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Tea Plant (Camellia Sinensis) Breeding Mechanisms Role in Genetic Improvement and Production of Major Producing Countries

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ABSTRACT

Despite applications of breeding in tea are difficult, entire varietal development in tea and other Camellia species has been done through conventional breeding which started way back in 1939. Since then, several developments of genetics and breeding have taken place, with objectives of developing high different types of tea variety, increase yield, improvement cup tea quality, and resistance to biotic and abiotic stress. This is through tea genetic improvement mechanisms like conventional selection, hybridization, marker-assisted selection, mutation breeding, polyploidy, genetic engineering, and micro propagation. In this paper, (1) the achievements of tea genetic improvement and breeding, (2) the current situation of collection, conservation, appraisal and evaluation of tea germplasms, (3) Genetic introgression to enhance germplasm innovation (4) the establishment and development of tea breeding system and (5) the main research emphases of tea genetics and breeding soon were reviewed.

Keywords: *Breeding, genetics, improvement, production, tea plant*

INTRODUCTION

Tea [Camellia sinensis (L.) O. Kuntze] plants are originated from southern China, Yunnan province (Hashimoto and Takasi, 1978; Yu, 1986). Tea has been known for more than 2000 years in China and is naturally distributed throughout tropical Asia (Banerjee, 1992). The present-day commercial tea population comprises three species, viz. China type [Camellia sinensis (L.) O. Kuntze], Assam type [Camellia assamica(M.) Wight] and the Cambod type [Camellia ssp. Lasiocalyx planch. ex. watt Weight] and their derivatives (Wood and Barua, 1958). The out breeding characters of tea species have led to a wide natural hybridization resulting in considerable heterogeneity in the existing populations. Therefore, it is difficult to assign a definite varietal status to a crop grown in a particular region. Tea production in India started in Assam in 1823 by Robert Bruce. Indian tea has diverse genetic resources since all existing plantation stocks are the progeny of the plants or seed stocks brought from different parts of Assam, China, and other sources. The genetic resource of tea is undoubtedly one of the most important sources of tea germplasm resources in India (Smith and Barua, 2011). Production of homozygous diploid tea plants through anther-culture followed by chromosome doubling is desirable due to the out-breeding nature of plants under the genus Camellia. Somatic hybridization via protoplast fusion holds tremendous potential in tea crop improvement (Mukhopadhyay et al., 2015). Beris et al. (2016) verified whether the qualitative morphological designations of the tea clones are genetically true by the ISSR markers thus, genetic diversity and relationships of 18 Turkish tea cultivars were determined using 15 ISSR markers with sizes ranging from 250 to 3000 base pairs.

A large number of controlled hybridization was attempted and some of the progenies were also recommended for planting (Satyanarayana and Sharma, 1993). Due to the development of high yielding clones and seed stocks, the productivity of tea in India rose from 1203 kg/ha in 2000 to 1693 kg/ha in 2008 (Statistical data from Tea Board). With an increase in productivity, the emphasis is also put on quality up-gradation of tea as per consumer demand.

However, the introduction of selected clonal materials and clonal seeds tends to result in the extinction of a wide range of genetic materials due to continuous uprooting programs of old tea

sections. The existing diversity will have to be preserved and characterized for future crop improvement programs that constitute the fundamental support structure for the tea industry. Leaf morphology has an important role in identifying taxa. The use of morphological characters is cost-effective when compared to that of biochemical and molecular markers for the preliminary characterization of many individuals to identify morphologically similar groups (Martinez et al., 2003). In tea, morphological characters especially leaf features have been used to study genetic diversity (Wickramaratna, 1981; Toyao and Takeda, 1999), variation (Gunasekara et al., 2001; Piyasundara et al., 2006; Su et al., 2007), phylogeny and classification (Chen et al., 2005; Vo, 2006; Piyasundara et al., 2008; Peng et al., 2009). Statistical methods have been reported (Kirchoff et al., 2004; Plotze et al., 2005; Kirchoff et al., 2007) and there are two main types of techniques to represent taxonomic structure: cluster analysis and principal component analysis (PCA). It should be useful for both the breeding program and the germplasm conservation of tea plants to understand the diversity and differentiation of morphology among those taxa (Smith and Barua, 2011).

The tea plants in China are of the broadest genetic variations in the world because of being the provenance of tea plants, long-term allogamy, and selection (Chen et al., 2005a). More than two hundred improved cultivars have been registered in the country so far, these cultivars have made a considerable contribution to the whole tea industry in China. The impact of the various breeding methods on the production of tea was not summarized before; this initiated the reviewer just to collect this dispersed information around the title. In this paper, (1) the current situation of collection, conservation, appraisal and evaluation of tea germplasms, (2), Genetic introgression to enhance germplasm innovation (3) the establishment and development of tea breeding system were reviewed, and (4) the achievements of tea genetic improvement and breeding.

LITERATURE REVIEW

The Current Situation of Collection, Conservation, Appraisal and Evaluation of Tea Germplasms

Different tea Producing countries' production levels correlate with their tea genetic resource collection, conservation, appraisal, and evaluation stage (Table 2). Tea germplasm is presently one of the most valuable fundamental materials for tea breeding and biotechnology, with valuable potential for the whole tea industry in the future. To fully make use of the plentiful tea germplasms, to breed more new varieties and serve the tea industry in China, great attention and effort have been paid to the collection, conservation, appraisal and evaluation of tea germplasms for half a century, particularly in the last two dozen years (Liang et al., 2007).

Table2. *The tea acreage, yield and export of top ten countries in 2005 the country order is sorted by yield.*

Country	Acreage(ha)	Yield (t)	Of total production (%)	Exports in 2004 (t)	Of the world Total export (%)
China	952,500	940,500	27.510	282,643	17.495
India	500,000	830,700	24.298	174,728	10.815
Sri Lanka	210,620	308,090	9.011	298,909	18.501
Kenya	140,000	295,000	8.629	284,309	17.598
Turkey	100,000	202,000	5.909	5,929	0.367
Indonesia	116,200	171,410	5.014	98,572	6.101
Viet Nam	104,000	110,000	3.218	99,400	6.152
Japan	49,000	100,000	2.925	923	0.057
Argentina	40,000	64,000	1.872	67,819	4.198
Bangladesh	54,000	55,627	1.627	10,635	0.658
Subtotal	2,266,320	3,077,327	90.013	1,323,867	81.942
Total in the world	2,561,001	3,418, 777	100	1,615,610	100

Data source: *Liang et al., 2007*

Collection and Conservation

The examination of tea germplasms was started in China during the 1930s. Nonetheless, enormous scale and well-arranged examination and assortment started during the 1980s. These generally fuse the assessment and arrangement of Yunnan, Shennongjia and Three Crevasses Locale, Hainan Island, Dabashan Area and Southwest Sichuan, Northwest Guangxi and Southwest Guizhou, Southeast Chongqing and Upper east Guizhou and, other tea developing areas (Chen et al., 2006a).

In 1990, the China National Germplasm Tea Stores (CNGTR), incorporating Hangzhou Tea Storehouse

in the Tea Exploration Organization Chinese Foundation of Horticultural Sciences (TRICAAS) and Menghai Tea Archive Branch in the TRI Yunnan Institute of Agrarian Sciences (TRIYAAS) were built up as national level lasting ex-situ preservation vaults (Chen et al., 2004). Around 2,665 germplasm promotions, including wild tea plants, landraces, improved clones, strains, hereditary materials, and others, from the tea developing areas of China and a few different nations around the globe, had been gathered and protected in the CNGTR before the finish of 2003 (Chen et al., 2004). In the meantime, vaults of various scales were set up in the TRIs of other tea creating regions essentially to ration their neighborhood landraces (Liang et al., 2007).

Early-Stage Appraisal Technique for Breeding

Cup tea quality, yield, and hindrances are fundamental tea reproducing goals. The appealing attributes for high harvest yield and maybe quality may not probably happen in more than one out of each at least 40,000 shrubberies (Wright, 1956; Hajra, 2001). It will take 22-25 years to successfully breed another clone utilizing ordinary strategies. The effectiveness of customary determination and reproducing is low. In this manner, to abbreviate the reproducing time and improve the rearing proficiency, heaps of research extends on beginning time examination procedure for rearing have been completed and accomplished altogether (Takeda, 2000). In the mid-1970s, explore chiefly centered around the basic connections between the morphological attributes and yield, cup tea quality and opposition. During the 1980s, biostatistics techniques, for example, way examination, poly-relapse investigation, and head part examination were utilized to efficiently break down the connections between a few morphological, physiological, compound attributes and the yield, quality, and obstruction (Liu and Zhou, 1994). Since the late 1990s, DNA sub-atomic markers have been utilized in beginning time evaluation (Chen et al., 2006c). The beginning period examination of tea reproducing is currently progressing from morphological, physiological and compound levels to progressively exact DNA level (Liang et al., 2007).

Appraisal and Evaluation

Somewhere in the range of 1986 and 2005, the agronomical attributes, cup tea quality, primary concoction segments, abiotic and biotic resilience, cytological and enzymological characteristics of 1,500 promotions of tea germplasms protected in the CNGTR were purposely surveyed and altogether assessed utilizing multidisciplinary approaches (Yu et al., 1992; Yang et al., 2003b; Chen and Zhou, 2005). The book "Descriptors and Data Standard for Tea (Camellia spp.)" was distributed (Chen et al., 2005b) and farming strategy standard of the Ministry of Agriculture "Technical Code for Crop Germplasm Evaluation Tea Plant (Camellia sinensis)" will be discharged to the open very soon (Chen et al., 2006b). These distributions were further direct and institutionalize the examination and assessment substance, strategies and the information quality control the executives. In the interim, atomic markers, for example, RAPD, AFLP, and ISSR are getting famous in the assessment of hereditary assorted variety and hereditary relationship of tea germplasms (Chen et al., 1998; Liang et al., 2000; Luo et al., 2002; Chen and Yamaguchi, 2002, 2005; Huang et al., 2004; Duan et al., 2004; Yao et al., 2005; Chen et al., 2005a). The deliberately assessed tea germplasms give first-class materials both to singular choice and parental choice for hybridization just as for transformation rearing (Liang et al., 2007).

Genetic Introgression to Enhance Germplasm Innovation

Germplasm development by far off hybridization has a significant job of widening the hereditary base. Ackerman (1973) endeavored an enormous number of interspecific crosses including 20 Camellia species. Tea could be effectively crossed with 10 distinct species. In Japan, the far off hybridization of the tea plant and 26 species in the variety Camellia were directed. An interspecific half breed between tea plant (C. sinensis) and bloom camellia (C. japonica) and named Chatsubaki was acquired. It demonstrated exceptionally impervious to tea anthracnose, dim scourge and cold harm in winter and had low caffeine content (Takeda et al., 1987). It has gotten one of the three promising parental materials for tea rearing in Japan. A clone TV 24 in Assam, India was delivered by going between F1 crossbreeds (C. irrawadiensis X C.assamica) and TV1, an Assam-China half breed (Bezbaruah, 1987).

The Establishment and Development of Tea Breeding System

Table:1 indicates that all the 30 cultivars registered in 1985 were landraces, and among them 17 were jats. In the 22 clones registered in 1987, most were selected from individuals of jats, or open-pollinated progenies. However, in the two batches registered in 1994 and 2002,

clones selected from hand-pollinated progenies increased significantly, and one clone was bred using a mutation method in 2002 (Liang et al., 2007). Among the 45 new clones in the on-going 3rd national adaptability test, the clones bred using controlled hybridization and mutation methods increased further (data not shown). The breeding objectives have been changing from high yield to high quality than to diverse objectives such as high quality, high efficiency, high functional components contents and high tolerance to stress. Meanwhile, the breeding technique is continually advancing. A highly efficient tea breeding system, in which controlled hybridization and individual selection are the main breeding approaches combined with the molecular marker-assisted selection and micro propagation techniques, has now being established and gradually developed (Liang et al., 2007).

Individual Selection Breeding

In both the 67 national (Table 1) and 101 provincial improved clones, about 76 percent were bred using the individual selection method from jats or open-pollinated progenies. So, the selection of natural exiting variations from high-quality local cultivars (jats) or open-pollinated progenies of elite cultivars is a dominant method for tea breeding. For example, six national clones, Longjing 43, LongjingChangye and Zhongcha 102 were selected from the seedlings of famous local cultivar Longjing Quntiand Anhui 1, Anhui 3 and Anhui 7 were from Qimen Qunti, respectively. In total, 15 clones had been selected from seedlings and open-pollinated progenies of Funding Dabaicha and/or Yunnan Dayecha as the parent(s). Many of them are now becoming widely cultivated popular clones in the tea gardens of China (Liang et al., 2007). Nevertheless, the percentage bred using the individual selection method decreased gradually, from 85 percent for the first time (1987) to 66.7 percent for the second (1994) and third (2002) time, respectively (Liang et al., 2007). The selection of elite mother bushes for quality attributes is based on fast fermentation using the chloroform test. Other attributes considered when selecting mother bushes include growth vigor, shoot size and tolerance to major pests and diseases. The chloroform test is very inexpensive (about USD 1/ genotype) and is used to classify plants as "slow", "medium" or "fast" fermenters. Using this test, the "slow" fermenters are eliminated from the selection program in year 4. This occurs in the nursery plants, thus eliminating them from expensive field trials (Table 1).

Since 1951 that has helped to prevent the spread of over the years there have been changes in the diseases. Weather pattern (characterized by the short rainy season and prolonged drought conditions), a lifestyle of people (leading to decreased desire to work on farms) and consumers' needs or taste (going for specific quality). These changes have strongly impacted on the breeding and selection strategy and establishment of the relevant selection criteria for elite cultivars (Table 3). The selection of these attributes requires the establishment of rapid and reliable selection criteria and methods (Apostolides et al., 2006).

Table1. *Brief introduction to the Chinese national registered cultivars*

no	Cultivars	Registered year	Breeding method	no	Cultivars	Registered year	Breeding method
1	Fuding Dabaicha	1985	Landrace	50	Yunkang 10	1987	Field clone
2	Fuding Dahaocha	1985	Landrace	51	Yunkang 14	1987	Field clone
3	Fu'an Dabaicha	1985	Landrace	52	Juhuachun	1987	OP
4	Meizhan	1985	Landrace	53	Guihong 3	1994	Field clone
5	Zhenghe Dabaicha	1985	Landrace	54	Guihong 4	1994	Field clone
6	Maoxie	1985	Landrace	55	Yangshuling 783	1994	Field clone
7	Tieguanyin	1985	Landrace	56	Wannong 95	1994	Field clone
8	Huangdan	1985	Landrace	57	Xicha 5	1994	Field clone
9	Fujian Shuixian	1985	Landrace	58	Xicha 11	1994	Field clone
10	Benshan	1985	Landrace	59	Hanlv	1994	Field clone
11	Daye Wulong	1985	Landrace	60	Longjing Changye	1994	Field clone
12	Mengku Dayecha*	1985	Landrace	61	Zhenong 113	1994	OP
13	Fengqing Dayecha*	1985	Landrace	62	Qingfeng	1994	Field clone
14	Menghai Dayecha*	1985	Landrace	63	Xingyang 10	1994	Field clone
15	Lechang Baimaicha*	1985	Landrace	64	Baxiancha	1994	Field clone
16	Hainan Daye*	1985	Landrace	65	Qianmei 601	1994	HP
17	Fenghuang Shuixian*	1985	Landrace	66	Qianmei 701	1994	HP

18	Damianbai	1985	Landrace	67	Gaoyaqi	1994	Field clone
19	Shangmeizhou Zhong	1985	Landrace	68	Zhuyeqi 12	1994	Field clone
20	Ningzhouzhong*	1985	Landrace	69	Baihaozao	1994	Field clone
21	Huangshang Zhong*	1985	Landrace	70	Jiebohuang 13	1994	Field clone
22	Qimenzhong*	1985	Landrace	71	Shuyong 703	1994	HP
23	Jiukengzhong*	1985	Landrace	72	Shuyong 808	1994	HP
24	Yuntaishanzhong*	1985	Landrace	73	Shuyong 307	1994	HP
25	Meitan Taicha*	1985	Landrace	74	Shuyong 401	1994	HP
26	LingyunBaimaocha*	1985	Landrace	75	Shuyong 3	1994	HP
27	Ziyangzhong*	1985	Landrace	76	Shuyong 906	1994	HP
28	Zaobaijie*	1985	Landrace	77	Yihongzao	1998	Field clone
29	Yichang Dayecha*	1985	Landrace	78	Fuzao 2	2002	Field clone
30	Yixingzhong*	1985	Landrace	79	LingtouDancong	2002	Field clone
31	Qianmei 419	1987	OP	80	Xiuhong	2002	Field clone
32	Qianmei 502	1987	HP	81	Wulinghong	2002	Field clone
33	Fuyun 6	1987	OP	82	Yunda Danlv	2002	Field clone
34	Fuyun 7	1987	OP	83	Gancha 2	2002	OP
35	Fuyun 10	1987	OP	84	Shuyong 808	2002	HP
36	Zhuyeqi	1987	Field clone	85	Shuchazao	2002	Field clone
37	Longjing 43	1987	Field clone	86	Wannong 111	2002	Mutation
38	Anhui 1	1987	Field clone	87	Zaobaijian 5	2002	Field clone
39	Anhui 3	1987	Field clone	88	Nanjiang 2	2002	Field clone
40	Anhui 7	1987	Field clone	89	Zhenong 21	2002	Field clone
41	Yingshuang	1987	OP	90	E'cha 1	2002	HP
42	Cuifeng	1987	OP	91	Zhongcha 102	2002	Field clone
43	Jingfeng	1987	OP	92	Mingke 2	2002	HP
44	Biyun	1987	OP	93	Yuemingxiang	2002	Field clone
45	Zhenong12	1987	OP	94	Mingke 1	2002	HP
46	Shuyong 1	1987	HP	95	Huangqi	2002	OP
47	Yinghong 1	1987	Field clone	96	Guilv 1	2003	Field clone
48	Shuyong 2	1987	HP	97	Mingshan Baihao	2005	Field clone
49	Ningzhou 2	1987	Field clone				

Source: *China Tea Varieties Compilation Committee, 2001; MOA Bulletin No. 191, 2002; Zakir, 2017.*

** Jat cultivars: (propagated by seeds), the others are clones Breeding methods:*

*Landrace**:** traditional cultivars, including jat cultivars and clones;*

Field clone: individual selected clones from seedlings/jats;

OP: Clones selected from open-pollinated progenies;

HP: Clones selected from hand-pollinated progenies

Table3. *Breeding and selection programme for new cultivars at the Tea Research Foundation in Central Africa (Malawi).*

Place	Year	Activity	Number of genotypes	Number of plants per genotype
Seed Garden	0	Controlled crosses of flowers in seed garden	5000	5000
Nursery	1	Germinate viable seeds in pots	3750	3750
Nursery	2,3	Select seedlings on the basis of plant vigor; Take single cuttings for vegetative propagation	2500	2500
Nursery	4	Select seedlings on the basis of rooting ability and nursery performance. Eliminate slow fermenters (chloroform test) take 30-50 cuttings from selected seedlings	350	350
Field	5	Plant cultivars in 2 x 8 = 16 bush observation plots in field. Mini-manufacture for organoleptic assessment by expert tea taster	150	2400
Field	6,7,8	Select cultivars on field performance and organoleptic quality	20	2400
Field	9	Establish cultivars in replicated field trials of 5 x 6 =	20	3000 per station

		30 bushes per plot replicated five times, on several research stations		
Field	10	Early release of cultivars to estates	5	as required
Field	11,12,13,14	Evaluation of cultivars on all traits for yield and quality	5	10,000 to 100,000
Industry	15	Possible release of 1-2 new cultivars to industry	0-3	as required

Source: *Apostolides et al., 2006*

Hybridization Breeding

Hybridization is one of the main methods of obtaining genetic variation, and it is an important method of breeding new varieties. The percentage of clones bred using the hybridization method increased significantly, from 9.1 percent for the first time (1987) to 29.1 percent for the second (1994) and 22.2 percent for the third (2002) time, respectively. Distant hybridization is a powerful method for broadening the genetic base of new varieties (Liang et al., 2007; Zakir, 2017). Thanks to sterility or extremely weak fecundity, currently it could not be a routinely used method in the breeding of tea plants. Young embryo rescuing tissue culture strategy is now being developed to improve the success ratio of distant hybridization in the TRICAAS (Liang et al., 2007).

Mutation Breeding

Mutation breeding is artificially using physical, chemical and biological factors to induce the tea plant to produce genetic variation and then breed new clones or get new valuable genetic materials for further breeding use according to the breeding objectives. The combined effects of c-ray and chemical mutagens on biological damage to tea plants were systematically analyzed (Yang and Lin 1992). The damage to tea plants treated with physicochemical mutagens was more significant than that treated with either c-ray or chemical mutagens. The suitable dose rate and physicochemical combined mutation technique and criteria of main Chinese tea cultivars and a math model between radiation dose and effect of dose rate were proposed (Zakir, 2017). The relationship between the moisture content, main indigenous components of tea seeds and the radiation damage was elucidated. One excellent new strain, which is very early sprouting in the spring, high cup tea quality, resistant to disease and suitable for fine green tea, has been selected from the offsprings of Longjing 43 cuttings under Co60c-ray radiation (Yang et al.,2003a). It is now in the 3rd national adaptability test and will hopefully become the first clone bred using cutting radiation mutation method. The TRI Hunan and Anhui Agricultural University had bred and registered a provincial and national clone using tea seedlings or seeds as radiation objects and Co60c-ray as a radiation source in 1997 and 2002, respectively. All these indicate that mutation breeding is becoming one of the practical breeding approaches for tea plants. Meanwhile, the molecular mechanism of cutting mutation was analyzed using ISSR markers in the author's lab. The amplified genomic DNA band patterns of twenty-four M1 off springs and their four M0 parents showed a significant difference, so they are of the potential for further selection (Liang et al., 2007).

Molecular Marker-Assisted Selection

Molecular biology techniques provide polymorphic DNA based molecular markers for plant genetics and breeding. Molecular markers have distinct advantages compared to other genetic markers. Firstly, it is the direct reflection of genetic variation on the DNA level, it is unaffected by the developmental stages and environmental conditions and can stably be inherited to offsprings. Secondly, some markers are co-dominant, suitable for the selection of recessive agronomical traits. Thirdly, the variation of the genome is plentiful and the potential markers are almost unlimited. Presently, several molecular markers, such as RFLP, RAPD, CAPS, AFLP, ALPs, SSR, ISSR, have been developed and widely applied in the tea plant. Remarkable advances have been achieved for the analysis of genetic diversity and relationship, discrimination of varieties and cultivars, studies on molecular phylogenetics, detection of genetic stability and fidelity and, genome mapping (Chen et al., 2006c). In the past ten years, some secondary metabolism, quality and stress-related important functional genes of tea plant, such as phenylalanine ammonia-lyase, chalcone synthase, dihydroflavonol 4-reductase, flavanone 3-hydroxylase, flavonoid 3¢,5¢-hydroxylase, leucoanthocyanidin reductase, anthocyanidin synthase, polyphenol oxidase for flavonoid biosynthesis, caffeine synthase and S-adenosylmethionine synthase for caffeine biosynthesis, beta-primeverosidase and beta-glucosidase for the formation of tea aroma, have been isolated, cloned and expressed (Chen et al., 2006c). Furthermore, the initiation and primary

progress of functional genomics of tea plants provide a novel and robust approach to understand the mechanisms of growth, development, differentiation, metabolism, quality, and stress resistance on the whole genome level. It is possible to genetically manipulate and control the tea plant. This will bring tremendous effects to tea genetic improvement and breeding in the foreseeable future (Chen et al., 2006c; Liang et al., 2007). Amplified Fragment Length DNA Polymorphism (AFLP) analysis of 49 tea cultivars from south India produced a total number of 1555 unambiguous polymorphic amplified DNA fragments (Balasaravnan et al., 2003).

Polyploidy and Its Application in Tea Breeding

Polyploidy plays a major role in increasing the amount of genetic material in plants and results in a change in the chromosome number. Polyploids have proportionally larger cells than their diploid counterparts; hence it is expected to contribute to larger plant size and higher yields (Allard, 1960). In tea, gigantism in various morphological characters was associated with tetraploids (Chaudhuri and Bezbaruah, 1985; Amma,1974). Apart from increasing the biomass of crops (Allard, 1960), induced polyploids could be used as an additional source of genetic variation to improve the overall performance of existing diploids, or to enhance particular characters such as the shoot size trait (Wachira and Kiplangat, 1991), while retaining most of the characteristics of the diploid progenitor. Also, they could be used as a source of breeding material for the production of secondary polyploidy cultivars by crossing with diploids (Singh, 1980). Although the value of polyploids in overcoming barriers to inter-specific gene introgression has been recognized in plant species (Allard, 1960), this has not been fully exploited in perennial crops (Wachira and Ng'etich, 1999).

However, owing to the highly heterozygous and self-incompatible nature of the tea plant, the introduction of a specific trait of interest into a proven cultivar, solely through conventional methods, has some limitations. On the other hand, non-conventional methods, such as polyploidy breeding, may induce more vigor and some degree of resistance to biotic and abiotic stresses in existing tea cultivars, without causing changes in the desired parts of the genome (Simura and Inabe, 1952). There is a positive correlation between the size of the leaf and the yield in tea. Therefore, the generation of polyploid tea genotypes with bigger leaves may be useful in developing high-yielding tea cultivars (Table 4). Further, in asexually-propagated perennial crops such as tea, where the vegetative organs are of economic value, polyploidy breeding can be used effectively in their genetic improvement (Gunasekara and Ranatunga, 2003).

Table4. *Identified polyploid clones, their chromosome number and ancestry*

Clone number	Ploidy-Chromosome No.	Original seed source
*TRFK 311/287	4n=60	TRFK 6/8 x TRFK 31/11 - hand-pollinated from TRIEA Uganda
*TRFK 31/30	4n=60	Seed from Ambangulu Estate, Tanzania
*TRFK 52/1	3n=45	“Between" seed from Kanywankoko Estate, Uganda
*TRFK 77/1	3n=45	Open-pollinated seed from Mimosa estate, Malawi
*Dimbolil 3	3n=45	Seedling from James Finlay (K) Ltd, Dimbolil Estate
*TRFK 77/2	3n=45	Open-pollinated seed from Koiwa Estate
*TRFK 383/1	3n=45	Open-pollinated BB35 X BB5, Koiwa Estate
*TRFK 331/2	3n=45	Seed from Chemosit Estate barie, Unilever tea
*TRFK 378/1	3n=45	Open-pollinated BB35 X BB7, Koiwa Estate
*TRFK 412/1	3n=45	Open-pollinated BB21 X BB5, Koiwa Estate
*TRFK 371/1	3n=45	Open-pollinated seed of AHP S15/10 from Chepgoiben Estate, James Finlay (K) Ltd
*TRFK 400/1	3n=45	Seed from Chepgoiben Estate barie
*TRFK 389/1	3n=45	Open-pollinated BB35 X BB152, Koiwa Estate
*TRFK 392/1	3n=45	Open-pollinated BB7 X BB35, Koiwa, Estate
*TRFK 394/1	3n=45	Open-pollinated BB2 X BB35, Koiwa, Estate
*TRFK 395/1	3n=45	Open-pollinated BB5 X BB35, Koiwa, Estate
*TRFK 54/49	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 386/1	3n=45	Seed from Sotik Tea Co.
TRFK 381/1	3n=45	Seed from BB5 X BB2
TRFK 84/1	3n=45	Mixed seed from Congo, Toro and Entebbe, Uganda
TRFK 84/2	3n=45	Mixed seed from Congo, Toro and Entebbe,Uganda
TRFK 85/1	3n=45	Seed collected from clones from Kakonde Estate

TRFK 382/2	3n=45	Seeds from BB5 X BB35
TRFK 382/1	3n=45	Seeds from BB5 X BB35
TRFK 386/2	3n=45	Seed from Sotik Tea Co.
TRFK 76/3	3n=45	Seed from Ramjat, Lugeri Estate, Malawi
TRFK 76/1	3n=45	Seed from Ramjat, Lugeri Estate, Malawi
TRFK 76/2	3n=45	Seed from Ramjat, Lugeri Estate, Malawi
TRFK 75/1	3n=45	Commercial seed from Lugeri Estate, Malawi
TRFK 31/36	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 31/38	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 31/39	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 31/40	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 31/41	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 18/7	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 18/27	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 18/26	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 18/28	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 54/50	3n=45	Seed from Ambangulu Estate, Tanzania
TRFK 550/1	3n=45	Open-pollinated seed from polyclonal mixture, Timbilil Estate, Kericho

Source: *Wachira and Kiplangat, 1991; Zakir, 2017) NB: in tea, n = x =15.*

The Achievements of Tea Genetic Improvement and Breeding

Different tea research institutes and dedicated planters had further developed several varieties with better yield, quality, and attributes such as tolerance to drought, diseases globally. More than 1,200 such commercial cultivars of tea have been developed and released for cultivation worldwide, and many of them have special traits (Mondal, 2014). By the end of 2005, China had 97 national registered cultivars, among them 17 are jats, 80 are clones, 30 are landraces and 67 are improved clones (Table 1). They are bred by 23 different institutions including the national and local tea research institutes, agricultural universities, local agricultural departments, tea experimental stations, etc. The level of clonal tea in plantations has expanded from less than 10% in the early1980s to 26% in 2005 (Yu, 2005). In India, the selected plants from old seed jats and progenies of biclonal hybrids, 153 locally adapted and 31 universal clones were developed for the tea industry. Marker development for drought resistance and blister blight disease is under progress using cDNA-AFLP techniques. The micropropagation technique has also been standardized for quick multiplication of these biotechnologically modified plantlets (Chen et al., 2012). To date, the Tea Research Foundation of Kenya has released a total of 50 high yielding and good quality tea clones for commercial utilization, not just in Kenya alone but also in the entire East African region. Furthermore, tea improvement activities integrating molecular markers and participatory clonal selection involving farmers and consumers are expected to taste-track the development and adoption of novel varieties within a relatively short period (Samson et al., 2012). From SriLanka; the first extensive study reported so far on tea germplasm characterization using morphological descriptors, both locally and internationally. Furthermore, the exceptional morphological descriptors identified in this study would facilitate cultivar identification, which has become one of the most demanding needs among tea growers after the introduction of new improved cultivars by the Tea Research Institute of Sri Lanka (Piyasundara et al., 2009).

Conclusion

Generally, the tea genetic improvement mechanisms like Conventional selection, hybridization, marker-assisted selection, mutation breeding, polyploidy, genetic engineering, etc.; were applied for tea production increments, quality and tolerance or resistance to biotic and abiotic stresses. The level of tea production is related to the level of intensive utilization of such breeding mechanisms.

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