## 'ICAC RESEARCHER OF THE YEAR 2018' **Nomination Package**



## **Personal Details**

Name (First, Middle, Last)	Baohong Zhang
Date of birth (dd/mm/yyyy)	17/11/1968
Gender	male
Educational Qualifications	Ph.D.
Field of Specialization	Plant molecular biology
Area of Research	Cotton genomics, genetics and molecular biology
Designation / Current Position	Professor
Address of the Organization /	Department of Biology, East Carolina University, Greenville,
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Part-1 Awards and Recognitions on Cotton Research (National)

I all -I A	1 art-1 Awards and Accognitions on Cotton Acsearch (National)				
S.No.	Year	Name of the Award / Recognition	Awarding	Remarks	
			Institution		
1	2017	Nominating the Outstanding Professorship	East Carolina		
			University		
2	2017	The Achievement in International Research	East Carolina	Only awarded	
		and Creative Activity Award	University	one faculty	
3	2016	Thomas Harriot College of Arts and	East Carolina		
		Sciences Reassignment Award	University		
4	2013	Five Year Research Achievement Award	East Carolina	Only awarded	
			University	two faculty	
5	2013	Academic Affairs Faculty Book	East Carolina		
		"Transgenic Cotton" Award	University		
6	2006	Fifth Annual Graduate Student Research	Texas Tech		
		Poster Competition	University		

Part-2 A	Part-2 Awards and Recognitions on Cotton Research (International)					
S.No.	Year	Name of the Award / Recognition	Awarding Institution	Remarks		
1	2017	Excellent Scholar Award	XIX International			
			Botanical Congress			
2	2006	Excellence in Science	Science/AAAS			
3	2006	Agrochemical Division Education Award	American Chemical			
			Society			
4	2002	The 10th IAPTC&B Fellowship on transgenic	SIVB			
		cotton				
5	2000	2nd place Award of Science and Technology	Henan Province			
		Progress, "The Establishment of Cotton Tissue	Government, China			
		Culture and High Frequency Plant				
		Regeneration"				

6	1999	Excellent Youth Award	Anyang, China
7	1999	First place Scientific Paper Award, "High frequency somatic embryogenesis and plant regeneration in cotton"	Chinese Academy of Agricultural Science
8	1997	First place Scientific Paper Award, "Anther culture and plant regeneration of cotton (Gossypium klotzschianium antherss)",	Henan Province, China
9	1997	Third place Scientific Paper Award, "Selection of cotton salt-resistant embryogenic cell lines and plant regeneration	Chinese Academy of Agricultural Science
10	1996	Scientific Paper Award	Chinese Association of Agronomy
11		More than 20 other scientific papers (on cotton) were awarded Excellent Scientific Papers by Henan Province, Ministry of Agriculture of China, respectively (1996-2000)	

Part-3 Research Papers on Cotton as First Author

	s Research Papers on Cotton as First Author	
S.No.	Paper Reference (*Harvard Style)	Cited by
1	<b>Zhang, B.H.</b> & Wang, Q.L. (2016) MicroRNA, a new target for engineering new crop cultivars. <i>Bioengineered</i> , 7(1): 7-10.	5
2	<b>Zhang, B.H.</b> (2015) MicroRNA: a new target for improving plant tolerance to abiotic stress. <i>Journal of Experimental Botany</i> , 66 (7): 1749-1761	
3	<b>Zhang, B.H.</b> and Wang, Q.L. (2015) MicroRNA-based biotechnology for plant improvement. <i>Journal of Cellular Physiology</i> , 230(1): 1-15.	
4	<b>Zhang, B.H.</b> & Pan, X.P. (2009) Expression of microRNAs in cotton. <i>Molecular Biotechnology</i> 42 (3): 269-274.	
5	<b>Zhang, B.H.</b> , Wang, Q.L., Liu, F., Wang, K.B. & Frazier, TP (2009) Highly efficient plant regeneration through somatic embryogenesis in 20 elite commercial cotton ( <i>Gossypium hirsutum</i> L.) cultivars. <i>Plant Omics</i> , 2(6): 259-268.	
6	<b>Zhang, B.H.</b> , Stellwag, E.J., & Pan, X.P. (2009) Large-scale genome analysis reveals unique features of microRNAs. <i>Gene</i> 443 (1-2): 100-109.	
7	<b>Zhang, B.H.</b> , Pan, X.P., Venne, L., McMurry, S.T., Cobb, G.P. & Anderson, T.A. (2008) Development of a method for the determination of 9 currently used cotton pesticides by gas chromatography with electron capture detection. <i>Talanta</i> 75(4): 1055-1060.	
8	<b>Zhang, B.H.</b> , Wang, Q.L., Wang, K.B., Pan, X.P., Liu, F., Guo TL, Cobb, G.P. & Anderson, T.A. (2007) Identification of cotton microRNAs and their targets. <i>Gene</i> 397(1-2): 26-37	
9	<b>Zhang, B.H.</b> , Pan, X.P., Cox SB, Cobb, G.P. & Anderson, T.A. (2006) Evidence that miRNAs are different from other RNAs. <i>Cellular and Molecular Life Sciences</i> (CMLS) 63(2):246-254.	
10	<b>Zhang, B.H.</b> , Pan, X.P., Cannon C, Cobb, G.P. & Anderson, T.A. (2006) Conservation and divergence of plant microRNA genes. <i>The Plant Journal</i> 46 (2): 243-259.	
11	<b>Zhang, B.H.</b> , Pan, X.P., Cobb, G.P. & Anderson, T.A. (2006) Plant microRNA: a small regulatory molecule with big impact. <i>Developmental Biology</i> 289: 3-16	
12	<b>Zhang, B.H.</b> , Pan, X.P., Wang, Q.L., Cobb, G.P. & Anderson, T.A. (2005) Identification and characterization of new plant microRNAs using EST analysis. <i>Cell Research</i> 15(5): 336-360	
13	<b>Zhang, B.H.</b> , Pan, X.P., Guo TL, Wang, Q.L. & Anderson, T.A. (2005) Measuring gene flow in the cultivation of transgenic cotton ( <i>Gossypium hirsutum L.</i> ). <i>Molecular Biotechnology</i> , 31:11-20.	
14	<b>Zhang, B.H.,</b> Pan, X.P. & Wang, Q.L. (2005) Development and commercial use of Bi cotton. <i>Physiology and Molecular Biology of Plants</i> 11: 51-64.	
15	<b>Zhang, B.H.</b> , Wang, Q.L. & Wang QP (2004) Bt cotton in India. <i>Current Science</i> 86(6): 758-760.	
16	<b>Zhang, B.H.</b> , Liu, F., Liu ZH, Wang HM & Yao CB (2001) Effects of kanamycin on tissue culture and somatic embryogenesis in cotton. <i>Plant Growth Regulation</i> 33(2): 137-149	
17	<b>Zhang, B.H.</b> , Wang, H.M., Liu, F., Li, Y.H. & Liu, Z.D. (2001) <i>In vitro</i> assay for 2,4-D resistant in transgenic cotton. <i>In Vitro Cell Developmental Biology-Plant</i> 37(2): 300-304.	5

18	<b>Zhang, B.H.</b> , Wang, Q.L. & Zhang WS (2001) Selection for salt tolerance in cotton tissue	8
10	culture and plant regeneration from NaCl-tolerant embryogenic callus. <i>Israel J Plant Sci</i>	0
	49: 187-191.	
19	<b>Zhang, B.H.</b> , Feng, R., Liu, F., Zhou DY & Wang, Q.L. (2001) Direct somatic	8
	embryogenesis and plant regeneration from cotton (Gossypium hirsutum L.) explants.	o l
	Israel J Plant Sci 49: 193-196.	
20	<b>Zhang, B.H.</b> , Wang, Q.L. & Liu, F. (2001) Phenotypic variation in cotton ( <i>Gossypium</i>	11
	hirsutum L.) regenerated plants. Current Science 81(8): 1112-1115.	
21	<b>Zhang, B.H.</b> , Feng, R., Liu, F. & Wang, Q.L. (2001) High frequency somatic	92
	embryogenesis and plant regeneration of an elite Chinese cotton variety. Bot Bulletin of	- <b>-</b>
	Acad Sin 42: 7-16.	
22	Zhang, B.H., Liu, F., Yao CB, Gong WK, Liu ZH, Wang HM & Liu YL (2001) Obtained	n/a
	callus resistant to kanamycin from cotton transformation by Agrobacterium tumefaciens	
	with GO gene. Cotton Science 13(2): 78-81. (In Chinese with English abstract)	
23	Zhang, B.H. & Wang, Q.L. (2001) Bt-cotton in China. Current Science, 81(4): 332-333	1
24	<b>Zhang, B.H.</b> (2000) Transgenic crops in China. <i>Science</i> , 290(5496): 1505-1506.	1
25	Zhang, B.H., Guo TL & Wang, Q.L. (2000) Inheritance and segregation of exogenous	25
	genes in transgenic cotton. <i>Journal of Genetics</i> , 79(2): 71-75	
26	<b>Zhang, B.H.</b> , Liu, F. & Yao CB (2000) Plant regeneration via somatic embryogenesis in	78
	cotton. Plant Cell, Tissue and Organ Culture 60(2): 89-94.	
27	Zhang, B.H., Liu, F., Yao CB & Wang, K.B. (2000) Recent progress in cotton	60
•	biotechnology and genetic engineering in China. Current Science 79(1): 37-44.	
28	Zhang, B.H., Liu, F. & Wang, Q.L. (2000) Germination of somatic embryos and plant	2
20	recovery in cotton (Gossypium hirsutum L.). International J Experiment Botany 68: 39-46.	,
29	Zhang, B.H. (2000) Regulation of plant growth regulators on cotton somatic	n/a
20	embryogenesis and plant regeneration. <i>Biochemistry</i> 39 (6): 1567.	
30	<b>Zhang, B.H.</b> (2000) Resistance management for Bt-transgenic cotton. <i>Cotton Sci</i> , 12(3):	n/a
31	7hong PH Liv E Voc CP Wong HM & Fong VA (2000) Scopping electron	n/o
31	<b>Zhang, B.H.</b> , Liu, F., Yao CB, Wang HM & Feng XA (2000) Scanning electron microscope observation on tissue culture and somatic embryogenesis of <i>Gossypium</i>	n/a
	hirsutum L. Chinese Journal of Crop Sciences 26(1):125-128. (In Chinese with English	
	abstract)	
32	<b>Zhang, B.H.</b> , Liu, F., Yao CB & Wang HM (2000) High frequency somatic embryogenesis	n/a
_	and plant regeneration from cotton elite variety cv. CCRI 19. Chinese Journal of Crop	12, 66
	Sciences 26(2):239-242. (In Chinese with English abstract)	
33	Zhang, B.H., & Guo TL (2000) Frequency and distance of pollen dispersal from transgenic	9
	cotton. Chinese Journal of Applied and Environmental Biology, 6(1):39-42.	
34	<b>Zhang, B.H.</b> , Guo TL & Wang, Q.L. (2000) Inheritance of transgenic cotton. <i>Life Science</i>	3
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35	Zhang, B.H., Liu, F., Liu ZH, Wang HM & Yao CB (2000) Hormone regulation on cotton	n/a
	somatic embryogenesis. Cotton Science 12(1): 17-21. (In Chinese with English abstract)	
36	<b>Zhang, B.H.</b> , Feng, R., Liu, F. & Yao CB (1999) Direct induction of cotton somatic	n/a
27	embryogenesis. Chinese Science Bulletin 44: 766-767. (In Chinese with English abstract)	/-
37	<b>Zhang, B.H.</b> , Li FL, Li XL, Li, F.G., Liu, F. & Yao CB (1999) Effects of genotypes on cotton anther response <i>in vitro</i> culture. <i>Cotton Sciences</i> 11(2): 92-99.	n/a
38	<b>Zhang, B.H.</b> , Feng, R., Du XM, Li FL, Wang CY, Feng XA & Li XL (1997) Scanning	n/a
30	electron microscope observation on embryogenesis and organogenesis in tissue culture of	II/a
	Gossypium klotzschianum Anderss. Chinese Journal of Electron Microscopy 16(2):81-86.	
39	<b>Zhang, B.H.</b> & Zhou Y (1999) Effects of salt-stress on cotton tissue culture and plant	n/a
	regeneration. Pakistan Journal of Biological Sciences 2(4):1085-1087.	11/4
40	<b>Zhang, B.H.</b> , Feng, R. (1998) Achievement, problems and strategies of transgenic insect-	7
	resistant cotton. Chinese Journal of Crop Sciences 24(2):248-246.	-
41	<b>Zhang, B.H.</b> , Feng, R., Li XL, Li FL (1996) Anther culture and plant regeneration of	33
	cotton (Gossypium klotzschianum Anderss). Chinese Science Bulletin 41(2): 145-148.	
42	Zhang, B.H., Li XL, Li FL & Li, F.G. (1996) Development of abnormal plantlets and their	n/a
1	normalization during cotton tissue culture. Chinese Journal of Plant Science 38(11):845-	
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43	<b>Zhang, B.H.</b> , Li XL (1996) Occurrence and transformation of abnormal embryoids in	6
	cotton tissue culture. Chinese Journal of Crop Sciences 22(1):107-111.	
44	Zhang, B.H., Wang, Q.L. & Feng, R. 1996. Somatic embryony patterns and plant	2

	regeneration in Gossypium hirsutum L. Journal of Agricultural Biotechnology 4(1):44-50.	
45	<b>Zhang, B.H.</b> , Feng, R., Zhang WS, Li FL & Wang CY (1996) Study of the method for	n/a
	smearing of cotton callus and the steady of chromosome in cotton tissue culture. Journal of	
	Agricultural Biotechnology 4(3): 224-229.	
46	<b>Zhang, B.H.</b> (1995) A methodology for tissue culture and plant regeneration in cotton.	n/a
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47	<b>Zhang, B.H.</b> , Feng, R., Li FL & Li, F.G. (1995) Embryogenesis and plant regeneration in	n/a
	cotton anther culture. Chinese Science Bulletin 40(17):1640-1642.	
48	<b>Zhang, B.H.</b> , Li FL, Li, F.G. and Li XL (1995) Plant regeneration from cotton anther	n/a
	culture. Chinese Journal of Agricultural Sciences 28(5):92-93.	

n/a means no citation information available from Google scholar

Part-4 Research Papers on Cotton as Co-Author

<ul> <li>S.No. Paper Reference (*Harvard Style)</li> <li>Pan, X.P., Nichols, R.L., Li, C. and Zhang, B.H. (2018) MicroRNA-target gene response to root knot nematode (<i>Meloidogyne incognita</i>) infection in cotton. <i>Genomics</i>, in press.</li> <li>Li, C, Unver T &amp; Zhang, B.H. (2017) A high-efficiency CRISPR/Cas9 system for target mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific Reports</i>, 7: 43902.</li> <li>Li C, Unver T &amp; Zhang, B.H. (2017) A powerful CRISPR/Cas9 platform for obtaining precise gene knockout mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). ISB New REPORT, 2017, p 5-9.</li> <li>Wang, M., Sun RR. Li C, Wang, Q.L. &amp; Zhang, B.H. (2017) MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Report</i> 7: 44454.</li> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhang B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analyst during abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. doi:10.1038/srep22980</li> </ul>	Cited by
<ul> <li>Pan, X.P., Nichols, R.L., Li, C. and Zhang, B.H. (2018) MicroRNA-target gene response to root knot nematode (<i>Meloidogyne incognita</i>) infection in cotton. <i>Genomics</i>, in press.</li> <li>Li, C, Unver T &amp; Zhang, B.H. (2017) A high-efficiency CRISPR/Cas9 system for target mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific Reports</i>, 7: 43902.</li> <li>Li C, Unver T &amp; Zhang, B.H. (2017) A powerful CRISPR/Cas9 platform for obtaining precise gene knockout mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). ISB New REPORT, 2017, p 5-9.</li> <li>Wang, M., Sun RR. Li C, Wang, Q.L. &amp; Zhang, B.H. (2017) MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Report</i> 7: 44454.</li> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhang B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analyst during abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. description of the control of the</li></ul>	Citcacj
<ul> <li>to root knot nematode (<i>Meloidogyne incognita</i>) infection in cotton. <i>Genomics</i>, in press.</li> <li>Li, C, Unver T &amp; Zhang, B.H. (2017) A high-efficiency CRISPR/Cas9 system for target mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific Reports</i>, 7: 43902.</li> <li>Li C, Unver T &amp; Zhang, B.H. (2017) A powerful CRISPR/Cas9 platform for obtaini precise gene knockout mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). ISB New REPORT, 2017, p 5-9.</li> <li>Wang, M., Sun RR. Li C, Wang, Q.L. &amp; Zhang, B.H. (2017) MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Report</i> 7: 44454.</li> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhang B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analyst during abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. decentific decentific reports, 6:22980.</li> </ul>	es
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<ul> <li>Li C, Unver T &amp; Zhang, B.H. (2017) A powerful CRISPR/Cas9 platform for obtaini precise gene knockout mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). ISB New REPORT, 2017, p 5-9.</li> <li>Wang, M., Sun RR. Li C, Wang, Q.L. &amp; Zhang, B.H. (2017) MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Report</i> 7: 44454.</li> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhang B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analysis during abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. december 1.</li> </ul>	
<ul> <li>precise gene knockout mutagenesis in cotton (<i>Gossypium hirsutum</i> L.). ISB New REPORT, 2017, p 5-9.</li> <li>Wang, M., Sun RR. Li C, Wang, Q.L. &amp; Zhang, B.H. (2017) MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Report</i> 7: 44454.</li> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhang B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analysis during abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. december 1.</li> </ul>	ng <b>n/a</b>
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<ul> <li>Sun RR *, Li CQ, Zhang JB, Li F, Ma L, Tan YG, Wang, Q.L., and Zhang BH (201 Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i>, 7:3.</li> <li>He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhan B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analysiduring abiotic stress in <i>Gossypium raimondii</i>. <i>Scientific Reports</i>, 6:22980. doi:</li> </ul>	1
Differential expression of microRNAs during fiber development between fuzzless-lintle mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i> , 7:3.  6 He QL, Jones DC, Li W, Xie F.L.*, Ma J*, Sun RR*, Wang, Q.L., Zhu SJ, and Zhan B.H. (2016) Genome-wide identification of R2R3-MYB genes and expression analysis during abiotic stress in <i>Gossypium raimondii</i> . <i>Scientific Reports</i> , 6:22980. de	7) 1
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17	Xie F.L.*, and Zhang, B.H. (2015) MicroRNA evolution and expression analysis in	20
	polyploidized cotton genome. <i>Plant Biotechnology Journal</i> , 13(3): 421-434.	
18	Xie F.L.*, Jones, D.C., Wang, Q.L., Sun, R.R., and Zhang, B.H. (2015) Small RNA	46
	sequencing identifies miRNA roles in ovule and fiber development. <i>Plant Biotech Journal</i> ,	
	13: 355-369.	
19	Xie F.L., Wang, Q.L., Sun, R.R., and Zhang, B.H. (2015) Deep sequencing reveals	64
	important roles of microRNAs in response to drought and salinity stress in cotton. J	
	Experiment Bot, 66: 789-804.	
20	Zhang ZY, Xin WW, Wang SF, Zhang X, Dai HF, Sun RR, Frazier T*, Zhang, B.H. and	18
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	stress response and cell wall development. Funct Integrative Genomics, 15(1): 17-26.	
21	Ma J*, Wang, Q.L., Sun RR, Xie F.L.*, Jones DC, and <b>Zhang, B.H.</b> (2014) Genome-wide	31
	identification and expression analysis of TCP transcription factors in Gossypium raimondii.	
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22	Sun RR*, Wang, Q.L., Ma J*, He QL and <b>Zhang, B.H.</b> (2014) Differentiated expression of	9
	microRNAs may regulate genotype-dependent traits in cotton. <i>Gene</i> 547(2): 233-238.	
23	He QL, Zhu SJ and Zhang, B.H. (2014) MicroRNA-target gene responses to lead-induced	15
	stress in cotton (Gossypium hirsutum L.). Funct Integrative Genomics, 14(3): 507-515.	
24	Li W, Liu W, Wei H, He QL, Chen JH, Zhang, B.H., Zhu SJ (2014) Species-specific	13
	expansion and molecular evolution of the 3-hydroxy-3-methylglutaryl coenzyme A	
	reductase (HMGR) gene family in plants. PLoS One, 9(4):e94172.	
25	Wang, M., Wang, Q.L. & Zhang, B.H. (2013) Response of miRNAs and their targets to	69
	salt and drought stresses in cotton (Gossypium hirsutum L.). Gene, 530(1):26-32.	
26	Wang, M., Wang, Q.L. & Zhang, B.H. (2013) Evaluation and selection of reliable	37
	reference genes for gene expression under abiotic stress in cotton. <i>Gene</i> , 530(1):44-50.	
27	Xie F.L.*, Xiao P, Chen DL*, Xu L* & <b>Zhang, B.H.</b> (2012) miRDeepFinder: a miRNA	259
	analysis tool for deep sequencing of plant small RNAs. <i>Plant Mol Biology</i> , 80 (1): 75-84.	
28	Xie F.L.*, Sun GL, Stiller JW & Zhang, B.H. (2011) Genome-wide functional analysis of	80
	the cotton transcriptome by creating an integrated EST database. <i>PLOS One</i> , 6(11):e26980	
29	Sun, G.L., Xie F.L.* & Zhang, B.H. (2011) Transcriptome-wide identification and stress	25
	properties of the 14-3-3 gene family in cotton (Gossypium hirsutum L.). Functional &	
	Integrative Genomics, 11(4): 627-636.	
30	Liu, F. & Zhang, B.H. (2004) Establishment of high frequency somatic embryogenesis and	n/a
	plant regeneration system in cotton. Cotton Science, 16: 117-122. (In Chinese)	
31	Wang, Q.L., Zhang, B.H., Guo TL & Xu XR (2001) Inheritance of exogenous genes in	n/a
	transgenic cotton. Life Science Research 5(4): 345-350.	
32	Wen X & Zhang, B.H. (2000) Current status and prospects of transgenic insect-resistant	12
22	cotton. Journal of Agricultural Biotechnology, 8(2): 194-199. (In Chinese)	
33	Liu, F., Zhang, B.H., Yao CB & Wang HM (1999) The effect of kanamycin on the growth	n/a
	and development of cotton embryogenic callus. <i>Cotton Sciences</i> 11(2): 70-72. (In Chinese)	
34	Liu, F., Zhang, B.H., Liu ZH & Yao CB (1999) Effect of kanamycin on induction and	n/a
2.5	growth of cotton callus. <i>Journal of Henan University</i> 29(3): 84-87. (In Chinese)	4.5
35	Feng, R., Zhang, B.H. (1997) Genotype analysis in cotton tissue culture and plant	13
26	regeneration. Acta Agriculturae Boreali-occidentalis Sinica 6(2):27-30. (In Chinese)	
36	Feng, R., <b>Zhang, B.H.</b> & Guo XM (1996) Effects of exogenous <i>Bt</i> gene on yield properties	14
25	and insect resistance of cotton. Cotton Science, 8(1): 10-13. (In Chinese)	
37	Feng, R., Guo TL & Zhang, B.H. (1996) Study on cotton somaclone variation and its	n/a
	application on cotton genetic and breeding. J Agricultural Biotechnology 4(3): 230-237	

n/a means no citation information available from Google scholar

Part-5 Oral Presentation on Cotton Research in International Conferences

Iuit	Of all 1 resentation on Cotton Research in International Comerences		
S.No.	Conference Proceedings Reference (*Style) as first Author	Countr	Year
		У	
1	<b>Invited speaker.</b> Roles of microRNAs during cotton fiber imitation and early	USA	2018

	development. International Plant & Animal Genome XXVI, Jan 12-18, 2018,	
2	San Diego, CA.	2017
2	<b>Invited speaker</b> . microRNA-based biotechnology for crop improvement. The China 3rd Int'l Conference on Agronomy and Horticulture. Sanya, China, Nov 28-30	2017
3	<b>Invited speaker</b> . MicroRNA-mediated mechanism during plant response to China	2017
3		2017
	abiotic stress and its application. XIX International Botanical Congress. Shenzhen, China, July 23-29, 2017	
4	Invited speaker. Impact of nanoparticles on plant growth and development and China	2017
7	the microRNA-mediated regulation 254th ACS National Meeting in	2017
	the microRNA-mediated regulation. 254th ACS National Meeting in Washington DC, August 19 <sup>th</sup> to 24 <sup>th</sup> , 2017	
5	Invited speaker. MicroRNA-based biotechnology for crop improvement. China	2017
	Ningxia Academy of Agricultural Science, July 4, 2017	2017
6	<b>Invited speaker</b> . MicroRNAs and its regulatory role in plant development. China	2017
	Jiangsu Normal University, July 2, 2017	2017
7	Invited speaker. MicroRNAs and its regulatory mechanism during plant China	2017
<b> </b>	response to abiotic stress. Fujiang Agri and Forestry University, June 30, 2017	2017
8	Invited speaker. MicroRNA-based plant biotechnology. Henan Institute of China	2017
	Sciences and Technology, June 28, 2017	2017
9	<b>Invited speaker</b> . MicroRNAs as a novel target for crop improvement. Anyang China	2017
	Institute of Technology, June 23, 2017	
10	Invited speaker. MicroRNA Expression Profiles during Cotton Fiber USA	2017
	Differentiation and Development. International Plant & Animal Genome XXV,	
	January 14-18, 2017, San Diego, CA.	
11	Invited speaker. MicroRNA Roles in Cotton Fiber Initiation and Early USA	2017
	Development. International Plant & Animal Genome XXV, January 14-18,	
	2017, San Diego, CA.	
12	<b>Invited speaker</b> . Development of a comprehensive CRISPR/CAS9 genome USA	2016
	editing tool for knocking out microRNA genes for crop improvement.	
	Syngenta, Durham, December 9, 2016	
13	Invited speaker. MicroRNAs: a New Target for Crop Improvement. Syngenta, USA	2016
	Durham, December 9, 2016	0011
14	Invited speaker. MicroRNAs: a new target for improving plant tolerance to China	2016
	abiotic environmental stress. College of Life Science, Nanjing Agricultural	
1.5	University. November 24, 2016	2016
15	Invited speaker. MiRNA roles during cotton fiber differentiation and early China development. China U.S. Cotton General Workshop, Nov. 18, 2016. Politing	2016
16	development. China-US Cotton Genome Workshop, Nov 18, 2016, Beijing  Invited speaker. MicroRNA roles in cotton fiber initiation and early  China	2016
10	development. The 2016 World Science Life Conference (2016 WSLC),	2010
	November 1 -3, 2016, Beijing, China	
17	Invited speaker. MicroRNA: a new target for improving plant tolerance to China	2016
1 /	abiotic stress. The 2016 World Science Life Conference (2016 WSLC),	2010
	November 1 -3, 2016, Beijing, China	
18	Invited speaker. Roles of microRNAs during cotton fiber differentiation and China	2016
	early development. College of Agronomy, Nanjing Agri Univ. Nov 24, 2016	
19	<b>Invited speaker</b> . MicroRNAs and its function during cotton fiber development. China	2016
	Cotton Research Center, Shandong Academy of Agri Sciences. Nov 22, 2016	
20	Invited speaker. MicroRNAs and its role in plant response to abiotic China	2016
	environmental stress. Biotechnology Research Center, Shandong Academy of	
	Agricultural Sciences. November 21, 2016	
21	<b>Invited speaker</b> . MicroRNA roles during cotton fiber differentiation and early China	2016
	development. China-US Cotton Genome Workshop, Nov 18, 2016, Beijing	
22	Invited speaker. Impact of Nanoparticles on Plant Growth and Development China	2016
	and the MicroRNA-mediated Regulation. The 1st International Conference on	
	Nanotechnology Applications and Implications of Agrochemicals toward	
22	Sustainable Agriculture and Food Systems, November 17-18, 2016, Beijing	2011
23	Invited speaker. MicroRNA-based biotechnology for plant improvement and USA	2016
	functional study. The 30th Annual Plant Molecular Biology Retreat. September	
24	23 - 25, 2016, Wrightsville, NC	2016
24	Plenary speaker. MicroRNA genetic transformation and its application on China	2016
	crop improvement. 7th International Crop Science Congress (7th ICSC),	

25	August 14-19, 2016, Beijing, China  Invited speaker. MicroRNAs and its role in cotton development. Henan China	a 2016
	Institute of Sciences and Technology. August 12, 2016	
26	<b>Invited speaker</b> . Small RNAs in Cotton. Institute of Cotton Research, Chinese China Academy of Agricultural Sciences. August 10th, 2016.	a 2016
27	<b>Invited speaker</b> . MicroRNA-mediated gene regulation and its application in China crop improvement. Jiangsu Normal University. August 9th, 2016.	a 2016
28	<b>Keynote speaker</b> . The role of microRNAs during cotton fiber development. China The 2016 Annual Meeting of Chinese Cotton Associate. August 7-9, 2016. Xuzhou	a 2016
29	<b>Keynote speaker.</b> MicroRNA-based biotechnology for crop improvement for China abiotic stress. The 3rd Conference on Botany. March 2nd to 4th, 2016. Beijing	a 2016
30	<b>Invited speaker</b> . MicroRNAs: a new target for improving cotton. Institute of China	a 2015
31	Cotton Research, Chinese Academy of Agricultural Sciences. August 4, 2015  Invited speaker. MicroRNAs: a new target for improving plant tolerance to China chiceti stress. Hence Institute of Sciences and Tachnology. August 2, 2015	a 2015
32	abiocti stress. Henan Institute of Sciences and Technology. August 2, 2015  Invited speaker. MicroRNAs: Identification and Functional Analysis in Plants. USA  The Department of Prininformatics and Conomics. University of North Coroling	2013
22	The Department of Bioinformatics and Genomics, University of North Carolina at Charlotte. November 1, 2013	2012
33	<b>Invited speaker</b> . Method on identification and functional analysis of China microRNAs in plants. College of Life Sciences, Henan Institute of Science and Technology, China, May 24, 2013	
34	<b>Invited speaker</b> . Function of microRNAs in plants. Henan Institute of Science China and Technology, China, May 23, 2013	a 2013
35	<b>Invited speaker</b> . MicroRNA-mediated gene regulation. North Carolina USA Biotechnology Center, East Carolina University and Sigma Xi. Feb 22 2010.	2010
36	Invited speaker. MicroRNAs: Identification and Functional Analysis in Plants. USA Department of Plant Biology, North Carolina State University, January 26, 2010.	2010
37	Invited speaker. MicroRNAs: a new insight into gene regulation and functions China in plants. College of Life Sciences, Henan Ins Sci Tech, China, June 15, 2008	a 2008
38	Invited speaker. MicroRNA-mediated gene regulation. Department of Botany, USA Miami University, February 15-17, 2007.	2007
39	He QL & <b>Zhang, B.H.</b> Lead-induced physiological and biochemical changes in USA cotton. The 7th SETAC World Congress/SETAC North America 37th Annual Meeting, November 6–10, 2016, Orlando, FL	2016
40	<b>Zhang, B.H.</b> & He QL. Heavy metal lead induced aberrant expression of microRNAs in cotton. The 7th SETAC World Congress/SETAC North America 37th Annual Meeting, November 6–10, 2016, Orlando, FL	2016
41	Sun RR, Xie F.L. & <b>Zhang, B.H</b> . MicroRNA regulation of ovule and fiber development in cotton. The 7th International Crop Science Congress (7th ICSC), August 14-19, 2016, Beijing, China	a 2016
42	Zhang, B.H. & Wang, Q.L. MicroRNA-based biotechnology for plant improvement. The 7th International Crop Science Congress (7th ICSC), August 14-19, 2016, Beijing, China	a 2016
43	He QL & <b>Zhang</b> , <b>B.H</b> . Genome-Wide Identification of R2R3-MYB Genes and China Their Expression Analyses during Abiotic Stress in Cotton. The 7th International Crop Science Congress (7th ICSC), August 14-19, 2016, Beijing	a 2016
44	Li C, Nichols RL, Pan, X.P., <b>Zhang, B.H.</b> , Xie F.L. and Zhang YQ (2016) Identification of microRNAs in the Cotton Root-Knot Nematode. The 2016 Beltwide Cotton Conferences, New Orleans, Jan 5-7, 2016.	2016
45	Li C, <b>Zhang, B.H.</b> , Zhu LF and Zhang XL (2016) GbWRKY1 Transcription Factor Is a Key Molecular Switch for Plant Defense-to-Development Transition in Cotton. The 2016 Beltwide Cotton Conferences, New Orleans, Louisiana. Jan 5-7, 2016.	2016
46	Li C, <b>Zhang, B.H.</b> , Zhu LF and Zhang XL (2015) Cotton GbWRKY1 Transcription Factor Is a key Molecular Switch for Plant Defense- toDevelopment Transition during Infection of Cotton by <i>Verticillium dahlia</i> .	2015
47	The 29th Annual Plant Molecular Biology Retreat, Asheville, NC, Sept 18-20.  He QL, Ma J, Sun YY and <b>Zhang, B.H.</b> (2014) Lead-Induced Physiological USA	2014
	<del></del>	

	Changes and Stress-Responsive Mirnas Expression in Cotton. The 2014	
	Beltwide Cotton Conferences, New Orleans, Louisiana. January 6-8, 2014.	
48	Xie F.L., Sun YY and <b>Zhang, B.H.</b> (2014) Deep Sequencing Identifies Cotton USA	2014
	miRNA Roles in Response to Stress of Drought and Salinity. The 2014	
40	Beltwide Cotton Conferences, New Orleans, Louisiana. January 6-8, 2014.	2014
49	Zhang, B.H., Xie F.L., Wang, Q.L. and Jones D. Small RNA sequencing China	2014
	identifies miRNA roles in fiber development. 2014 ICGI Research Conference.	
50	Wuhan, China. September 25-28, 2014.	2013
30	He QL, Ma J, Sun RR & <b>Zhang</b> , <b>B.H</b> . Lead-induced physiological changes and USA stress responsive miRNA expression in cotton. Society of Environmental	2013
	Toxicology and Chemistry (SETAC) North America 34th Annual Meeting,	
	Nashville, TN, 17-21 November. 2013	
51	Sun GL & Zhang, B.H. Identification, Characterization and Expression USA	2011
	Analysis of MicroRNAs in Cotton. In Vitro Biology Meeting, Raleigh, NC. June	2011
	4-8, 2011.	
52	Sun GL & Zhang, B.H. MicroRNAs and Their Diverse Functions in Plants. In USA	2011
	Vitro Biology Meeting, Raleigh, NC. June 4-8, 2011.	
53	Xie F.L., Xiao P & Zhang, B.H. Target-align: a Tool for Plant MicroRNA USA	2011
	Target Identification. In Vitro Biology Meeting, Raleigh, NC. June 4-8, 2011.	
54	Zhang, B.H., Pan, X.P. & Wang, Q.L. Identification of conserved cotton USA	2008
	microRNAs and their targets. The International Cotton Genome Initiative	
<i>==</i>	(ICGI) 2008 Research Conference, Anyang, China, July 8-11, 2008	2007
55	Zhang, B.H. Identification of Conserved Cotton MicroRNAs and Their USA	2007
	Targets. The 2007 Beltwide Cotton Conferences, New Orleans. Jan 9-12, 2007.	
56	<b>Zhang, B.H.</b> , Feng, R., Li, F.G., Liu CL, Liu, F. & Yao CB. Somatic Australi	1008
50	embryogenic patterns and production of artificial seeds in Gossypum hirsutuma	1770
	L. Proceedings of the 4th Asia Pacific Conference on Agricultural Biology,	
	Darwin, Australia, 1998	
57	Zhang, B.H., Feng, R., Li, F.G., Liu, F. & Yao CB. Plant regeneration from Australi	1998
	another culture of cultivated and wild species of Gossypium genus. In: Larkina	
	PJ (ed.) Agricultural Biotechnology: Laboratory, Field and Market.	
	Proceedings of the 4th Asia-Pacific Conference on Agricultural Biotechnology,	
<b>=</b> 0	Darwin 13-16 July 1998. Canberra, UTC Publishing. pp. 164-165.	1000
58	Feng, R., Zhang, B.H., Zhang WS & Wang, Q.L. Genotype analysis in cotton Australi	1998
	tissue culture and plant regeneration. In: Larkin PJ (ed.) Agricultural a	
	Biotechnology: Laboratory, Field and Market. Proceedings of the 4th Asia-	
	Pacific Conference on Agricultural Biotechnology, Darwin 13-16 July 1998.	
	Canberra, UTC Publishing. pp.161-163.	1

Part-6 Books / Book Chapters on Cotton as First Author

S.No.			Year	
1	Zhang, B.H. (2012). Transgenic Cotton. Springer Science+Business Media,		2012	
	New York			
2	<b>Zhang, B.H.</b> & Feng, R. (2000) Cotton Pest-resistance and Transgenic Pest-	China	2000	
	resistant Cotton. Beijing: Chinese Agri Science and Technology Press			
3	<b>Zhang, B.H.</b> & Zhang, L.Z. (1998) <i>Pest-resistant Cotton and its Cultivation</i> .			
	Jinan: Shangdong Science and Technology Press.			
4	<b>Zhang, B.H.</b> & Zhao, B.S. (1997) Cotton Biotechnology and its Application.	China	1997	
	Beijing: Chinese Agricultural Press.			
5				
	agricultural application. In Zhang, B.H. (ed.), Transgenic Cotton. Springer			
	Science+Business Media, New York.			
6	<b>Zhang, B.H.</b> (2012) Agrobacterium-mediated transformation of cotton. In	USA	2012	
	Zhang, B.H. (ed.), Transgenic Cotton. Springer Science+Business Media,			
	New York.			
7	<b>Zhang, B.H.</b> , Wang, M., Zhang, X, Li CQ & Wang, Q.L. (2012)	USA	2012	
	Overexpression of miR 156 in cotton via Agrobacterium-mediated			
	transformation. In Zhang, B.H. (ed.), Transgenic Cotton. Springer			
	Science+Business Media, New York.			

8	<b>Zhang, B.H.</b> , Wang, H.M., Liu, F., & Wang, Q.L. (2012) A simple and rapid	USA	2012	
	method for determining transgenic cotton plants. In Zhang, B.H. (ed.),			
	Transgenic Cotton. Springer Science+Business Media, New York.			
9	<b>Zhang, B.H.</b> & Wang, Q.L (2003). Transgenic cotton. In Singh RH & Jiwal USA			
	PK (eds), Plant Genetic Engineering. Houston: Sci-Tech Publisher Company			
10	Zhang, B.H. (1999). Cotton biotechnology. In Mao SC (ed), Cotton	China	1999	
	Development in China. Beijing: China Agricultural Press			

Part-7 Books / Book Chapters on Cotton as Co-Author

	Books / Book Chapters on Cotton as Co-Author			
S.No.	Reference (*Harvard Style)	Country	Year	
1	Wang, Q.L., <b>Zhang, B.H.</b> et al. (2005) Cotton Production. Beijing: Chinese	China	2005	
	Agricultural Science and Technology Press			
2	Wang, Q.L., Zhang, B.H. et al. (2003) Plant Tissue Culture. Beijing:	China	2003	
	Chinese Agricultural Science and Technology Press			
3	Wang, M., <b>Zhang, B.H.</b> & Wang, Q.L. (2012) Cotton transformation via	USA	2012	
	pollen tube pathway. In Zhang, B.H. (ed.), Transgenic Cotton. Springer			
	Science+Business Media, New York.			
4	Wang, M., Wang, Q.L., & Zhang, B.H. (2012) An efficient grafting	USA	2012	
	technique for recovery of transgenic cotton plants. In Zhang, B.H. (ed.),			
	Transgenic Cotton. Springer Science+Business Media, New York.			
5	Sun GL, Wang, Q.L. & Zhang, B.H. (2011) MicroRNAs in Cotton. In	USA	2011	
	Erdmann VA and Barciszewski (Ed.), Non Coding RNAs in Plants. Springer			
	Science+Business Media, New York			
6	Pan, X.P., Murashov, A.K., and <b>Zhang, B.H.</b> (2010) Monitoring microRNA	USA	2010	
	expression during embryonic stem cell differentiation using quantitative			
	real-time PCR. In Zhang, B.H. & Stellwag E (ed.), RNAi and MicroRNA-			
	mediated Gene Regulation in Stem Cells. New York, Springer.			
7	Frazier, T. & Zhang, B.H. (2010) Identification of plant microRNAs using	USA	2010	
	expressed sequence tag analysis. In Pereira A (ed.), Plant Reverse Genetics.			
	New York, Springer.	G1 :	2002	
8	Huang, J.Q., Zhang, X.L. & Zhang, B.H. (2003). Cotton biotechnology. In	China	2003	
	Huang ZK (ed), Cotton Genetics and Breeding. Beijing: Chinese			
	Agricultural Science and Technology Press	GI :	2002	
9	<b>Zhang, B.H.</b> is one of the major authors (2003) Cotton Genetics and China 2003			
40	Breeding in China. Jinan: Shangdong Science and Technology Press.	GI :	2002	
10	<b>Zhang, B.H.</b> is one of the major authors (1999) Studies on the Sustainable China		2003	
44	Development of Cotton in China. Beijing: Chinese Agricultural Press.	G1 :	1000	
11	Jing, S.R., Zhang, B.H. & Zhang, L.Z. (1999) Transgenic Insect-resistant China 199			
	Hybrid Cotton. Beijing: Chinese Agri Science and Technology Press.	G1 :	1000	
12	<b>Zhang, B.H.</b> is one of the major authors (1999) Theory and Practices of	China	1999	
	Cotton Hybrid Breeding. Beijing: Science Press.			

Part-8: Three Most Innovative and Impactful Achievements

S.No.	Achievements in not more than 100 words each		
1	Dr. Zhang developed an advanced CRISPR/Cas9 genome editing tool and its application		
	on cotton genetics and breeding. Dr. Zhang is the first scientist who successfully employed		
	CRISPR/cas 9 genome editing technology to knockout an individual functional gene in cotton,		
	including the fiber-related MYB25-like and miRNA genes. Additionally, Dr. Zhang also		
	developed a high efficient approach for obtaining cotton somatic embryogenesis and plant		
	regeneration and a high efficient Agrobacterium-mediated gene transformation in cotton.		
	<b>Impact</b> : This power tool and resources open a new strategy and direction for cotton research		
	and breeding community for performing cotton gene functional studies and molecular		
	breeding.		
2	Dr. Zhang's innovative research on small regulatory RNAs. Dr. Zhang is a pioneer for		
	cotton microRNA study. In the past 10 years, Dr. Zhang has been employing different		
	technologies (deep sequencing, transgenics, genome editing and bioinformatics) to identify and		
	functional analysis of microRNAs in cotton fiber development as well cotton response to		

	different biotic and abiotic stress. Among those, many microRNA are identified for genetic	
	and breeding purpose. <b>Impact</b> : this provides new targets for cotton improvement, including	
	fiber yield and quality and tolerance to environmental biotic and abiotic stresses.	
3	Breeding 5 cotton cultivars and they are being used in China and internationally. Dr.	
	Zhang is one of the major contributors for breeding transgenic Bt cotton in China, which has	
	been widely adopted globally. Except the Bt cotton, with collaborating with other breeders, Dr.	
	Zhang have gotten involved in breeding five cotton cultivars that has been widely adopted by	
	cotton farmers in China and also in several Middle-Asian countries. Additionally, Dr. Zhang	
	also created many elite cotton germplam lines using transgenic, somatic variant screening and	
	genome editing. <b>Impact</b> : the bred cultivars have generated huge economic benefits for cotton	
	farmers.	

## Part-9: **Brief Biographical Note** (Not more than 300 words)

Dr. Zhang grew up in a small village in China. Since he was a kid, he helped his parents working in cotton field, which attract his interests on cotton genetic and breeding. He attended China Agricultural University with a major of plant genetic and breeding. After graduated with a bachelor degree in 1991, he joined the Institute of Cotton Research, Chinese Academy of Agricultural Science (ICR-CAAS) where he had worked for more than one decade before he joined Texas Tech University for Ph.D. study in 2003. During he worked in ICR-CAAS, Dr. Zhang majorly worked on cotton biotechnology; he is one of the major contributors for transgenic Bt Cotton in China. After Dr. Zhang received his Ph.D in 2006, he was immediately offered a faculty position by East Carolina University (ECU). Since then, developing cotton genetic tool and resource and cotton small RNA study is Dr. Zhang's major focus. Dr. Zhang is the pioneer for cotton small RNA study. He also develop a high-efficient CRISPR/Cas9 tool for cotton research community for the first time to knockout an individual gene in cotton. Because his great achievement and contribution, he is frequently invited by the international conferences for giving keynote lectures or invited talks, he also frequently serves on grant reviewing panels for more than 40 national and international funding agents. Dr. Zhang is also serving as co-Editor-in-Chief, associate editor or guest editor for 10 international journals, including *Scientific* Reports, Plant Biotechnology Journal, and The Crop Journal. Dr. Zhang frequently reviews manuscripts for more than 100 international journals, including *Nature*. Additionally, Dr. Zhang won the ECU Five Year Excellent Research and Creative Award, the highest award for ECU faculty and he was also awarded early tenure and early promotion to associate professor in 2006 and then to full professor in 2012.

Part-10: Citations (from Google Scholar) and RG Score

Citation Indices	All	Since 2013
Citations	10460	6505
h-index	46	41
I10 index	104	81
Research-Gate RG Score	41.56	

I hereby affirm that the entire information furnished in this application is true to the best on my knowledge.

March 21<sup>st</sup>, 2018
Greenville, North Carolina, USA
Date & Place