Journal of Applied Life Sciences International

11(3): 1-7, 2017; Article no.JALSI.31137
ISSN: 2394-1103

Physiological and Agronomic Performance of Domesticated and Wild Cotton Germplasm from Selected Regions of Kenya

Njagi Anthony Kiranga[1], Fredrick M. Njoka[1*] and Charles W. Nderito[2]

[1]Department of Agricultural Resource Management, University of Embu, P.O.Box 6-60100, Embu, Kenya.
[2]Kenya Agriculture and Livestock Research Organisation, Thika, P.O.Box 220-01000, Thika, Kenya.

Authors' contributions

This work was carried out in collaboration between all authors. Author NAK designed the study and collected the field data. Authors FMN and CWN performed the statistical analysis and wrote the first draft of the manuscript. All authors managed the literature searches. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JALSI/2017/31137
Editor(s):
(1) Muhammad Kasib Khan, Department of Parasitology, University of Agriculture, Pakistan.
(2) Martin Koller, University of Graz, Research Management and Service, c/o Institute of Chemistry, Austria.
Reviewers:
(1) Ayona Jayadev, All Saints'College, Thiruvananthapuram, Kerala, India.
(2) Mohammed Suleiman, Umaru Musa Yar'adua University, Katsina, Nigeria.
Complete Peer review History: http://www.sciencedomain.org/review-history/18931

Original Research Article

Received 22nd December 2016
Accepted 18th April 2017
Published 5th May 2017

ABSTRACT

Aims: Cotton (*Gossypium* species) occupies a prime position as a fibre crop of the world used for making cooking oil, soup and seed cake for animal feed industry among other uses. Performance of wild cotton germplasm in Kenya has not been well studied and therefore there is need for understanding the correlation of traits influencing seed cotton productivity for effective improvement of the standard HART 89M. The study aimed at determining the correlation in performance between domesticated cotton HART 89M with wild cotton.
Experimental Layout: Four wild cotton species and HART 89M were planted in three experimental blocks, each measuring 6 m by 30 m. There were three replications per experimental block, the distance between blocks was 2 m. The experimental blocks were then divided into 5 plots of 5 m by 5 m, with 1 m separating plots. The cotton seeds were planted in rows of 1 m by 0.5 m at depth of 2 cm.

**Corresponding author: E-mail: njokafm@yahoo.co.uk, njokafm@gmail.com;*

Methodology: Data on agronomic traits such as germination rate, flowering rate, height, number of fruiting branches, length of the longest fruiting branch, internodal length, number of nodes on the longest fruiting branch and yield per plant was collected from a sample of forty-five plants. One way Analysis of Variance (ANOVA) was used to determine the significant difference among the studied species and varieties at P = 5%.
Results: There was a significant difference between the standard genotype (HART 89M) and studied wild genotypes with *G. barbadense* having highest height (203.37 cm), number of fruiting branches (66.93 cm), length of the longest fruiting branch (68.36 cm), number of nodes on the longest fruiting branch (5.38) and productivity (205.21 g) compared with other genotypes. *G. kirkii* had the longest intermodal length of 6.36 cm.
Conclusion: On boll traits the highest significant difference with HART 89M was found with *G. kirkii* on boll weight (3.71 g), seed weight (2.30 g), and lint weight (1.41 g). Cotton breeding programs should consider traits such as plant height, number of fruiting branches, number of nodes on the longest fruiting branch, boll weight, seed weight and lint weight during selection as they were the major attributes of the seed cotton productivity. *G. herbaceum* and *G. kirkii* were recommended for seed production.

Keywords: Genotype; gossypium species; agronomic performance; traits; wild genotype.

1. INTRODUCTION

Cotton (*Gossypium* species) occupies a prime position as a fibre crop of the world. Today cotton is used as a natural fibre, while seeds are used for making cooking oil, soup and seed cake for animal feed industry [1]. Commercial cotton fibre is produced from only four species. Two diploids are *G. arboreum* and *G. herbaceum* while the two tetraploid are *G. barbadense* and *G. hirsutum* [2]. The species *G. hirsutum* is however usually the early-maturing and higher yielding [3]. In Kenya *G. hirsutum* was introduced in the year 1902 by the British colonial administration [4]. It is grown in several agro-ecological zones, mainly in the semi-arid regions of Eastern, Central, Coast and Western regions of Kenya. The cotton variety HART 89M was developed at the National Fibre Research Centre (NFRC), Mwea, Kenya and it is now the most extensively cultivated variety in Kenya [4]. The level of genetic diversity is low in *G. hirsutum* as revealed by [5]. Hybridization of new varieties of cotton is done by crossing plants of different gene types selected amongst the resultant hybrids [6]. Desirable characteristics are introduced from wild species relative to the cultivated cotton [7]. Cotton is among the few crops where the farmer cannot retain his seeds for planting because all seeds go to the ginneries, which then sell them back to the farmers. In the ginnery the cotton seeds are most likely to be of unknown genetic origin [4]. This recycling of seed has led to deterioration of yield and fiber quality [8].

Lack of genetic diversity or narrowness in genetic base creates a potential threat to sustain productivity due to rapid vulnerability of genetically uniform cultivars caused by new biotic and abiotic stresses [9,10]. A wider genetic diversity of crop species ensures potential to protect crops from new pathogens, pest epidemics and global environmental changes. This provides an opportunity for further improvement of complex traits of interest by pyramiding genetic variation within populations [9,11]. The current cultivars that grow today in Kenya have a narrow genetic base. For this reason, it is necessary to take advantage of the available gene pool, hence important to identify and study the wild cotton germplasm to provide the necessary gene pool for evaluation and selection of traits that are superior [12]. Cotton is cultivated in different soil-climate areas, each having entomofauna and microfrora of its own. Due to adaptive variation of pathogens and pests of cotton under these conditions, agronomists, geneticists and breeders should keep on searching for new resources and donors of cotton resistance and adaptation. The varieties losing disease and pests resistance could be replaced with the ones blend for resistance and possessing a series of economically valuable traits, along with the high yielding ability [6]. The understanding of the correlation of factors influencing productivity is a pre-requisite for designing an effective plant-breeding program. These include correlations between of cotton seed weight per plant and plant height, number of fruiting branches and number of nodes per plant [13,14,15]. The aim of this study was to characterize wild cotton genotypes grown in Kenya using morphological and physiological parameters. The results from this study will serve as a guide to cotton producers and breeders in initiating a cotton improvement program.

2. MATERIALS AND METHODS

2.1 Study Area and Duration

The reported work was carried out at the Kenya Agricultural and Livestock Research Organisation (KALRO) Thika centre, beginning May 2010 to June 2013. The Centre is located at 0 59 S and 37 04 E. It is 5 Kms from Thika Town in Kiambu County and 43 Kms from Nairobi. The Centre is located at an altitude of 4800 ft above the sea level. The soils are classified as sandy loam to clay and depth ranges from deep to shallow with good to poor drainage.

2.2 Study Materials and Design

Kenya Agricultural and Livestock Reaserch Organisation (KALRO) - Thika, provided wild cotton germplasm and domestic cotton. The studied germplasm were collected from various regions in Kenya including Lamu, Kilifi, Kwale and Siaya counties. The domestic cotton used in the study was HART 89M while four wild cotton species, *G. kirkii, G. hirsutum*, *G. barbadense*, *G. herbaceum* were included. The four wild cotton species and HART 89M were planted in three experimental blocks, each measuring 6 m by 30 m. There were three replications per experimental block, the distance between blocks was 2 m. The experimental blocks were then divided into 5 plots of 5 m by 5 m, with 1 m separating plots. The cotton seeds were planted in rows of 1 m by 0.5 m at depth of 2 cm. The cultural practices such as application of fertilizer, hoeing, irrigation and pest control were done at appropriate time. Crops were grown under uniform conditions to minimize environmental variation. The data collected included monthly rainfall, average monthly temperature, germination percentage, flowering, bush height, internode length, and number of branches in the main stem, lint and seed weight, lint and seed weight ratio, productivity per genotype. The percent germination was recorded every seven days per plot from the date of the first germination. Fifteen bushes from each plot were randomly marked and used for all subsequent sampling as proposed by [16]. Picking of bolls extended from December 2011 to April 2012.

2.3 Data Analysis

One way Analysis of Variance (ANOVA), was used to determine the significant difference among the studied species and varieties at P = 5%. T-test was used to determine the significance difference between agronomic traits and boll traits between the standard species HART 89M and wild cotton at P = 5% per method proposed by [17]. The t-test was also used to determine agronomic and boll performances at P = 0.05. Correlation coefficient and coefficient of determination were used to determine the relationship between the cotton boll yield with other agronomic traits such as height, number of fruiting branches, length of the longest fruiting branch and number of nodes on the fruiting branches at P = 0.05 as proposed by [18].

3. RESULTS AND DISCUSSION

The results on weather conditions during the vegetative period revealed that, the mean monthly temperatures were high during sowing 21.6℃ (October). Temperatures were low, from 19.8℃ to 20.2℃ between June 2011 and August 2011. The mean monthly rainfall was unevenly distributed, ranging from 1 mm in January 2011 and July 2011 to 155.4 mm in November 2010 and March 2011 during the vegetative period. On 29th October 2010, fifty cotton seeds were sown per plot and by the 8th week they differed in germination percent ranging from *G. barbadense* having the highest percent of 74.3%, G. *herbaceum* 64%, HART 89M 56.7%, *G. hirsutum* 53.3% and lowest was *G. kirkii* 35.3% which never attained 50% germination. The results revealed that, all the other genotypes took eight weeks to attain 50% seed germination. There was delayed germination in all the studied genotypes, which can be associated with hard seeds found among the genotypes. Four genotypes took eight week to attain 50% flowering may be due to delay in germination, except *G. kirkii* which by eighth week had attained 86.7%. The study showed an interesting scenario where *G. kirkii* plant which shed the shoot at early stage was the first in flowering compared with the unsheded shoot which extended flowering from ten to eighteen weeks.

Results in Table 1 present the mean agronomic performances of genotypes at p=0.05. Results on plant height indicated significant differences in plant height among the studied genotypes (F =136.2, p=0.001). The mean height among the genotypes ranged from the lowest height being HART 89M (103.42 ± 8.08 cm) and the highest being *G. barbadense* (203.37 ± 7.18 cm). The results on the number of fruiting branches

per plant indicated significant differences in the number of fruiting branches, among the studied genotypes (F = 36.6, p=0.001). The highest mean number of fruiting branches was found in *G. barbadense* with 66.93 ± 3.9 branches and the lowest was found in HART 89M with 36.47 ± 2.81 branches. The results on internodal length from the first fruiting branch per plant indicated a significant difference among the four studied genotypes (F = 30.06, p=0.001). *G. kirkii* had the highest internodal mean length of 6.36 ± 0.30 cm and the lowest was found in HART 89 M of 4.07 ± 0.23 cm. The results showed a significant difference (F=30.06, p=0.001) in mean length of the longest fruiting branch per bush among the studied genotypes. *Gossypium barbadense* had the highest mean of 68.36 ± 3.34 cm and the lowest being HART 89M with a mean of 34.02 ± 2.98 cm.

Results showed that *G. barbadense* had the highest number of nodes on the longest fruiting branches of 5.38 ± 0.34 and the lowest mean being HART 89M (2.89 ± 0.17). The results on plant productivity revealed a significant difference among the genotypes (F= 182.9, p=0.001). *G. barbadense* had the highest mean production per plant of 205.21 ± 15.61 g and *G. kirkii* had the lowest productivity of 40.29 ± 2.29 g, *G. hirsutum* had 100.27 ± 8.27 g, *G. herbaceum* had 88.38 ± 9.74 g and HART 89M had 71.48 ± 3.28 g.

Table 2 presents results of mean boll traits on the studied genotypes at p=0.05. Mean boll weight ranged from 2.77 ± 0.14 g (*G. hirsutum*) to 3.71 ± 0.14 g (*G. kirkii*). There was a significant difference (F=21.18, P=0.000) in seed weight among the studied genotypes ranging between 1.78 ± 0.09 g (HART 89M) and 2.30 ± 0.08 (*G. kirkii*). Lint weight ranged between 0.98 ± 0.05 g (G. *herbaceum*) and 1.41 ± 0.06 g (*G. kirkii*). Number of seeds per boll ranged between 19.01 ± 0.89 (HART 89M) and 21.05 ± 0.59 (*G. kirkii*). The results on mean percentage lint weight per boll among the studied genotypes revealed a significant difference (F = 13.613, P=0.000). The results showed that HART 89M had the highest % lint weight of 39.71 ± 2.49, *G. kirkii* had 37.82 ± 0.66%, *G. hirsutum* had 37.82 ± 2.56%, *G. barbadense* 34.59 ± 2.00% and *G. herbaceum* had the lowest lint weight percentage of 32.31 ± 2.10. The result on mean seed weight percentage revealed a significant difference among the genotypes (F = 16.364, P=0.004). *G. herbaceum* had highest percentage of 68.68 ± 0.86%, *G. hirsutum* had 62.17 ± 0.66%, *G. barbadense* had 65.46 ± 2.52%, *G. kirkii* had 62.17 ± 0.64% and HART 89M had 60.28 ± 1.85% (Table 2).

The results on seed lint ratio per boll, revealed that species were significantly different (F = 2.264, P=0.004). The average lint-seed ratio ranged as follows: *G. barbadense* had 2.31 ± 0.268, *G. hirsutum* had 1.98 ± 0.13, HART 89M had 1.79 ± 0.13, G. *herbaceum* had 1.65 ± 0.047, and the lowest was *G. kirkii* with 0.65 ± 0.13.

The analysis of variance (ANOVA) indicated significant difference among traits of the studied genotypes. Results on different traits revealed different potentials in agronomic performance for different wild cotton traits. This provides the evidence for the genetic variability present for the traits among the studied genotypes. Plant height has a direct influence on the number of fruiting branches and therefore cotton seed productivity. There was a significant difference in height between *G. barbadense* and HART 89M. Similar results were reported by [6,10]. The result enunciated that, there was significant difference in the number of fruiting branches among the genotypes and a significant and positive correlation between number of fruiting branches and seed cotton yield. The number of fruiting branches is desirable and attention should be paid in the selection in the breeding for seed cotton yield. The internodal length has influence on maturity rate on cotton plant, the cotton plant with short internodal value have early maturity compared with the one having longer internodal length. The internodal length had an influence on maturity rate on cotton genotypes. Therefore, HART 89M with short internodal value matured earlier compared with the others having longer internodal length and flowered earlier than other studied genotypes. Therefore, internodal length should be kept in mind while breeding for early maturity. [15] studied the earliness in *Gossypium hirsutum* varieties and reported similar findings.

The length of fruiting branch has a direct influence on flowering point, in that the longer the length the more the nodes that produces flowering points, which determines the cotton seed productivity. This was found in *G. barbadense*, which had the longest fruiting branch and the highest number on nodes on the fruiting branch. Similar results were reported by [1,11]. Therefore, selection of the length of fruiting branch can be effective in breeding for seed cotton productivity when paired with other traits that have a significant correlation with seed cotton yield.

Table 1. Mean agronomic performances of genotypes

Parameter	Genotypes					F, P=0.05
	G. herbaceum	*G. hirsutum*	HART 89M	*G. barbadense*	*G. kirkii*	
N	45	45	45	45	45	DF=4
Plant height, cm	143.89±6.98^{c}	160.06±9.86^{b}	103.42±8.08^{d}	203.37±7.18^{a}	18.15±6.09^{e}	136.2, 0.001
Number of fruiting ranches	47.93±4.19^{d}	61.49±5.52^{b}	36.47±2.81^{e}	66.93±3.90^{a}	55.89± 85^{c}	36.6, 0.001
Inter nodal length, cm	5.22±0.22^{d}	5.78±0.48^{b}	4.07±0.23^{e}	5.50±0.25^{c}	6.36± 0.30^{a}	30.06, 0.001
Length of the longest fruiting branch, cm	39.69±3.27^{c}	50.40±4.70^{b}	34.02±2.98^{e}	68.36±3.34^{a}	38.60±2.84^{d}	30.06, 0.001
Number of nodes of the longest fruiting branch	3.87±0.35^{c}	4.69±0.42^{b}	2.89±0.17^{d}	5.38±0.34^{a}	3.78±0.34^{c}	25.78, 0.001
Productivity, g	88.38±9.74^{c}	100.27±8.27^{b}	71.48± 3.28^{d}	205.21±15.61^{a}	40.29±2.29^{e}	182.9, 0.001

Parameters marked with the same letter on a row had no significant difference

Table 2. Mean boll traits on studied genotypes, P=0.05

Traits	Genotypes					F value	P value = 0.05
	G. herbaceum	*G. hirsutum*	HART 89M	*G. barbadense*	*G. kirkii*		
Boll weight, g	3.19±0.16^{a}	2.77±0.14^{d}	2.98±0.15^{c}	2.98±0.12^{c}	3.71±0.14^{b}	25.938	0.000
Seed weight, g	2.18±0,09^{b}	1,85±0.11^{b}	1.78±0.09^{d}	2.05±0.10^{c}	2.30 ± 0.08^{a}	21.181	0.000
Lint weight, g	0.98±0.05^{d}	1.03±0.07^{c}	1.21±0.10^{b}	0.99±0.05^{d}	1.41± 0.06^{a}	26.592	0.002
No. of seeds per boll	20.73±0.74^{d}	20.83±1.05^{c}	19.01±0.89^{e}	20.83±0.62^{b}	21.05±0.59^{a}	4.309	0.000
Lint weight %	32.31±2.10^{d}	37.82±2.56^{b}	39.71±2.49^{a}	34.59±2.00^{c}	37.82±0.66^{b}	13.613	0.000
Seed weight %	68.68±0.86^{a}	62.17±0.66^{c}	60.28±1.85^{d}	65.46±2.52^{b}	62.17±0.64^{c}	16.364	0.001
Lint seed ratio	1.65±0.047^{d}	1.98±0.13^{b}	1.79±0.13^{c}	2.31±0.268^{a}	0.65±0.13^{e}	2.264	0.004

Parameters marked with the same letter on a row had no significant difference

The number of nodes has direct influence on flowering point hence determines the seed cotton productivity. The genotype that had the highest number of nodes on the longest fruiting branch was *G. barbadense*. This plays an important role in cotton crop, which should be considered by breeders while breeding for seed cotton productivity. This is in agreement with the results reported by [1,13].

There was a positive effect of the number of seeds per boll to the seed cotton productivity through increasing boll weight. The genotypes having high number of seed per boll have a relatively good production potential in comparison with those with less number of seeds per boll. Number of seeds per boll is an important yield component, it determines boll weight, seed cotton yield, lint, and cotton seeds for oil. The number of seeds per boll should be considered while breeding for seed cotton yield and cooking oil extraction and animal feed industry. Seeds are also very important for future propagation of the plant. The results revealed a significant difference in seed cotton yield, number of fruiting branches, length of fruiting branch and number of nodes of fruiting branch between *G. barbadense* and all the other genotypes. The results were in agreement with those reported [19,20,21,22].

4. CONCLUSIONS

Genetic variance in most traits was similar to that of phenotypic variance consequently giving high heritability estimates and significant genetic gains. Therefore, selection based on traits such as height, number of fruiting branches, boll weight, number of nodes on fruiting branch, lint weight and seed weight should be exploited for improvement of yield. On morphological traits, the result revealed a significant difference among the genotypes with *G. barbadense* being the best performer in height, cotton seed yield, number of fruiting branches and number of nodes on the fruiting branches. On boll traits the highest significant difference with HART 89M was found with *G. kirkii* on boll weight, seed weight and lint weight. Cotton breeding programs should consider traits such as plant height, number of fruiting branches, number of nodes on the longest fruiting branch, boll weight, seed weight and lint weight during selection as they were the major attributes of the seed cotton productivity. *Gossypium herbaceum* and *Gossypium kirkii* were recommended for future seed production.

ACKNOWLEDGEMENTS

The Kenya Agriculture and Livestock research Organisation (KALRO – Thika) is highly acknowledged for providing the cotton germplasm seeds and facilities used in the experiment. Technical staffs and Scientists of KALRO (Thika) and University of Embu are acknowledged for their valuable support, advice and assistance.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Khan NU, Marwat KB, Hassan G, Farhatullah HA, Batool S, Makhdoom K, Ahmad W. Genetic variation and heritability for cotton seed, fiber and oil traits in *G. hirsutum* L. Pakistan Journal of Botany. 2010;2(1):615-625.
2. Vafaie-tabar M, Chndrashekaran S, Rana MK, Bhat KV. RAPD analysis of genetic diversity in Indian tetraploid and diploid cotton (*Gossypium spp*). Journal of Plant Biochemistry and Biotechnology. 2004;13: 81-84.
3. Lacape JM, Nguyen TB, Courtois B, Belot JL, Giband M, Gourlot JP, Gawryziak G, Roques S, Hau B. QTL analysis of cotton fiber quality using multiple *Gossypium hirsutum* × *Gossypium barbadense* backcross generations. Crop Science Journal. 2005;45:123-140.
4. Ikitoo EC, Onzere BB, Karani EW, Maobe SN. Cotton agronomy research in Eastern Kenya and Kerio Valley. In KARI-NFRC Annual Report. 1989;23-35.
5. Gutierrez OA, Basu S, Saha S, Jenkins JN, Shoemaker DB, Cheatham CL, McCarty JC. Genetic distance among selected cotton genotypes and its relationship with F_2 performance. Crop Science Journal. 2002;44:1841-1847.
6. Suinaga FA, Bastos CS, Rangel LEP. Phenotypic adaptability and stability of cotton cultivars in Mato Grosso State, Brazil. Pesquisa Agropecuaria Tropical. 2006;36(3):145-150.
7. Kameswara R. Plant genetic resources. Advancing conservation and use through biotechnology. Madras Agricultural Journal. 2004;18:430-432.

8. Invest in the growing and ginning of cotton. Available:Mwaithaka@Kenyaepzkenya.com (Accessed July 2012)
9. Van Esbroeck GA, Bowman DT. Cotton germplasm diversity and its importance to cultivar development. Journal of Cotton Science. 1998;2:121-129.
10. Ulloa M, Stewart JM, Gaytan EA, Goday AS, Gaytan MN, Acostan N. Cotton genetic resources in the Western State of Mexico: *In situ* conservation status and germplasm collection for *ex situ* preservation. Crop Genetic Resources. 2006;53:653-668.
11. Khan NU, Hassan G, Kumbhar MB, Marwat KB, Khan MA, Parveen A, Aiman U, Saeed M. Combining ability analysis to identify suitable parents for heterosis in seed cotton yield, its components and lint percentage in upland cotton. Industrial Crops and Production. 2009;29:108-115.
12. Taohua Z, Haipeng Z. Comparative study on yield and main agri-characters of five hybrids coloured cotton varieties. Journal Anhui Agricultural University. 2006;33(4): 533-536.
13. Hussein SS, Azhar FM, Sadiq M. Association of yield with various economic characters in *G. hirsutum* L. Pakistan Journal of Biological Sciences. 2000;3(8):1237-1238.
14. Soomro AR, Kakar RG, Ali H, Abid SA. Comparison of yield and its components in some commercial cotton varieties. Industrial Journal of Plant Science. 2005;4(4):545-552.
15. Igbal J, Reddy G, El-zik KM, Pepper AE. A genetic bottleneck in the evolution under domestication of upland cotton *Gossypium hirsutum* L. examined using DNA. Genetics. 2006;103:547-554.
16. Bird LS. Cotton seed and germination stand establishment. Beltwide Cotton Production Research Conference. 1981;3:18-21.
17. Steel RGD, Torrie JH. Principle and procedure of statistics, a biometrical approach 2nd edition. McGraw 2005 Hill Inc: New York. 1980;234-238.
18. Qayyum SM, Chondhry NA, Ansari MM, Baig MA, Memmon MI. Correlation and regression analysis among yield and its economic character in upland cotton *G. hirsutum L.* Journal of Agricultural and Vetinary Sciences. 1992;8(12):28-34.
19. Ansari AH, Qayyum SM, Malik SM, Ansari NN. Phenotypic correlation and regression analysis in cotton (*Gossypium hirsutum* L.) CV TH-1174. Journal of Agricultural Research, Lahore. 1989;27(2):89-93.
20. Arshad MM, Noor I, Shah SM. Correlation studies on some commercial cotton varieties of *G. hirsutum* L. Sarhad Journal of Agriculture. 1993;9(1):49-56.
21. Fonseca S, Paterson FL. Yield components heritability and interrelationship in winter wheat. Crop Science Journal. 1968;8:614-617.
22. Larik AS, Kakar AA, Naz MA, Shaikh MA. Character correlation and path analysis in seed cotton yield of *G. hirsutum* L. Sarhad Journal of Agriculture. 1999;15(4):269-274.

Peer-review history:
The peer review history for this paper can be accessed here:
http://sciencedomain.org/review-history/18931