Scientific Papers. Series B, Horticulture. Vol. LX, 2016
Print ISSN 2285-5653, CD-ROM ISSN 2285-5661, Online ISSN 2286-1580, ISSN-L 2285-5653

OVERVİEW OF DAHLIA BREEDING

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Abstract

Dahlias are popular ornamental plants cultivated in many countries. It is an important garden plant owing to its diversity in colours, size, shapes, forms and profusion of flowering. Dahlia,member of the Asteraceae family. This review describes and compares the conventional and molecular genetics methods being used for breeding. Dahlia is vegetatively propagated with tubers commonly. Breeding programmes have focussed on improving various characteristics to enhance ornamental values, including flower colour, size and form, and production quality. Although desirable traits have been introduced by classical breeding, there are limitations to this technique. Firstly, distant crosses may be limited by incompatibility or differences in ploidy level that is very common in dahlias. Secondly, characteristics such as uniform growth and synchronous flowering are polygenic. Thirdly, several viruses are known to infect dahlia. The dahlia breeding and its methods are described and discussed in this review. Alternative breeding methods will provide faster procedures. In the past, classical breeding approaches like introduction, hybridization, composite crossing, multiline, and backcross breeding were utilized for this purpose. However, each of these methods has advantages and disadvantages. Recent developments in plant biotechnology such as directed mutation, genomics and recombinant DNA technology were adapted by breeders to develop more improved cultivars of dahlias.

Key words: *Ornamental plant, landscape, Asteraceae, mutation breeding, hybridization.*

INTRODUCTION

Dahlias are popular ornamental plants cultivated in many countries. Dahlias are high-value flower crop in several countries in the world. *Dahlia* spp. are members of the *Asteraceae* family. The genus Dahlia's cultivated forms are known as either *D. pinnata* or *D. variabilis* (Sahar et al., 2009). It is popular ornamental plant owing to its diversity in colours, size, shapes, forms and profusion of flowering (De Hertegh, 1989).

Dahlias are allopolyploid with chromosome number 2n = 64 (Lawrence, 1929; Gatt et al., 1998). According to Sorensen (1969), the modern cultivars have 64 chromosomes and are now generally regarded as tetraploids (2n = 4x = 64), though they have also been classed as octoploids (2n = 8x = 64). Crosses between double and single flowered types produce a continuous range of form, indicating that doubleness is controlled by relatively few genes. However their interaction gives rise to great variation in colours (Phetpradap, 1992).

Because of high occurrence of polyploidy, *Dahlia* spp. exhibits various colors, sizes and flower shapes. In particular, dahlias exhibit a wide range of ray floret colors, such as ivory, red, yellow, pink and purple. The pigments accumulated in ray florets are flavonoids, butein, mainly anthocyanin's and flavones and their derivatives that produce yellow, red and ivory colours (Yamaguchi et al., 1999). It is grown as both annual and perennial plant. Many important diseases of dahlia are caused by fungal, bacterial and viral sources leading to diverse types of impairment (Bose and Yadav, 1989) and can be successfully eliminated using micro-propagated plant material (Sediva et al., 2006, Fatıma et al, 2007). It can be more susceptible to bacterial, fungal, and viral infections if is propagated by conventional vegetative methods.

Dahlia is a dicotyledonous plant and a leaf type is composite formed of 3-7 leaflets (Dole & Wilkins 1999). Dahlia plants reproduce vegetative tuberous roots and sexually by seed.

Dahlia is vegetatively propagated with tubers more commonly. Breeding programmes have focused on improving various characteristics to enhance ornamental values including flower colour, size and form (Rout et al., 2006). Although classical breeding contributed improved cultivars, limitations as discussed

below avoid speed of breeding methods. Firstly, crosses may be limited by incompatibility or differences in ploidy level. Secondly, characteristics such as uniform growth and synchronous flowering are polygenic. Thirdly, several viruses are known to infect dahlia. They are dahlia mosaic virus (DMV), cucumber mosaic virus (CMV), impatiens necrotic spot virus (INSV), tobacco streak virus (TSV), and tomato spotted wilt virus (TSWV) (Lobenstein et al., 1995; Pappu et al., 2005). Objective of this study are to summarize and discuss breeding methods of dahlia in relation to conventional breeding methods.

1. MUTATION BREEDING

For various reasons, mutation breeding has been especially successful in ornamentals as well as in many other horticultural plants such as citrus and apples. Firstly, the selection of mutations of directly perceptible characteristics including flower form or size, colour, is generally not difficult. The other reason is that a lot of cultivars are heterozygous that may allow extended variation through mutations and hybridizations. Moreover, *in vitro* or *in vivo* propagation methods frequently allow the successful production of mutants that can be recognized later (Broertjes, 1967). Ornamental bulb and tuber crops contain large, economically important varieties. As many of them indicate segregation after seed propagation, the majority of these crops is propagated vegetatively. This coupled with low speed of propagation, is one of the main obstacles to breeding. This low process cannot be speeded up since pruning, to support the growth of axillary buds, is often impossible. It is therefore not surprising that irradiation at the right moment is recognized as being of great significant; that is, irradiation should be carried out at the earliest possible stage of development, when a mutated cell has the largest feasible opportunity to make a substantial contribution to the genesis of the new plant, tuber or bulb.

In Dahlia, freshly harvested tubers were more suitable for irradiation. For many reasons *D. variabilis* must be considered as a promising species for mutation breeding. The high polyploidy and the great number of flower colour genes brings attention to this species (Broertjes, 1967). Flower colour and other distinguishable mutations ranging from dominant to recessive can be observed in the material due to the high degree of heterozygosity and vegetative propagation. Furthermore, genetic composition of a given cultivar is not altered significantly. Cross-breeding of a certain dahlia variety, on the other hand, will never result in a genotype which is identical except for recently introduced one like change in lower colour. For this reason, mutation breeding is important way of development in those varieties important (Broertjes, 1968).

Material selection is highly difficult due to complicated genetics and unknown genetic history of the current cultivars, which makes it impossible to choose cultivars. Thus mutation breeding is more promising than hybridization breeding (Broertjes, 1976).

It is of crucial importance to irradiate the buds at the earliest possible stage of development, for the purpose of give a mutated cell the best chance to take part in the formation of the shoot. Irradiation should therefore take place immediately after harvest, when no visible eyes can be detected on these so-called dormant tubers.

There are chemical (DMS, EMS, etc.) and physical (^{60}Co-gamma) reagents for mutation breeding. Although chemical mutagens usually cause point mutations (minor alteration in sequences), physical mutagens bear larger modifications in the chromosomes. List studies related to mutation breeding are reported in Table 1.

2. HYBRIDIZATION BREEDING

Hybridization remains significant component of a lot of plant breeding programs. Hybridization can include crosses between distinct species (interspecific hybridization), or crosses between genetically distinct individuals (selections, breeding lines, or cultivars) within a species (intraspecific hybridization) (Murray, 2003). Hybridization is generally significant for two main reasons: to transfer genes and therefore, the characters they control, from one plant to another; or to exploit the vigor that is

often observed when genetically distinct plants are crossed.

2.1. Intraspesific gene transfer

In general, modern dahlias have been developed through conventional breeding such as hybridizations and selections. Particularly, intraspecific hybridizations may have advantages due to less occurrence of complications such as incompatibility and early embryo losses. Breeders might expect lower incidence of chromosome imbalance within species crosses. Eriksen et al (2014) propose that multiple intraspecific hybridization events may have created especially potent conditions for the selection of a noxious invader, and may explain differences in genetic patterns among North and South America populations in *Centaurea solstitialis* L. (*Asteraceae*) inferred differences in demographic processes, as well as morphological differences previously reported.

2.2. Interspecific gene transfer

Interspecific hybridization, also named wide hybridization, is generally used when a specific character or group of characters is missing from a cultivated species. A research of related wild species is then needed to identify which of them may be beneficial as potential gene donors. Not all species are able to hybridize, and there can be remarkable variation in the ease of hybridization, even between closely related species.

Interspecific gene transfer through hybridization is possible among many dahlia cultivars and has occurred naturally. An extensive search of the relevant literature did not reveal evidence of gene transfer between dahlias and unrelated plant species yet. Thus gene transfer through wide hybridizations should be investigated.

3. MODERN APPROACHES

The molecular markers have contributed research on genetic variation among dahlia genetic resources. They are very useful identification of differences, germ plasm management and discriminating commercial cultivars for protecting breeders' rights (Ben-Meir et al., 1997; Rout et al. 2006).

In traditional breeding, selections were made on morphological bases that were extremely influenced by the environment. This created confusion in selection of creditable parents for breeding programs. However, the exploration of DNA based markers such as RAPD, AFLP, ISSR, SSR and SNPs linked to various economically significant traits has provided the opportunity to plant breeders to select their desired parents for further improving cultivars. (Hussain et al., 2012; Hussain, 2015).

Chebet et al. (2003) reported the use of biotechnological approaches to develop horticultural plant production especially the application of biotechnology on in vitro propagation of ornamental plants.

Many important diseases of Dahlia can be successfully eliminated using micro propagated plant material. In vitro culture is one of the key tools of plant biotechnology. Furthermore, micro-propagation of plants is a well-known strategy for effective production and propagation of the elite plant material. It helps in the improvement and rapid propagation of selected plants with requested characters in shortest possible time and new cultivars can also be developed by genetic modifications and protoplast fusion.

The regeneration of Dahlia plants has been reported either directly from explants without callus formation or indirectly through callus induction and regeneration. There are a few reports available on in vitro proliferation of *Dahlia sp.*. Fatima et al (2007) produced the largest number of dahlia plants by indirect organogenesis technique when used the cotyledon leaf, hypocotyls and shoot tip as explants. Salman et al (2010) reported similar results when they cultured the shoot tips on MS medium. Majid et al (2015) studied in order to produce large number of dahlia plants free of pathogens and matching the genetic traits of the mother plant by plant tissue culture technique.

List of relevant studies are given in Table 1.

Table 1: Studies conducted in the *Asteraceae* family

Study subject	Genus	Reference of study
Intergeneric hybridization	*Chrysanthemum naktongense x Chrysanthemum xmorifolium 'Aifen'*	Wu et al., 2015
DNA sequence analysis	*intergeneric hybrid (Argyrotegium mackayi x leucogenes leontopodium)*	Smissen et al., 2015
In suti hybridization	*Chrysanthemum*	Xiangyu et al., 2015
Hybridization and genomic in situ hybridization	*Tragopogon castellanus*	Mavrodiev et al., 2015
Intergeneric hybrids	*Anaphalioides bellidioides x Ewartiothamnus sinclairii and Leucogenes grandiceps x Raoulia eximia*	McKenzie et al., 2015
Hybridization	*Calendula maritima*	Plume et al., 2015
Natural hybridization	*Ligularia cymbulifera and L. tongolensis*	Yu et al., 2014
Intergeneric genomic shock	*Chrysanthemum morifolium x Leucanthemum paludosum*	Wang et al., 2014
Hybridization	*Cyanus triumfetti and C. montanus*	Olsavska et al., 2013
Hybridization	*Chrysanthemum nankingense x Tanacetum vulgare and C. crassum x Crossostephium chinense*	Wang et al., 2013
Karyotypic changes followıng hybrıdızatıon at the polyploid level	*Tragopogon mırus and T. mıscellus*	Lipman et al., 2013
Interspecific hybridization	Genus *Tolpis*	Gruenstaeudl et al.,2013
Hybridization	Members of the *Artemisia tridentata*	Garrison et al., 2013
Intergeneric hybridization	*Senecio sect. Crociseris*	Calvo et al., 2013
Interspecific and intraspecific polymorphisms	*Cichorium* L.	Bernardes et al., 2013
Natural hybridization	*Sphagneticola trilobata*	Wu et al., 2013
Intraspecific hybridization	*Artemisia tridentata*	Richardson et al., 2012
Hybridization	*Tithonia tubaeformis and T. rotundifolia*	Tovar-Sanchez et al., 2012
Intersectional hybridization	*Helichrysum orientale and Helichrysum stoechas*	Galbany-Casals et al., 2012
Natural hybridization and introgression	*Ligularia species*	Yu et al., 2011
Hybridization	diploid *Centaurea pseudophrygia and the* tetraploid *C. jacea*	Koutecky et al., 2011
Hybridization	Boltonia asteroides (L.)	DeWoody et al., 2011
Hybridization and genome duplication	*Secenio*	Hegarty et al., 2011
Intergeneric hybridization	*Chrysanthemum grandiflorum (Ramat.) Kitam. 'Zhongshanjingui' (female parent) and Ajania przewalskii Poljak. (male parent)*	Deng et al., 2010
Molecular, morphological, and experimental evidence for hybridization	The *Galapagos* endemic plants *Scalesia aspera, Scalesia crockeri,* and *Scalesia pedunculata*	Lindhardt et al., 2009
Molecular study of hybridization and homoploid hybrid speciation	*Argyranthemum sundingii*	Fjellheim et al., 2009
Mutation breeding by radiation technology	domestic and foreing ornamentals	Sup Song et al., 2005
Induced mutations	-	Ahloowalia et al., 2001
Applıcatıon of ın-vıvo and ın-vitro mutation techniques	-	Maluszynskı t.al.,1995
Mutations breeding	*Dahlia* spp.	Broertjes et al., 1966

CONCLUSIONS

This review describes and compares the conventional and molecular genetics methods being used for breeding. In the past, classical breeding approaches like introduction, hybridization, composite crossing, multiline, and backcross breeding were utilized for this purpose. However, these methods have low speed, and expensive. Furthermore, breakdown of resistance due to fast evolving pathogens could not be coped with using these time consuming methods. Therefore, molecular genetics approaches like mutation, genomics, recombinant DNA technology, were adapted by breeders to develop effective resistance in crop plants in a shorter time.

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