGS	Reduced-representation genome sequencing
RRS	Reduced-representation sequencing
RSA	Root system architecture
RSAMPL	Random selective amplification of microsatellite polymorphic locus
RSLs	Recombinant substitution lines
RT-PCR	Real-time PCR
RT-PCR	Reverse transcription PCR
RXBS	Rongxian black sesame
SAM	Sequence alignment map
SAT	Semi-arid tropics
SBA	Soybean aphid
SbDV	Soybean dwarf virus
SBL	Soybean looper
SbNHX1	*Salicornia brachiata* reverse transporter protein gene
SC	Sesamin content
SCAR	Sequence-characterized amplified region
scFv	Single-chain variable fragment
SCMR	SPAD chlorophyll meter reading
SCoT	Start codon targeted polymorphism
SD	Short day
SDS	Sudden death syndrome
SEA	Singular enrichment analysis
SFW	Sesame Fusarium wilt
SG	Selective genotyping
SGMD	Soybean Genomics and Microarray Database
SGP	The Sesame Genome Project
SGWG	The Sesame Genome Working Group
SHA	Shattering
SIM	Simple interval mapping
SiNPs	Silicon nanoparticles
SLA	Specific leaf area
SLAF	Specific length amplified fragment

SLAF-seq	Specific length amplified fragment sequencing
SMA	Single marker analysis
SMG	Suppressor with morphogenetic effects on genitalia
SMV	Soybean mosaic virus
SN	Seed number per plant
SNC	Seed number per capsule
SNP	Single nucleotide polymorphism
SOD	Superoxide dismutase
SoyGD	Soybean Genome Database
SR	Shatter resistant
SRAP	Sequence-related amplified polymorphism
SSCP	Single-strand conformational polymorphism
SSH	Semi-shattering
SSR	Simple sequence repeat
STE	Stearic acid
STF	Days from sowing to flowering
STS	Sequence tagged site
SUS	Super-shattering
TAG	Triacylglycerols
TALEN	Transcription activator-like effector nuclease
TE	Transpiration efficiency
TFL-like	Terminal flower-like
TIGR	The Institute for Genomic Research
TILLING	Targeting induced local lesions in genomes
TIR	Temperature induction response
TL	Tip length without the capsule
TP	Training population
TRAP	Target region amplification polymorphism
TRAP	Tartrate-resistant acid phosphatase
TSS	Total soluble sugars
TSW	Thousand seed weight
TSWV	Tomato spotted wilt virus
TT	Triazine tolerant
TUFGEN	Total Utilization Flax Genomics
UGM	Ungrouped matches
UPM	The Universidad Politécnica de Madrid
UPOV	International Union for the Protection of New Varieties of Plants
USDA	United States Department of Agriculture
UTRs	Untranslated regions
VBC	Velvet bean caterpillar
VIR	Vavilov Institute of Plant Industry
VNIIMK	All-Russia Research Institute of Oil Crops
VPD	Vapor pressure deficit
WGR	Whole genome re-sequencing
WGS	Whole genome shotgun

WSC	Water soluble carbohydrates
WUE	Water use efficiency
ZFN	Zinc-finger nucleases