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Technical Analysis

Price outlook for Gujarat-ICS-105, 29mm and ICE cotton futures

(The author is Director of Commtrendz Research and the views expressed in this column are his own and the author is not liable for any loss or damage, including without limitations, any profit or loss which may arise directly or indirectly from the use of above information.)

We will look into the Gujarat-ICS-105,29mm prices along with other benchmarks and try to forecast price moves going forward.

As mentioned in the previous update, fundamental analysis involves studying and analysing various reports and data and based on that arriving at some possible direction for prices in the coming months or quarters.

Some of the recent fundamental drivers for the domestic cotton prices are:

- Cotton prices are extending its fall due to slowing exports from India amid higher arrivals while farmers and ginners take advantage of higher prices.

- Weak demand and an appreciating local currency along with higher yarn exports further pressured prices lower. Cotton yarn exports

in December rose 9% from a month earlier to 119 million kilogram, according to data from Directorate General of Foreign Trade (DGFT).

- Cotton demand from textile industry is however is expected to support prices on increase due to better sale prospects of clothing in the midst of the marriage season.

Some of the fundamental drivers for international cotton prices are:

- Cotton futures edged higher on Friday, as the market continued to struggle to sustain closer to the key technical and psychological level of 90 cents a pound.

- Despite the ongoing Lunar New Year in China, a modest dip in cotton future prices helped push (export) sales up further above 120,000 bales, during the week ending

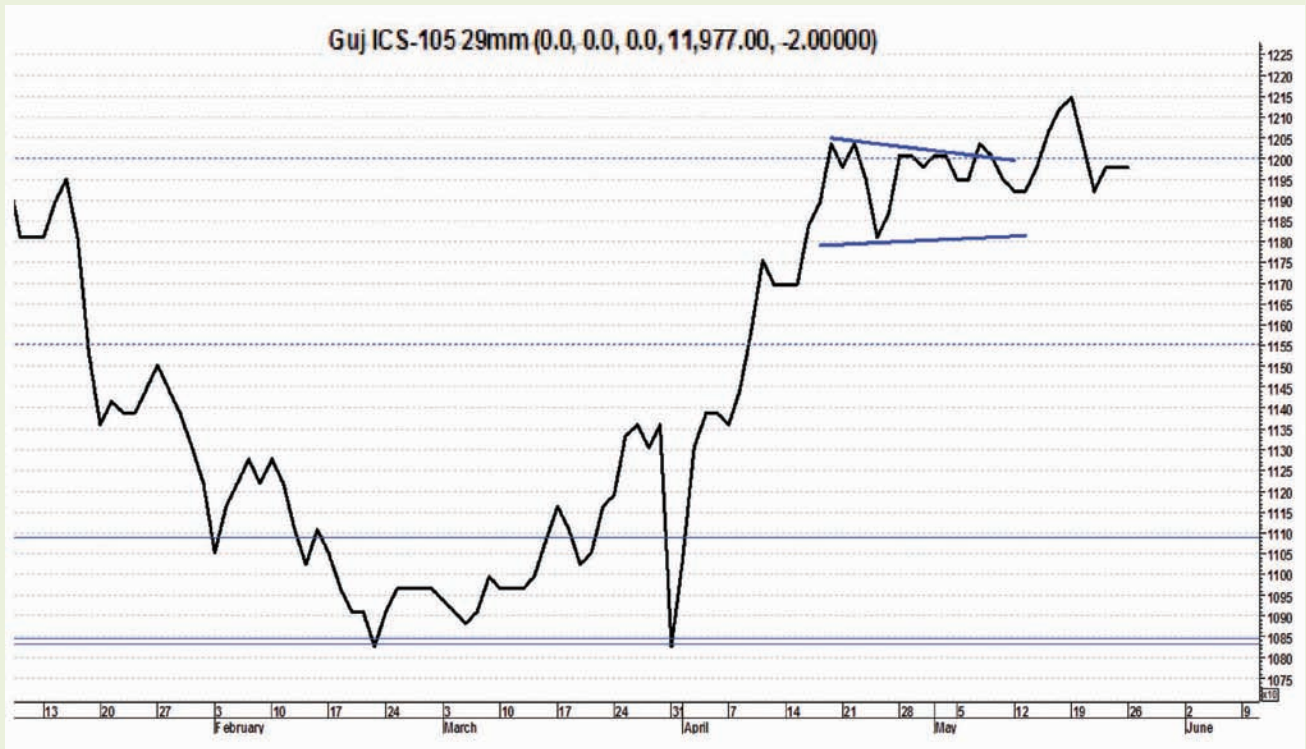
Feb. 6. Beijing's decision to scrap the controversial program has stoked fears that China's import demand will plunge and set prices up for a steep tumble.

- The USDA kept its estimate for U.S. exports at 10.50 million bales. A Wall Street Journal survey of analysts and traders had predicted the agency could raise its forecast by 1.7% to 10.68

EXPERT'S Column



Shri Gnanasekar Thiagarajan



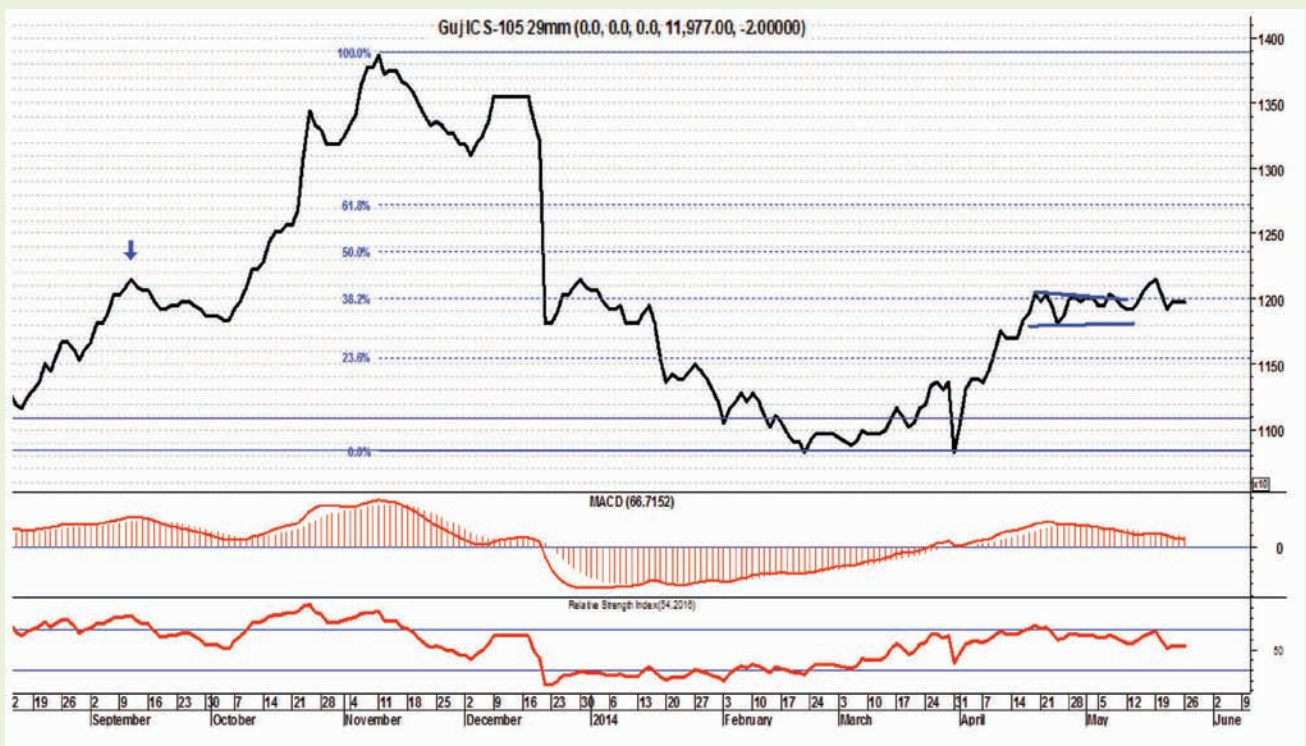
million bales of exports. Higher exports would crimp U.S. domestic supplies of cotton.

Both the domestic and international prices have hit multi-month highs. Whether prices could follow-through higher or not depends on news flows from here on.

We will now dwell into the various tools

in technical analysis and forecast a possible direction.

As mentioned in the previous update, price structures have turned very friendly, and therefore further gains of 12,350-450 /qtl looks likely in the short-term. A bullish flag pattern was identified with upwards targets ranging from 12,350 or even higher to 12,725/qtl, both





being Fibonacci retracement levels. Key support now lies at 11,700/qtl and fall below here could dash our bullish hopes. Such a fall could push prices even lower to 11,350-400 /qtl levels.

As anticipated in the previous update, chart indicates further upside to 12,365 or even higher to 12,725 levels in the coming weeks. Prices moved as per expectations, so far testing a high of 12,175/qtl. Further upside to 12,365 or even higher to 12,725 levels looks likely from where a corrective decline can be seen towards 11,700 /qtl levels. Both the above mentioned price targets are Fibonacci projected resistance levels as seen in the chart above. Prices now have to go below 11,500, for the picture to turn weak again, which we still do not favour presently.

We will also look at the ICE cotton futures charts for possible direction in international prices.

As explained in the previous update, further upside to 88-89c could face strong resistance and a minor corrective move to 85-86c is possible before prices eventually test 94c on the upside in

the coming weeks. Prices moved exactly in line with our expectations. We continue to maintain this view in the coming weeks as well. Price structures now favour a mild decline initially towards 85c while 89c caps upside attempts. As explained earlier, technical indicators are hinting at a possible bullish trend reversal. The averages in MACD have gone above the zero line indicating a bullish reversal. So, the trend remains bullish, but there could be a strong corrective downward move within this uptrend in the coming weeks.

CONCLUSION:

Both the domestic and international prices are stagnant after recent highs. Potential exists for prices to correct lower in the coming weeks. Supports are seen both for ICE March cotton futures at 85-86c and for Gujarat-ICS-105 29mm at 11,350-500 levels. We expect prices to hold support on the downside in ICE futures, and the bullish rally to continue. The Guj-ICS-105 29mm could initially correct lower towards 11,350-500 /qtl levels and then edge higher again towards 12,350-500 /qtl again in the coming weeks.

Role of Genomic Studies in Boosting Yield

(Continued from the last issue...)

Marker-assisted Selection: Its Role, Success and Perspectives in Cotton Yield Improvement

As an alternative approach being developed by the genomics research community as a result of decoding entire crop genomes and the development of sufficient genomic resources during the 21st century “omics” era, is molecular breeding or so called marker-assisted selection (MAS). Being distinct from GE approaches, MAS has great potential to improve both intrinsic and operational yields of crop species (Edgerton, 2009; Gruian-Sherman, 2009) including cotton.

Marker-assisted selection (MAS) is based on identification and tracking of genomic regions in introgression programs using DNA markers and quantitative trait loci (QTL), or association mapping results to select and further breed plant genotypes with minimal genomic fragment introgression; this allows only desirable alleles of interest to be transferred and minimizes the ‘linkage’ drag effects that negatively affect non-targeted but agronomically important traits. In this regard, DNA markers linked to the genomic regions of interest serve as an important tool, enabling breeders to conduct early-stage selection of the best plant(s) on the basis of genotype rather than phenotype. MAS provides many advantages over conventional breeding, a characteristic that is widely discussed by many review papers.

The most important requirement to conduct a MAS program is the availability of a sufficient number of polymorphic marker panels evenly covering the target genome and associated with a trait of interest, mapping details with flanking loci, the extent of linkage disequilibrium blocks, donor genotypes bearing the QTL of interest, and breeders ability and capacity to use available molecular resources. User-friendly automated genotyping platforms are vital to perform large-scale MAS programs.

The MAS approach is considered to be an efficient breeding tool to improve crops. According to Google Scholar, as of September 15, 2013, there were about 42,200 articles/ documents containing the keyword “marker-assisted selection” although many of them related to describing the future perspectives of MAS. MAS articles targeting improved yield traits or discussing yield traits resulted in 33,000 hits. The PubMed search resulted in 2,256 scientific publications with the keyword “marker-assisted selection.” Some early successful applications of MAS were improvements in maize and soybeans, and MAS has been limited to the major crops for which reference sequences are available, e.g., rice and maize.

Cotton is the world’s leading cash crop but lags behind other major crops for marker-assisted selection (MAS) due to limited polymorphisms and ‘a genetic bottleneck’ through historic domestication. MAS programs are in their early experimental phases in cotton, and MAS platforms are being developed for fiber quality traits, yield potential and biotic stress tolerance traits; however, there has been only limited success in utilization of MAS for complex traits in cotton.

Large-scale genomics resources have been developed, and significant advances in cotton genomics have been made for fostering cotton MAS programs that should facilitate better and more rapid cotton improvement programs worldwide, with the potential to raise yields. For instance, recently a researcher released a set of 17 disomic alien chromosome substitution (CS-B) lines through hypoaneuploid-based backcross chromosome substitution lines in a near-isogenic genetic background of TM-1. Researchers documented the chromosomal effects on agronomic properties, including increased yield and fiber quality using these CS-B. The chromosome substitution lines serve as a new tool for both MAS and conventional breeding programs to rapidly and efficiently improve genetic diversity and yield potential in Upland cotton.





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Cotton Genome Sequencing and Re-sequencing Efforts

The recent completion of sequencing of a diploid cotton *Gossypium raimondii* genome with the draft and the first “gold-standard” versions has provided a golden opportunity to study orthologous and paralogous genes and gene families in allotetraploid cotton. The completed genome sequencing for ancestral cotton, being the basis for near-future sequencing tetraploid genomes of commercial importance, further sequencing and re-sequencing of cotton genomes foster (1) the development of a whole genome map of DNA markers, (2) development of ‘candidate’ gene markers based on single nucleotide polymorphisms (SNP), (3) genome-wide association studies to identify biologically meaningful variations, (4) clearer understanding of transcriptome, proteome and metabolome complexes conditioning the complex traits like yield and quality, (5) allele mining efforts, and (6) understanding the genome-wide gene interactions and epigenetic regulations of agronomic traits in cotton genomes with commercial importance. These will be vital steps to enhance cotton genetic engineering as well as marker-assisted selection programs to develop novel GE technologies and design more complex MAS programs including genomic selection (GS) and virtual breeding platforms. Unlike MAS, the comprehensive information on all possible loci, haplotypes and marker effects across the entire genome is used in genomic selection to estimate trait effects coming from the genomic regions; thus, increasing the efficiency of breeding for the interested trait. Therefore, modern biotechnology and “omics”-science based breeding with the ability to exploit contemporary breeding tools and agro-technologies have great power to boost cotton yields and provide sustainable cotton production in the future.

Cotton in Uzbekistan

Cotton is one of the priority agricultural cash crops in Uzbekistan and has a significant impact on annual income in the country by providing work and supporting livelihoods in rural areas. Uzbekistan accounts for ~4% of world cotton production and 8% of world exports, and Uzbekistan is the sixth largest cotton producer and the second largest cotton exporter in the world.

Out of 4.4 million hectares of cultivable crop land in Uzbekistan, 1.3-1.4 million ha are occupied with cotton, producing 3.5 to 4 million tons of seedcotton, and exporting cotton fiber valued at ~US\$0.9 to 1.2 billion. In recent seasons, Uzbekistan has usually produced between 900,000 and 1

million tons of lint. In addition, the Uzbek cotton crop is produced primarily for the export market and represented 11% of all Uzbek exports in 2012. Sustainability and bio-security of cotton production is pivotal for the Uzbekistan economy because agriculture accounts for 24-28% of total GDP of Uzbekistan (State Statistics report, 2007: <http://www.gov.uz/en/helpinfo/agriculture>), with the cotton share being 11-17% of the country's exports.

Cotton Yield Status in Uzbekistan: Issues, Solutions and Efforts

There has been a noticeable downward trend in cotton production in Uzbekistan during the past few decades. This decline is due to both a reduction in area and lower yields caused by environmental factors. The issues associated with the decline in cotton production in Uzbekistan were addressed by Abdullaev et al., (2007), which is outside the scope of this paper. Although this report concluded that overall, minor yield decrease in cotton were caused by policy choices (such as food security or the quota system for production). However, environmental stresses are the main bio-security issue threatening agricultural production in Uzbekistan, including cotton, and these stresses are related to irrigation and water deficiencies, as well as soil salinization. These issues will pose significant dangers for the region. The current water deficit may further be intensified by over 500% this century, spreading from 2 cubic kilometers in 2005 up to 13 cubic kilometers in 2050. The cotton yield in Uzbekistan was 669 kg/ha in 2011/12, 778 kg/ha in 2012/13 and 738 kg/ha in 2013/14. In the 1970s, yields in Uzbekistan were routinely above 800 kilograms per hectare.

Recent ‘ominous forecast’ for the region projects the possibility of significant temperature increases (2-3°C) for the next 50 years. “Additionally, average annual rainfall may drop by about 10 mm in the highlands and increase by 40 to 50 mm in the desert areas of the country. If no adaptation measures are taken beyond changing planting dates in response to climate change, and taking reduced water availability into account, nearly all crop yields could fall 20 to 50 percent by 2050”. Further, based on a vulnerability index formed by the World Bank report, Uzbekistan is classified as a highly stressed region compared to most of countries in Central Asia and elsewhere.

Cotton production also suffers from pathogen attacks such as wilting disease in cotton, caused by *Fusarium oxysporum*, which is particularly dangerous for Upland cotton (*G. hirsutum*) cultivars in Uzbekistan. Reports from 2007 to 2011

demonstrated that several other varieties of Upland cottons also became highly susceptible to Fusarium wilt. Therefore, safeguarding of crop production from biotic and abiotic threats and the development of biosecure agricultural regional and national programs and strategies is vital for Uzbekistan.

In Uzbekistan, the government and research institutions put huge efforts into developing high-yielding, better quality cotton varieties using conventional breeding approaches. These efforts have produced many new cotton cultivars with increased yield and better adaptation for local farming environments. This paper is focused on cotton biotechnology and genomics efforts to address efforts at boosting yields.

Cotton Genomics and Biotechnology Research

History and the Main Factors for the Development of Biotechnology

Considering the prominent role of cotton in the economy of Uzbekistan, Mr. Islam Karimov, President of the Republic of Uzbekistan, signed a decree right after the independence of the country

in 1992 to establish the Institute of Genetics and Plant Experimental Biology under the Academy of Sciences of Uzbekistan. The Uzbekistan government invested a significant amount of foreign currency in the development of genetic engineering and the genomics of cotton, and in training qualified scientists in related disciplines. During the past 20 years, the scientists have developed an effective research environment, build a well-equipped modern laboratory for genomics and biotechnology research, and they have established wide international scientific networks of collaborators.

The “Center for Genomic Technologies” was established in 2008 within the Institute of Genetics and Plant Experimental Biology. Scientists targeted applied issues confronting Uzbek cotton farmers, as well as basic problems of cotton biotechnology and genomics in the global arena. Further, with the purpose of enhancing cotton genomics efforts and expanding the expertise gained over the past several decades, the government of Uzbekistan has established a fully genomics-dedicated interagency research institute called the Center of Genomics and Bioinformatics (CGB) under the Academy of Sciences, Ministry of Agriculture and Water Resources and the “UzCottonIndustry” association. The CGB is the

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successor agency to the former "Center of Genomic Technologies" of the Institute of Genetics and Plant Experimental Biology. The Uzbekistan government invested a large amount of funding to build a modern genomics and bioinformatics facility, provide funding for cotton genomics and biotechnology basic and applied projects, and to prepare a young generation of cotton scientists and breeders.

At the same time, the Center developed strong international collaborations with leading cotton genomics and biotechnology laboratories worldwide to support world cotton research programs. The Center received a number of international grants, which helped to enhance the research facilities, the equipment park and a reagent-material base as well as to promote young scientists and their training in leading research laboratories in the USA. For example, fruitful collaborations were established with Texas A&M University and USDA-ARS (at Starkville, Mississippi; College Station, Texas; Shafter, California; and Lubbock, Texas). These collaborations accelerated the cotton genomics and biotechnology of Uzbekistan, enhancing the development of genetically engineered cotton varieties, promoted technology transfer, and jointly patented newly developed products.

Genetic Mapping and Marker-Assisted Selection Efforts

Uzbek researchers participated in the development of pioneer cotton SSR marker collections (JESPR) consisting of 309 microsatellite markers, which found wide application in cotton genome investigations worldwide, and JESPR was widely utilized in cotton genomics research in Uzbekistan.

As cotton production in many ways is connected with earliness, boll maturation and plant senescence, a natural leaf defoliation QTL was mapped using SSR markers, and a unique naturally leaf shedding Upland cotton line was developed ($2n=2x=52$), derived from tri-species crosses between *G. thurberi* (D1D1, $2n=2x=26$, natural defoliant) \times *G. harknessii* (D2D2, $2n=2x=26$, wilt resistant) \times *G. hirsutum* (variety Tashkent-1, AADD, $2n = 2x = 52$). These QTL associated SSR markers were assigned to the short arm of chromosome 18, suggesting indirectly that gene(s) associated with natural leaf defoliation is located on this chromosome.

A set of unique recombinant inbred cotton lines (RILs) segregating for lint percentage, derived from the cross of lintless/fuzzless mutant and linted/fuzzy cottons, were exploited to tag QTL

loci responsible for lint percentage traits using SSR markers. Multiple QTL-mapping (MQM) revealed that at least, two highly significant fiber development QTLs exist around regions TMB0471 and MGHES-31 (which explained about 23-59% of the phenotypic variation of lint percentage) and around markers MGHES-31 and TMB0366 (which accounted for 5.4-12.5% of the phenotypic variation of lint percentage). These lint-percentage-trait associated SSR markers have been located on chromosomes 12, 18, 23, and 26 using deletion analysis in aneuploid chromosome substitution lines.

Considering the importance of day-neutral cotton flowering for Uzbekistan (the northernmost cotton growing country) that helped to develop cultivars with early flowering and maturation, researchers investigated a collection of photoperiod-converted radiomutants (32P), including their wild-type parental lines using SSR markers. Impact and pressure of radiomutagenesis to the SSR mutation patterns were studied, bi-parental mapping of populations via crossing the photoperiod-converted, day-neutral flowering radiomutants to the original photoperiodic wild parents were created, and consequent progenies segregated for the early flowering trait were obtained. Utilizing a collection of large SSR markers, QTL regions responsible for photoperiodic conversions and causing the day-neutral flowering after the mutation were mapped. These QTL regions were localized on chromosome 5 of cotton.

Due to the emerging threat of Fusarium wilt disease in Uzbekistan, Uzbek cotton germplasm resources were evaluated for Fusarium oxysporum sp. Vasinfectum (FOV) resistance, a race/genotype distribution of FOV fungi in Uzbekistan was studied, including frequently occurring races and their pathogenicity were identified, and a bi-parental mapping population segregating for FOV resistance was created in order to map QTL loci controlling FOV resistance in cotton. Several QTL loci contributing for FOV resistance in cotton were mapped using SSR markers.

A large number of *G. hirsutum* varieties and exotic accessions from Uzbek germplasm were characterized for both fiber quality characteristics and molecular diversity within the framework of international collaborative projects. Researchers estimated the extent of genome-wide linkage disequilibrium (LD) and association mapping of fiber quality traits using >200 microsatellite markers in narrow and broad-based *G. hirsutum* germplasm grown in two diverse environments, agronomically useful genetic diversity within a large

cotton germplasm collection was demonstrated. Researchers found the level of LD between SSR sites in broad-based exoticgermplasm (11-12%) was greater than in narrow-based cultivar germplasm (4-9%) groups. A genome-wide average of LD extended up to genetic distance of 25 cM and ~5-6 cM at $r^2 > 0.2$ in variety germplasm at the significance threshold ($r^2 > 0.1$). A genome-wide average of LD declines within the genetic distance at < 10 cM in the landrace stocks germplasm and > 30 cM in photoperiodic variety germplasm. Genome wide LD at $r^2 > 0.2$ was reduced on average to ~1-2 cM in the landrace stock germplasm and 6-8 cM in variety germplasm, providing evidence of the potential for association mapping of agronomically important traits in cotton. These results suggest that linkage, selective sweeps, inbreeding and genetic drift are the potential LD-generating factors in cotton.

Two diverse environments and analysis of a large sets of cotton germplasm found on the average of 20 SSR markers per specific environment (Uzbekistan and Mexico) associated with one of each of the five main fiber quality traits. The mixed liner model (MLM), considering both kinship (K) and population structure (Q) to minimize spurious associations, was used. The LD-based association mapping, using the MLM approach, was found to be effective in cotton,

and a number of SSR markers associated with the fiber quality traits, reported herein, provide insight into understanding environment specific functions of genes controlling fiber development, which increases the effectiveness of cotton marker-assisted breeding programs at similar latitudes.

Association mapping efforts in a large number of Upland cotton germplasm allowed Uzbek researchers to design an “association mapping” study to find biologically meaningful marker-trait associations for important fiber quality traits that account for population confounding effects. Several SSR markers associated with main fiber quality traits along with donor accessions were identified and selected for MAS programs of important fiber traits in Uzbekistan. As a result, researchers were able to mobilize novel haplotypes of quantitative trait loci (QTLs), “still - underutilized” in current Uzbek cotton breeding, from donor genotypes to several commercialized recipient cultivars using traditional backcrossing with the aid of trait-associated molecular markers. Testing the major fiber quality traits using high volume instruments (HVI) in MAS hybrids revealed that mobilization of the specific marker bands from donors has positively improved the trait of interest in recipient genotypes. Currently, fourth generation MAS

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hybrids (F1BC4) carrying new markers and having a better quality of fiber compared to the recipient parents are being grown and tested. Using these effective molecular markers as a breeding tool, researchers are pyramiding major fiber quality traits into a single genotype of several commercial Upland cotton cultivars of Uzbekistan. Thus, these genetic mapping and MAS efforts are developing in Uzbekistan that will help to address many problems associated with improving, boosting and sustaining cotton yields and quality.

Characterization of Novel Genes and Sequence Signatures

Several genes involved in cotton photomorphogenesis, flowering, and disease resistance were cloned and characterized in Uzbekistan to develop cotton biotechnology and produce Uzbekistan's own biotech cottons. For instance, two paralogous PHYA1 and PHYA2 genes in diploid cottons, the result of a Malvacea-specific PHYA gene duplication were characterized that occurred approximately 14 million years ago (MYA) - before the divergence of the A- and D-genome ancestors. One of each PHYB, PHYC, and PHYE genes in diploid cottons was cloned. Allotetraploid genomes retained all gene complements observed in putative diploid genome ancestors with at least four PHYA genes, and two genes of each PHYB, PHYC and PHYE in AD-genome *G. hirsutum* and *G. barbadense*.

Several phytochrome gene specific CAPs and dCAPs markers were developed using SNP sites for PHYA1/BbvI, PHYA1/ MboI CAPs, PHYB/AluI dCAPs, PHYB2/MboI, and PHYB2/ TaqI dCAPs that were polymorphic between *G. hirsutum* and *G. barbadense*. Cotton phytochrome A genes were found localized into chromosome 2 and 11, while cotton phytochrome B was localized into chromosome 10 using CAPs and dCAPs markers in cytogenetic stocks and linkage analysis. Further, PHYA1-derived single nucleotide polymorphism marker was associated with fiber quality traits in an interspecific cross between Pima S-7 (*G. barbadense*) and Tamcot SP37 (*G. hirsutum*) consisting of 96 F2 individuals. In addition, the orthologs of the Arabidopsis HY5 gene were cloned and characterized from *Gossypium* species. It was revealed that tetraploid cottons *G. hirsutum* and *G. barbadense* have at least two orthologous genes for HY5 that were acquired from the putative diploid ancestors - *G. raimondii* (D-genome) and *G. herbaceum* (A-genome) through allopolyploidy. Each of these consensus contig sequences shared $\pm 56\%$ nucleotide identity and 72% amino acid

similarity with the orthologous region of the Arabidopsis HY5 gene. The results should be useful in understanding cotton photomorphogenesis and the involvement of the light signal transduction system in fiber elongation through the genetic-developmental view.

A large number of small RNAs from 0-10 days post anthesis were cloned and annotated. Results provided the first direct evidence of siRNA/miRNA-mediated regulation of complex fiber development in cotton. Using the same strategy, several small RNA/microRNA signatures from developing roots, and FOV and root knot nematode (RKN) infected, as well as salt treated cotton tissues, were annotated. These signatures currently are being used for creating biotech crops with improved pathogen resistance and salt tolerance.

Further, a family of cotton MIC-3 genes were cloned and sequenced. The MIC-3 gene family plays an important role in plant defense as a PR-protein. Molecular evolution of different cotton genomes was studied, and for the first time the pathogen-dependent gene duplication pattern in the cotton MIC-3 gene was identified that completely fit with «bait and switch» and «guard and decoy» evolution models of resistant genes in plants. This gene and/or its regulatory elements family should have great potential to be used in GE cotton development due to its association with PR-processes, uniqueness to cotton, and tissue specific activity.

Cotton Transgenomics and Biotechnology

An efficient high-throughput cotton transformation system was established using modern transgenomics tools with the specific aim of developing Uzbekistan's own tissue culture derived biotech crops as well as to study the biological function of these de novo characterized cotton genes mentioned above. This includes RNAi (RNA interference) technology using available RNAi vector systems as well as newly developed synthetic RNAi constructs, which are highly specific to a gene or small RNA/microRNA signature of interest that reduce (knock-out) gene function.

Because of multiple gene effects in plant development, as well as its association with yield potential and productivity, plant flowering and architecture, and cotton fiber quality as well as its possible involvement in salt tolerance, in regulation of nitrate reductase, in cold/freezing and drought tolerance in model plant Arabidopsis, in fungal disease resistance in rice, researchers targeted RNAi

of the cotton phytochrome gene family and its signal transduction system for developing genetically engineered cottons for Uzbekistan. The work was done in collaboration with Texas A&M University and USDA-ARS laboratories. The phytochrome RNAi study provided the first molecular evidence of the importance of the phytochrome gene family in cotton fiber development and demonstrated the potential of phytochromespecific RNAi, simultaneously improving several important agronomic (e.g., early maturity, high yield) and fiber quality traits (length, strength, fineness, elasticity, and uniformity) in somatically single-cell regenerated RNAi Coker 312 cotton plants.

Previous studies in model plant *Arabidopsis* have shown physiological consequences associated with modulation of expression of phytochromes and cross-regulatory effects as the manifestations of a compensatory regulatory network of phytochromes. Results sharply contrast with findings from *Arabidopsis* in which loss-of-function *phyA* mutations showed no increase in *PHYB* expression. *PHYA1* RNAi cotton lines with a 70% decreased level of *PHYA1* expression showed increased transcript levels for *PHYA2*, *PHYB*, *PHYC* and *PHYE*. These observations indicate that the phytochrome regulatory network of cotton may have a fundamentally different dynamic architecture than that of *Arabidopsis*.

Researchers showed a transfer of phytochrome-associated RNAi phenotypes from somatically regenerated RNAi Coker-312 to other 'recipient' commercial Upland cotton cultivars via sexual crosses, effectively converting recipients to the superior genotypes. Using this RNAi approach, as the first generation biotech cottons in Uzbekistan, a number of genetically modified cotton varieties with improved fiber quality (38-40 mm fiber length), improved micronaire (3.9-4.2), early maturity (earlier by 5-10 days) and higher seed cotton yield (~10-18% higher) with improved root system (two fold) have been developed. This technology demonstrates the great potential to develop superior cultivars in a globally important crop species in a short time without any adverse effects on yield. Large-scale field trials to further commercialize phytochrome derived biotech cotton varieties are being conducted for future commercialization of phytochrome gene specific RNAi varieties and to quickly boost cotton production in Uzbekistan. Similarly, biotech cottons for drought, salt, wilt (FOV) resistance traits (using RNAi approach) are being developed using characterized genes and sequence signatures in Uzbekistan. To put this in perspective, researchers

will work on new genetic engineering technologies such as "Zinc-finger" and/or "TALEN" for sitespecific genome editing of genes with proven RNAi effects (e.g. cotton *PHYA1*) to develop native biotech cotton cultivars for Uzbekistan farmers.

Conclusion

A careful review of current cotton production reports and world statistics shows that the demand for cotton fiber will likely keep increasing, but cotton production will be constrained by food security concerns associated with population growth, complex policy factors affecting a gradual decrease of cotton planted area, declining cotton yield potential associated with the narrowness of genetic diversity of cotton cultivars, and a worsening of environmental and biotic stresses. Global climate change and projected temperature increases generate alarming forecasts for even larger yield decreases, including for cotton, over the next few decades. Advances in conventional cotton breeding programs and the success of biotech cottons, widely implemented by cotton farmers in the last several decades, have resulted in significant yield gains. These yield gains contributed to the profitability and sustainability of world cotton production.

Future success in boosting cotton yields can be achieved through the development and application of new "omics"-based modern technologies. These include marker-assisted selection, genomic selection and virtual breeding, and the development of a new generation biotech cottons through modification and targeting of multiple-effect genes, improving photosynthetic rates and plant architecture with more bolls, fruiting branches and well-developed roots, resistant to environmental stress and biotic invasions, and plants with better nitrogen and water use efficiencies. In this mission, the newly completed cotton genome sequence and completion of genome sequences of commercially important allotetraploid cottons will boost the development of innovative technologies in the near future. This should help to rapidly improve yields of cotton to cover the projected needs for fiber and other associated cotton products. These challenges require more coordinated efforts, wider international collaborations, and better funding and investment. Similarly, cotton yield improvement is the priority objective and mission of the research programs in Uzbekistan. Current efforts on application of novel genomics tools and biotechnologies, in combination with contemporary breeding knowledge and expertise, will provide a basis to boost yields and other agronomic properties of Uzbek cotton.

(Source: ICAC Recorder - December 2013)

UPCOUNTRY SPOT RATES							(Rs./Qtl)					
Standard Descriptions with Basic Grade & Staple in Millimetres based on Upper Half Mean Length [By law 66 (A) (a) (4)]							Spot Rate (Upcountry) 2013-14 Crop FEBRUARY 2014					
Sr. No.	Growth	Grade Standard	Grade	Staple	Micronaire	Strength /GPT	10th	11th	12th	13th	14th	15th
1	P/H/R	ICS-101	Fine	Below 22mm	5.0 - 7.0	15	11220 (39900)	11220 (39900)	11164 (39700)	11164 (39700)	11164 (39700)	11107 (39500)
2	P/H/R	ICS-201	Fine	Below 22mm	5.0 - 7.0	15	11360 (40400)	11360 (40400)	11304 (40200)	11304 (40200)	11304 (40200)	11248 (40000)
3	GUJ	ICS-102	Fine	22mm	4.0 - 6.0	20	8942 (31800)	8942 (31800)	8886 (31600)	8942 (31800)	8886 (31600)	8858 (31500)
4	KAR	ICS-103	Fine	23mm	4.0 - 5.5	21	9561 (34000)	9505 (33800)	9448 (33600)	9505 (33800)	9448 (33600)	9420 (33500)
5	M/M	ICS-104	Fine	24mm	4.0 - 5.5	23	10967 (39000)	10911 (38800)	10854 (38600)	10911 (38800)	10854 (38600)	10826 (38500)
6	P/H/R	ICS-202	Fine	26mm	3.5 - 4.9	26	12035 (42800)	11923 (42400)	11979 (42600)	12035 (42800)	11979 (42600)	11979 (42600)
7	M/M/A	ICS-105	Fine	26mm	3.0 - 3.4	25	11304 (40200)	11192 (39800)	11135 (39600)	11192 (39800)	11135 (39600)	11107 (39500)
8	M/M/A	ICS-105	Fine	26mm	3.5 - 4.9	25	11473 (40800)	11360 (40400)	11304 (40200)	11360 (40400)	11304 (40200)	11276 (40100)
9	P/H/R	ICS-105	Fine	27mm	3.5 - 4.9	26	12092 (43000)	11979 (42600)	12035 (42800)	12148 (43200)	12092 (43000)	12092 (43000)
10	M/M/A	ICS-105	Fine	27mm	3.0 - 3.4	26	11529 (41000)	11389 (40500)	11445 (40700)	11473 (40800)	11473 (40800)	11473 (40800)
11	M/M/A	ICS-105	Fine	27mm	3.5 - 4.9	26	11642 (41400)	11501 (40900)	11557 (41100)	11585 (41200)	11585 (41200)	11585 (41200)
12	P/H/R	ICS-105	Fine	28mm	3.5 - 4.9	27	12345 (43900)	12260 (43600)	12317 (43800)	12373 (44000)	12345 (43900)	12345 (43900)
13	M/M/A	ICS-105	Fine	28mm	3.5 - 4.9	27	11810 (42000)	11642 (41400)	11726 (41700)	11726 (41700)	11726 (41700)	11726 (41700)
14	GUJ	ICS-105	Fine	28mm	3.5 - 4.9	27	11923 (42400)	11810 (42000)	11867 (42200)	11867 (42200)	11867 (42200)	11867 (42200)
15	M/M/A/K	ICS-105	Fine	29mm	3.5 - 4.9	28	11895 (42300)	11726 (41700)	11810 (42000)	11810 (42000)	11810 (42000)	11810 (42000)
16	GUJ	ICS-105	Fine	29mm	3.5 - 4.9	28	12035 (42800)	11923 (42400)	11979 (42600)	11979 (42600)	11979 (42600)	11979 (42600)
17	M/M/A/K	ICS-105	Fine	30mm	3.5 - 4.9	29	12063 (42900)	11923 (42400)	12007 (42700)	12007 (42700)	12007 (42700)	12007 (42700)
18	M/M/A/K/T/O	ICS-105	Fine	31mm	3.5 - 4.9	30	12232 (43500)	12092 (43000)	12176 (43300)	12232 (43500)	12232 (43500)	12232 (43500)
19	K/A/T/O	ICS-106	Fine	32mm	3.5 - 4.9	31	12485 (44400)	12373 (44000)	12457 (44300)	12513 (44500)	12513 (44500)	12513 (44500)
20	M(P)/K/T	ICS-107	Fine	34mm	3.0 - 3.8	33	17997 (64000)	17997 (64000)	17997 (64000)	18109 (64400)	18109 (64400)	18109 (64400)

(Note: Figures in bracket indicate prices in Rs./Candy)