~~yield and quality through their respective interactions in the cotton production environment. Their influence is in terms of controlling pests, diseases and weeds, providing nutrients to the cotton plant and controlling growth for the appropriate allocation of assimilates in favor of yield and quality components. The cotton quality can be approached in terms of cleanliness and freeness from foreign contaminants and neps, appearance of the cotton in terms of color or radiance and intrinsic fiber and spinning quality parameters. Therefore, balancing input use in cotton production is paramount for high quality cotton.~~

~~The issue of stickiness, caused by whitefly and aphids, came under discussion but no newer technologies are yet available to eliminate the causal organisms.~~

~~The Committee on Cotton Production Research of the ICAC decided that the 2015 Technical Seminar will be on the topic 'Elimination of insecticides from cotton production: Is this possible?' In addition, it recommended that an Open Session should be dedicated to 'International exchange of germplasm' and a Breakout Session on 'Mechanization of cotton picking.'~~

~~The 6th World Cotton Research Conference (WCRC-6) will be held in Brazil in the city of Goiânia, Goiás, from June 20 to 24, 2016. Pre-registration is now open and additional information on the Conference is available at www.wcrc-6.com. CABI, the Food and Agriculture Organization of the United Nations (FAO) and the Centre de coopération internationale en recherche agronomique pour le développement (CIRAD) are sponsoring the Conference. Major support comes from the ICAC. The WCRC-6 will be organized under the auspices of the International Cotton Researchers Association (ICRA). The International Committee headed by the Chairman of ICRA is advising the local organizing committee.~~

Role of Genetic and Genetic Engineering in Optimizing Input Use

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The cultivation of cotton – a source of natural fiber for the textile industry worldwide, bred under high-performance environments (extensive use of fertilizers, irrigations, pesticides, etc.) for achieving maximum yields may result in rapid depletion of energy sources. Performance of cotton varieties is much more vulnerable in low input farming systems, especially in resource-poor farming communities. The impact of climate change would result in a gradual escalation in temperature and depletion of fresh water resources and would further depress cotton productivity. For realizing maximum sustainability, policies for sustainable on-farm management practices and improvement in cotton genetics together can achieve maximum profitability under an optimal level of inputs. Efforts towards developing cotton varieties with excellent genetics have been initiated by deploying the genomic tools for incorporating alien genes conferring resistance to glyphosate (weedicide) and bollworm complex. For example, the *Cry1Ac* gene was initially incorporated in cotton and commercialized in 1996, and varieties containing *Cry2Ab* and herbicide tolerant genes were subsequently released. All these efforts illustrated a significant reduction of pesticides sprayed to control bollworm complex and conservation of farm resources. Extensive collaborative efforts through bridging conventional and genomic tools are needed for incorporating genes involved in enhancing water use efficiency, heat tolerance, maintaining high net photosynthetic rate, improving plant architecture and root structure, in order to scavenge more water and nutrients, improve the lint-to-seed ratio, etc. Such efforts would set a firm foundation for meeting the demands of the world's population beyond 2050.

Extensive characterization of the available untapped genetic resources – underexploited cotton species (cultivated and wild) – to transfer traits of interest into the cultivated cotton varieties is needed. For example, root traits can be improved for scavenging and capturing more water and nutrients from the deeper layers of soil. In this regard, the identification of genomic regions conferring this trait followed by their introgression in the cultivated varieties using DNA markers as diagnostic tool would accelerate breeding for the purpose of developing resilience cotton varieties. Few important genes present in the diverse untapped genetic resources are difficult to transfer through crossing; such genes would be the best targets for engineering the cotton genome through transgenic approaches. Genes from other plant species can also be transferred. For example, genes such as P5CS, DREB, AVP1, etc., which confer tolerance to drought at cellular level, are being introgressed. Similarly, some of the MADS Box genes, which confer resistance to stresses, can be helpful in pyramiding multiple important genes in one cultivar. The

HARDY gene, which confers ethylene-responsive transcription factor, has been identified in *Arabidopsis thaliana*, elucidating high tolerance to drought and salinity in rice. Increased level of ABA, responsible for conferring tolerance to stress, is encoded by *ESKIMO1*. Responses of these genes are being studied in cotton. All these efforts would be instrumental in reducing the amount of irrigation without risking yield potential. In contrast to drought, cotton crops in a few parts of the world experience cold stress. Improvement in the cotton genome by incorporating genes such as superoxide dismutase (SOD) would make cotton more resilient to cold stress.

At the moment, use of nutrients (nitrogen, phosphorus, potassium, etc.) is at peak levels for achieveing high seedcotton yield. A shift is mandatory for developing cotton varieties that can respond equally at the minimum level of nutrients. In this regard, understanding the genetics of nitrogen use efficiency, especially in low input systems, and various mechanisms, such as root morphology and its architecture, delayed leaf senescence etc., remain a top priority target for molecular biologists. In addition, root traits, such as its density and the length of hairs, can scavenge phosphorus more efficiently. At the cellular level, selection for efficient membrane transport systems would complement the other mechanisms involved in phosphorus uptake. Root traits of the available germplasm resources have not yet been studied at length. It would be instrumental to introgress these genomic regions in cultivated cotton species or to excise, characterize and introgress genes through genetic engineering approaches.

Rubisco is one of the vital enzymes that determine the photosynthetic efficacy of the plant. Owing to its high importance in determining the yield of plant species, genes conferring Rubisco from cynabacterium have been successfully transferred in chloroplast genome of tobacco – showing a higher rate of CO_2 fixation. These genes can be utilized to make the cotton plant more photosynthetically competent, and thus ultimately enhance productivity in cotton.

Another option is to grab genetic resources/land races that are low yielding but show high adaptability to the natural environment and evolve them for low-input regions with high adaptability. Deployment of genomic-based selection procedures would be the best choice for transferring desirable genes into domesticated high-yielding types. For this, extensive screening of germplasm would be mandatory for identifying genotypes/accessions depicting traits such as resistance to various insect pests and diseases, better nutrient economy, delayed leaf senescence, and yield consistency in different environments. These would be precious assets both for breeders and biotechnologists. In this regard, exchange of germplasm would be instrumental for indenting valuable genetic resources. For example, the gene bank of the US Department of Agriculture shared about 3,000 cotton accessions for screening against cotton leaf curl disease in Pakistan. In total, more than ninety asymptomatic cotton accessions were identified that are being utilized in breeding programs as well as in developing mapping populations for identifying DNA markers. The disease is a potential threat to cotton in those regions where the whitefly is prevalent. Thus, the findings of the study undertaken in Pakistan can be translated in other parts of the world, if unfortunately, this disease infects the cotton crop. Other genomic technologies, like RNAi using various pathogen (virus) genes (REP, CP, V2 etc.) for the reduction of the virus titer in the infected cotton cells, and also to control the whitefly population using sex lethal genes, are new strategies for complementing hosts' resistance to buffer rapidly evolving viral genomes.

During the last decade of the 20th century, cotton containing three genes conferring tolerance to bollworm complex and glyphosate was released and covered ~75% of the total cotton area. However, issues related to the reduced expression of these genes and evolution of new strains of the pests are the new challenges that require further attention. Efforts towards identification of new genes of the Cry series and also from other sources such as Hvt gene derived from a spider can be used in cotton for controlling chewing insect pests. Similarly, several other genes encoding phytohormons, such as jasmonates, that mediate the defense and growth of insect herbivores have recently been identified. These can be utilized in cotton for combating bollworm strains. Pyramiding of all these genes into one genotype would develop durable resistance.

Sucking insect pests (jassid, whitefly, thrips, aphids, etc.) are being largely controlled through the application of pesticides, escalating the cost of production. Efforts to identify genes that confer high tolerance to sucking pests have not been successful. Use of new genomic methods, such as RNAi, are being investigated to engineer resistance to sucking insect pests in the cotton plant—though nothing has been commercialized yet, a great potential lies ahead.

World population is projected to exceed ten billion in 2050, requiring 40% more natural fiber production than today. Thus, sustaining lint fiber yields, especially in a context of squeezed land resources and limited availability of inputs in upcoming years, requires the exploration of underutilized avenues in cotton. For instance, impact of hybrid vigor has been witnessed in multifold increase in corn production worldwide but showed limited increase in lint production. Developing hybrids showing a 30% increase in lint production over the standard open pollinated cotton variety may convince farmers to cultivate hybrid cotton. This task is difficult but achievable through exploring the best combiners. Also, breeding hybrid cotton is handicapped by the non-availability of reliable genetic and/or mechanical procedures for emasculation. Various genes encoding sterility and restoring fertility have been identified. However, most are temperature sensitive.

Natural genetic variations for high lint-to-seed ratio were found in cotton germplasm. In most countries lint recovery of cotton ranges from 30 to 45%. This trait is very complex and difficult to improve using conventional breeding approaches, but can be tailored using DNA markers. A significant improvement in the quality of fiber has been made, but a plateau has been reached. In the present scenario, modest advances demand further explorations in understanding the cotton genome through conventional and non-conventional genomic approaches. Genetic maps dominantly developed using populations derived from interspecific crosses (between *G. hirsutum* and *G. barbadense*), are available. Genomic regions conferring quality traits can be utilized in breeding programs by initiating DNA-based selection procedures – previously not possible. In the whole scheme, extensive backcrossing followed by probing of cotton plants containing the desired loci using DNA markers is a vital breeding tactic for developing improved cotton germplasm. Other approaches, including the exploration of genetic pathways involved in conferring fiber traits, can supplement genetic engineering approaches. The ancestral species of the cultivated cotton species have been sequenced, and the genome sequencing of tetraploid cultivated cotton species would be released soon. Exploitation of bioinformatics for unraveling various mechanisms in cotton would pave the way for isolating important genes. Next-generation sequencing technologies are becoming increasingly cost-effective. Important cotton genotypes can be sequenced for exploring new genes, which can be a useful asset for transgenic approaches, would add synergy for sustaining cotton production. Such genomic approaches also help in the identification of new tissue-specific promoters, unlike the constitutive promoter, which may save plant energy.

In conclusion, the immediate adoption of high-tech management practices coupled with cultivation of improved cotton varieties developed through bridging conventional and genomic approaches would pave the way for sustaining fiber production at an optimum level of input application.

~~Deficit Irrigation Effects on Growth, Water Status and Yield of Cotton Cultivated in Central Greece~~

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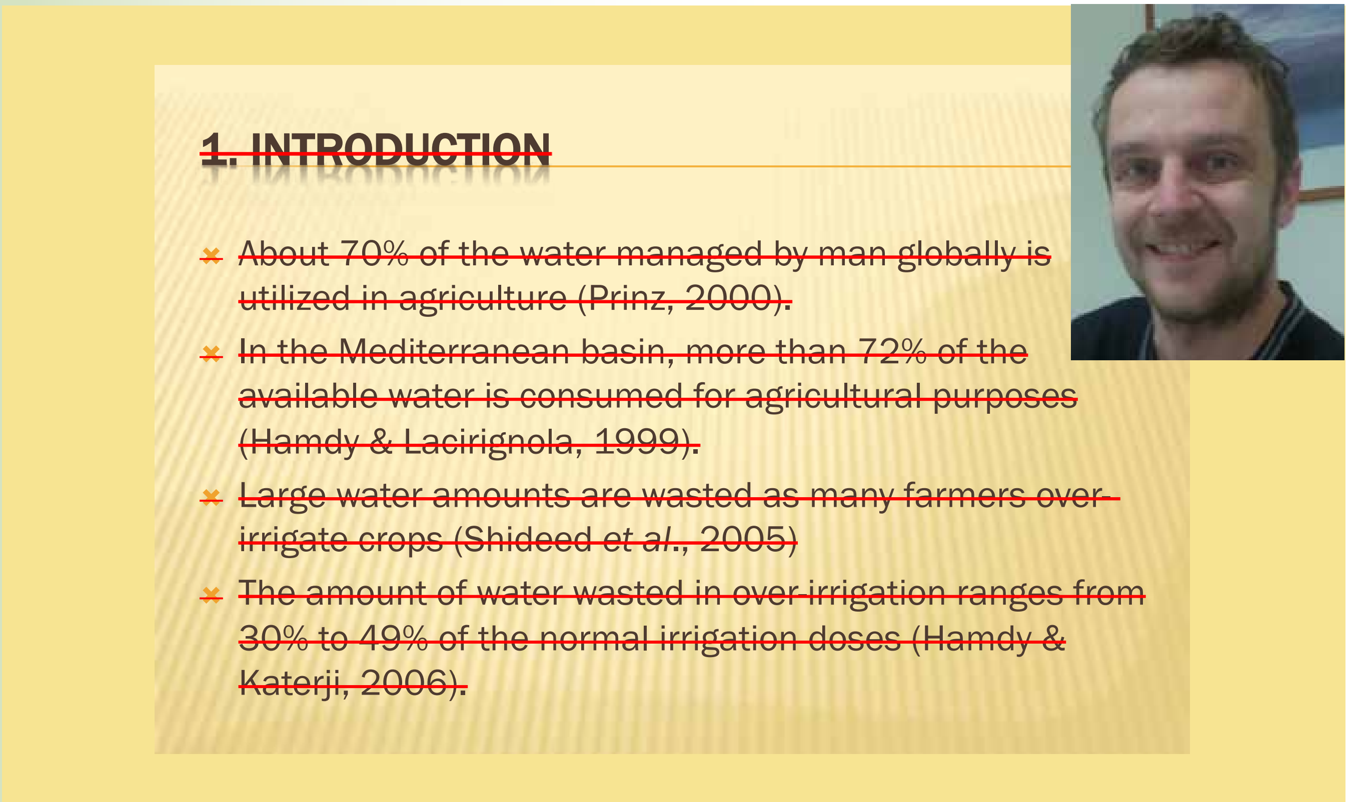

~~1. INTRODUCTION~~

- ~~About 70% of the water managed by man globally is utilized in agriculture (Prinz, 2000).~~
- ~~In the Mediterranean basin, more than 72% of the available water is consumed for agricultural purposes (Hamdy & Lacirignola, 1999).~~
- ~~Large water amounts are wasted as many farmers over-irrigate crops (Shideed *et al.*, 2005)~~
- ~~The amount of water wasted in over irrigation ranges from 30% to 49% of the normal irrigation doses (Hamdy & Katerji, 2006).~~