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Discovery of *UPSTREAM OF FLOWERING LOCUS C* (*UFC*) and *FLOWERING LOCUS C EXPRESSOR* (*FLX*) in *Gladiolus ×hybridus, G. dalenii*

Jaser A. Aljaser, Neil O. Anderson*, and Andrzej Noyszewski

Department of Horticultural Science, University of Minnesota, 1970 Folwell Avenue, Saint Paul, MN 55108, USA

* Corresponding author, E-mail: ander044@umn.edu

Abstract

The lack of identified flowering genes in ornamental geophytic crops, such as *Gladiolus,* is critical to further genetic research. The *UPSTREAM OF FLOWERING LOCUS C (UFC)* gene is adjacent to *FLOWERING LOCUS C (FLC)* which is a floral repressor; *FLC EXPRESSOR (FLX)* upregulates *FRIGIDA* which upregulates *FLC* expression. The purpose of this research was to determine whether two flowering genes exist in *Gladiolus ×hybridus* and *G. dalenii*: *UFC* and *FLX*. Seventeen early flowering and commercial cultivars possess the *UFC* gene with four exons in two allelic forms. The sequenced *UFC* gene, when translated into its amino acid sequence and set in pair-alignment to other species, has < 57% in amino acid identity to *Musa acuminata*. The *FLX* gene in gladiolus has 3/5 (60%) exons in common with *Ananas comosus*; pair-alignment of the exons has ~65% identity of *FLX* to *A. comosus*. The *UFC* protein consists of a conserved domain, *DUF966*, which is higher in identity (86%) and pair-alignment with *Elaeis guineensis*. The two newly-discovered genes in gladiolus, *UFC* and *FLX*, provide insight into the flowering mechanism, flowering pathway genes, and vernalization response.

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INTRODUCTION

In angiosperms or flowering plants, 'Florogenesis' is the transitioning process from vegetative tissue to reproductive organs or flowers in a plant's apical meristem[1]. This transition is governed by flowering genes in which expression is influenced by environmental factors such as vernalization, photoperiod, gibberellins, an autonomous pathway[2]. In *Arabidopsis*, several genes have been discovered which are involved in flowering and act as floral integrators. These flowering genes include *FT, SOC1, CO, VRN1, PPD, FCA, FLD*, and *FLK*[3,4]. These floral integrator genes specifically upregulate flowering by promoting transition from vegetative to flowering or repressing floral repressor genes. Repressor genes act as repressors of floral integrator genes and upregulate the expression of repressors, including genes such as *FLC, FRI, FLX, VRN2*, and *SVP*[3,5–6].

FLC and *FLC*-like are floral repressors found in many dicotyledon plants, such as *Malus*[7], *Rosa*[8], *Coffea*[9] and *Brassica*[10]. The *FLC* gene is regulated by temperature changes throughout the year, both in annuals and perennials. In summer, *FLC* expression is upregulated through *FRIGIDA (FRI)* by binding the *FLC* promoter through the DNA-binding protein *SUPPRESSOR OF FRIGIDA4 SUF4*[11]. In addition, *FRI* expression is upregulated by *FLX*; both *SUF4* and *FLX* are in the *FRI*-specific pathway[12]. In winter, *FLC* is down-regulated through a process of vernalization as prolonged exposure of low temperature in winter in the meristem gradually reduces the expression of *FLC*[13]. In addition to the vernalization pathway, the autonomous pathway reduces the expression of *FLC* both in the meristem and leaves[13]. Gradual reduction of *FLC* allows *FLOWERING LOCUS T (FT)* to be expressed in the leaves and transported through the phloem to reach to the meristematic tissue and stimulate the MADS box genes, thereby inducing flowering in *Arabidopsis*[14].

In wheat and barley, the flowering pathway is regulated by photoperiod, vernalization and the circadian clock[15]. *Vernalization gene-2 (VRN2)* is a dominant repressor or inhibitor of flowering in winter wheat (*Triticum aestivum*; a monocot grass) that is down-regulated by vernalization (a cold period; winter)[15]. Subsequently, the floral integrator leads to flowering in winter wheat while spring wheat doesn't require vernalization due to a non-functional *VRN2* gene. However, vernalization is a facultative stimulus for earlier flowering in spring wheat[16]. In contrast, maize (*Zea mays*) and rice (*Oryza sativa*) rely on plant age to build up sufficient energy requirements in order to transition to flowering through epigenetic action of *miR172*[17]. In monocot geophytes (defined as herbaceous perennial plants with underground storage organs, e.g. bulbs, corms, tubers, etc., that promote winter survival), such as *Gladiolus, Lilium, Tulipa, Narcissus* and *Crocus*, the flowering pathway is poorly understood. Factors of plant growth influencing flowering in commercial geophytes for commercial production are well known[1,18]. A clearly delineated genetic pathway for monocots has yet to be explored and characterized for many floricultural crops, such as gladiolus. In contrast, the *Arabidopsis* model is readily applicable to temperate dicotyledon plants[19] but may be only partially useful for monocots. Only a few flowering genes have been discovered in monocot ornamental geophytes[1], such as *FT*-like in *Allium cepa*[20,21], *FT* in *Narcissus*[22], *NLF* in *Narcissus*[23], *LFY* in *Allium sativum*[24,25] and in *Lilium*[26]. Recently, many flowering genes have been discovered in *Lilium ×formolongi* (*FT, CO-like, AP2, GA1, SOC1)* and/or proposed for *L. formosanum* (*VER1, VER2*)[27,28]. The discovery of flowering genes in geophytes

serves as a valuable resource to model flowering pathway(s) therein.

Geophytes such as *Gladiolus, Lilium, Tulipa, Narcissus* and *Crocus* are floricultural crops with ornamental value wherein flowering is essential to maintain the marketing value for these crops. *Gladiolus* ×*hybridus* Rodigas, commonly known as gladiolus(-i), is commercially cultivated as a cut flower and as garden or landscape plants. Gladioli are geophytic plants with underground modified stem structures known as corms, producing cormels as a means of vegetative propagation[29]. Flower initiation and development are crucial steps for its success as a cut flower. Therefore, understanding the flowering pathway is vital for genetics and breeding to improve the floral market value.

Gladiolus has a genome size of 1,100 Mbp, although it is unclear whether this is for haploid or diploid and the species is unknown[30]. The genome weight for gladiolus was recently measured in *G. communis* as 0.67–0.68 pg for monoploid *G.s.* (1Cx, pg) and in *G. italicus* at 0.61 pg for monoploid *G.s.* (1Cx, pg)[31]. The limited knowledge of the gladiolus genome is also reflected in the lack of identified gladiolus flowering genes, since none have been discovered except for the gibberellin receptor gene *GID1a*[31]. The relationship of *GID1a* with flowering has not been established. In *Arabidopsis*, gibberellin binds to the gibberellin receptor forming the *GID1* complex that binds to *DELLA*, causing its degradation, thereby enabling *SOC1* and *LFY* to be upregulated, leading to flowering[32–33].

Understanding the flowering pathway and gene expression is important for efficient selective breeding of gladiolus for rapid generation cycling (RGC) or early flowering types that flower in < 1 year from seed. An important flowering gene is *FLC*, a major flowering repressor found in *Arabidopsis* and many dicot species. *FLC* plays a vital role in the control of flower initiation[13]. *Gladiolus* (Iridaceae) has both summer and winter flowering species. It had been hypothesized that there was no *FLC* gene in monocot species until the *FLC* homologue was discovered in some cereal crops, such as *Triticum aestivum*[34], *Hordeum vulgare*[35] and *Brachypodium distachyon*[36]. These studies did not discover *FRI* genes, which upregulate *FLC* expression in *Arabidopsis thaliana*[11]. A hypothesis to test would be that some monocots do not possess the flowering repressor *FLC* gene and rely on alternative gene(s) to acts as a *miR172* repressor as in *Zea* and *Oryza*[17]. Additionally, it remains unknown whether there is a *FLC*-dependent pathway in all other monocots.

In *Arabidopsis*, *FLC* is located between two flanking genes, *UFC* (located 4.7 Kb upstream of *FLC*) and *DOWNSTREAM OF FLOWERING LOCUS C (DFC*; found 6.9 Kb downstream of *FLC*)[37]. The *UFC* gene expression is repressed by vernalization and independent of *FLC* repression due to vernalization[37]. Thus, both *FLC* and *UFC* are repressed by vernalization, yet are not dependent on each other for expression; the suppression is through chromatin modification in an epigenetic manner[37]. The *VRN1* gene is expressed with vernalization and acts as a floral integrator whereas *UFC* is repressed and required by *VRN1* expression dependently[38]. The potential role for *UFC* in flowering has yet to be discovered and it may not involve flowering at all since vernalization only represses *UFC* in seeds while *DFC* is repressed by vernalization of the plant[38]. Insertion of the *NPTII* gene between the *UFC* and *FLC* region confirmed *NPTII* response to cold as the whole cluster region of *FLC* responded to cold[37]. In the *UFC* protein of *A. thaliana*, a conserved domain *DUF966*, has 92 amino acids, although its function is still unknown[39]. This lack of knowledge in *DUF966* function creates a challenge to identify the function of *UFC* protein. A recent study showed the role of *UFC* in *A. thaliana*, with the genes *SOK2* (with a role in embryogenesis, root initiation, growth and branching of the primary and lateral roots)[39] and DUF966 (with a defense-stress response)[40,41].

The *FLX* gene encodes a putative leucine zipper domain which is required for *FRI*-mediated activation of *FLC* in *Arabidopsis*[42] (Fig. 1). Up-regulating *FLC* occurs in winter annual *Arabidopsis*[33], while late flowering phenotypes exhibit strong expression of *FLX* which indicates its role in the suppression of flowering[42]. Several genes have been discovered in the *FLX* gene family, e.g. *FLX-LIKE1 (FLL1), FLX-LIKE2 (FLL2), FLX-LIKE3 (FLL3), FLX-LIKE4 (FLL4)*[11,33]. *FLX* and *FLL4* are the most crucial genes in flowering time control in *Arabidopsis*[33].

In order to test whether *FLC* is present in gladiolus, the adjacent gene (*UFC*) will also be probed, along with *FLX,* which is part of the *FLC*-dependent mechanism. Therefore, the objective of this study is to identify whether *UFC* and *FLX* genes occur in the genetically diverse gladiolus germplasm of the University of Minnesota Gladiolus Breeding Program. The null hypotheses tested are: H_o1 = There is no difference among gladiolus genotypes in the existence of the *UFC* gene; H_o2 = There is no difference among gladiolus genotypes in the presence of *FLX*.

RESULTS

Rapid Generation Cycling (RGC) in gladiolus is the ability of flowering in the first year from seed as an annualized perennial. Eight such RGC genotypes were included in this study[43–45], along with six breeding genotypes and three commercial cultivars ('Vista', 'Glamini®' and 'Carolina Primrose'; Table 1). Classically, seed-propagated gladiolus have 3–5 years as juvenile, non-flowering (vegetative) seedlings before a phase change into flowering (reproductive) adults[44]. The University of Minnesota Gladiolus breeding program developed gladiolus genotypes with a reduced juvenility period and phase change to flowering in less than one year from seed[43–45].

The designed probe for the *UFC* gene in *Gladiolus* (RAPiD genomics® LLC; Gainesville, FL, USA; https://rapid-genomics.com) resulted in a total of 433 sequences; 161/433 sequences had read hits of the *UFC* gene with various percentages of coverage. Of these, 34 sequences were chosen, based on the largest length with two sequences per genotype due to the presence of two alleles per gene. These sequences represent the genomic variability of *UFC* in gladiolus. The sequences were analyzed for gene prediction using the HMM-based gene structure prediction of FGENESH using *A. thaliana* (Generic) as the specific gene-finding parameter since the gene prediction is optimized for *A. thaliana*. Results confirmed the presence of *UFC* exons of a protein and coding sequence. The *UFC* coding sequences of each gladiolus genotype were analyzed in Genoeious® by pair-alignment with its genomic sequence to determine each exon. After the pair-alignment, the coding sequence was translated and aligned in a multi-alignment process using MUSCLE alignment in the neighbor joining clustering method and CLUSTALW sequencing scheme

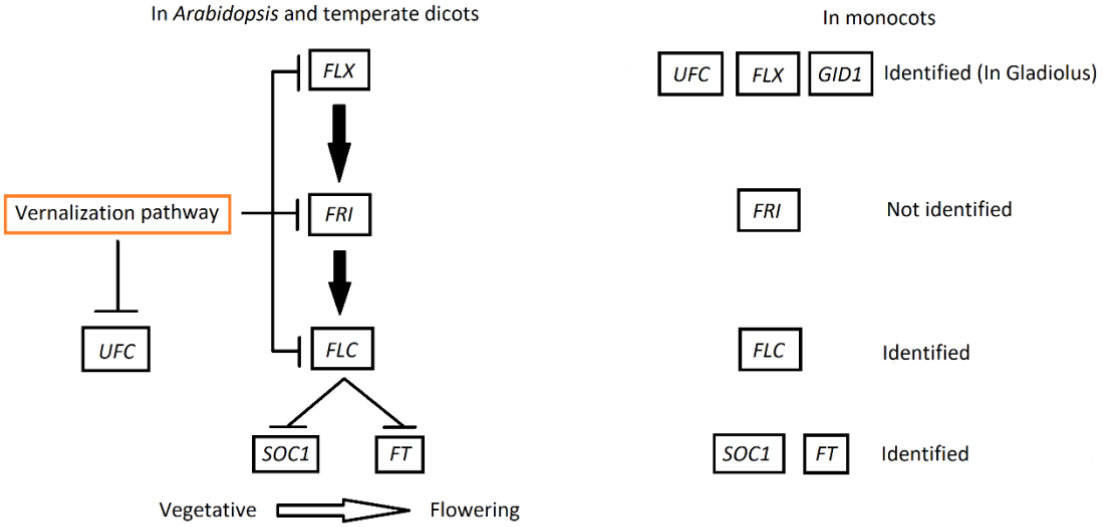

Fig. 1 Model represents portion of flowering pathway regarding the role of the *FLX* gene in flowering along with the *UFC* gene in *Arabidopsis* and temperate dicots. *FLX* upregulates *FRI* which also upregulates the expression of the *FLC* protein and suppresses flowering by repressing the expression of the floral integrator *SOC1* and *FT*. The vernalization pathway downregulates the expression of *FLX, FRI* and *FLC* genes, allowing the floral integrators to initiate flowering in vegetative state of dicots, while the vernalization pathway also downregulates the *UFC* gene[37]. In monocots, *FLX, FLC, GID1, SOC1* and *FT* have been identified[22,35,51], while *UFC* and *FLX* have just been identified in gladiolus (in the current study). *GIBBERELLIN-INSENSITIVE DWARF1 (GID1)* regulates GA synthesis. However, *FRI* was not identified either by lacking the presence of these repressor genes or monocots relying on other options of the flowering pathway genes.

Table 1. *Gladiolus* genotypes used in this study, their codes and whether they are Rapid Generation Cycling (RGC): + is for RGC genotypes and – for Non-RGC genotypes. All gladiolus genotypes were tested for the presence of *UFC*, *FLX* and *FRI* genes.

Genotype	Code	RGC
Gladiolus ×*hybridus* 21213	1	+
Gladiolus × *hybridus* 2220	2	+
Gladiolus ×*hybridus* 2231	3	+
Gladiolus ×*hybridus* 2337	4	+
Gladiolus ×*hybridus* 35314	5	+
Gladiolus ×*hybridus* 3923	6	+
Gladiolus ×*hybridus* 3931	7	+
Gladiolus × *hybridus* 74210	8	+
Gladiolus ×*hybridus* 7736	9	+
Gladiolus ×*hybridus* 28236	10	–
Gladiolus ×*hybridus* 15531	11	–
Gladiolus ×*hybridus* 20732	12	–
Gladiolus ×*hybridus* 60314	13	–
Gladiolus dalenii 'arolina Primrose'	14	–
Gladiolus ×*hybridus* 'Beatrice'	15	–
Gladiolus ×*hybridus* 'Glamini'®	16	–
Gladiolus ×*hybridus* 'Vista'	17	–

with *UFC* proteins of other monocot and dicot species: *Ananas comosus, Musa acuminata, Elaeis guineensis, Asparagus officinalis, Arabidopsis thaliana* and *Glycine max*. The *UFC* gene in *Gladiolus* ×*hybridus* was assigned to *GhUFC* as a label while genotype 14, *G. dalenii* 'Carolina Primrose', is assigned to *GdUFC*.

There are two alleles of the *UFC* gene found in gladiolus, designated as A and B. Thus, the genes are designated as *GhUFC*-A and *GhUFC*-B. The median number of amino acids of the *GhUFC*-A protein is 420 amino acids across all gladiolus genotypes, with some genotypes having less than 420 amino acids. One genotype has 451 amino acids which could be due to an insertion, while *GdUFC*-A also has 420 amino acids. The second allele, the *GhUFC*-B protein, has a range of 375 to 410 amino acids. *GdUFC*-B has 286 amino acids with an incomplete protein, missing many amino acids and a stop codon (Figs 2 & 3). *Gladiolus* genotypes 1 (*G.* ×*hybridus* 21213; Table 1) and 15 (*G.* ×*hybridus* 'Beatrice'; Table 1) were selected for pair-alignment with the species of comparison (Table 2). Similarities of identity protein sequences and the percentage of *GhUFC*-A and *GhUFC*-B occur at range of ~30% to 57% across all species (Table 2). The intron-exon organization of *GhUFC*-A in *G.* ×*hybridus* 'Beatrice' is similar to *Elaeis guineensis* and *Asparagus officinalis* in term of exon splicing (Fig. 4) while *GhUFC*-B in *G.* ×*hybridus* 21213 (genotype 1; Table 1) has some similarity with *Ananas comosus* exons splicing. The remaining genotypes fall into these two configurations of the exon; the configuration shows the location of the conserved domain for *UFC* gene *DUF966*, which is found in *Arabidopsis* and other selected species of comparison. The *DUF966* domain has the 92 and 93 amino acids of *Ananas comosus*. The multi alignment of the *UFC* protein conserved domain is conserved across species, although it is polymorphic (Fig. 5). With the high identity matching in *Gladiolus,* genotypes 1 and 15 exhibit a range of ~65% to ~86% across all investigated species for the *DUF966* domain of the *UFC* protein (Table 3). The *GhUFC*-A allele has a high identity across gladiolus genotypes (Fig. 6), with the polymorphic exception of *G.* ×*hybridus* 2231 (genotype 3; Table 1) and *G.* ×*hybridus* 3931 (genotype 7). *GhUFC*-B is also conserved and identical in sequence with *G.* ×*hybridus* 20732 (genotype 12), due to missing amino acids.

The *FLX* gene was identified in *Gladiolus* in 12/17 genotypes; 11 *G.* ×*hybridus* genotypes have *GhFLX* whereas *GdFLX* is identified in genotype 14, *G. dalenii* 'Carolina Primrose' (Table 4). The range of amino acid proteins are from 146 to 254 amino acids, missing the stop codon. Three genotype sequences in *G.* ×*hybridus* 2231, 3923, and 'Glamini'® (genotypes 3, 6 and 16, respectively; Table 1) have the longest amino acid chain. *FLX* is present in many species; in *Arabidopsis* it belongs to the *FLX* gene family, *FLX, FLOWERING LOCUS C*

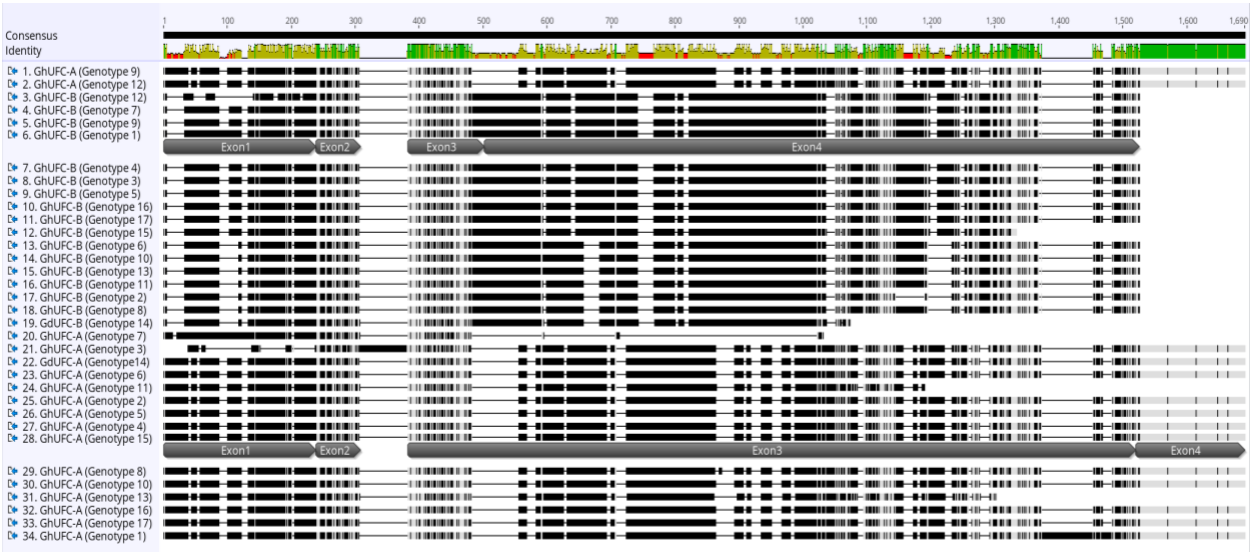

Fig. 2 Multi-alignment of *UFC* coding sequence in *G.* ×*hybridus* (*GhUFC*) and *Gladiolus dalenii (GdUFC)*, the alignment is for the 17 genotypes, each genotype has 2 alleles, allele A and allele B: *GhUFC*-A, *GdUFC*-A, *GhUFC*-B, *GdUFC*-B. Both alleles has 4 exons but allele A size is larger in coding sequence than allele B. The alignment shows insertion and missing coding sequences in some genotypes. The multi-alignment is done in MUSCLE pair-alignment using neighbor joining cluster method and CLUSTALW sequencing scheme (Geneious®).

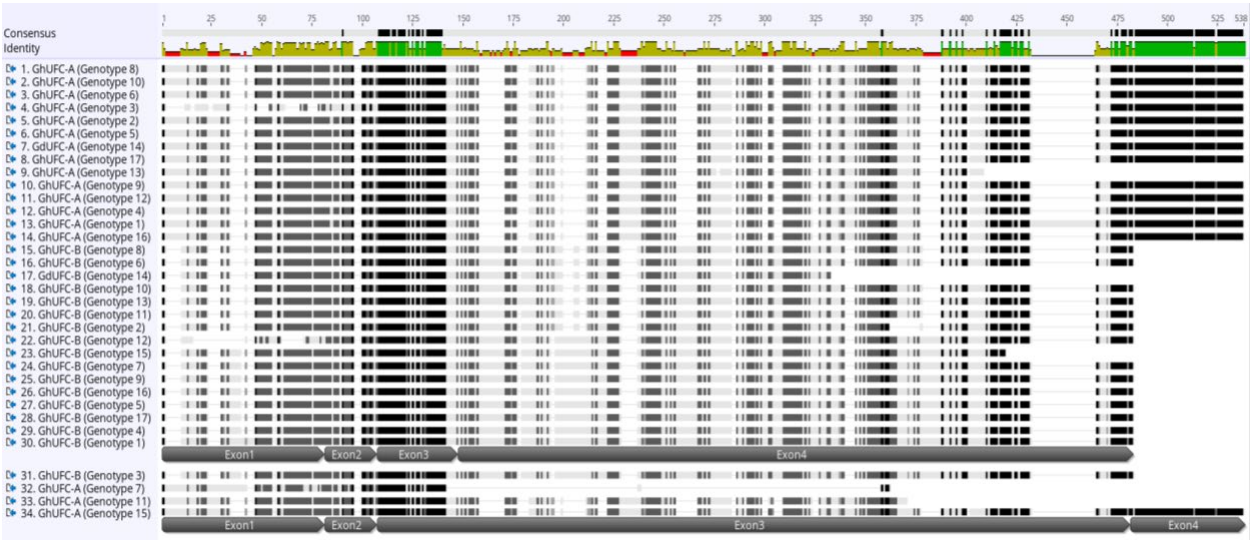

Fig. 3 Multi-alignment of *UFC* amino acid sequence in *Gladiolus* ×*hybridus* (*GhUFC*) and *G. dalenii (GdUFC)*, the alignment is for the 17 genotypes, each genotype has 2 alleles, allele A and allele B: *GhUFC*-A, *GdUFC*-A, *GhUFC*-B, *GdUFC*-B. Both alleles has 4 exons but allele A size is larger in amino acid sequence than allele B. The alignment shows insertion and missing amino acid sequences in some genotypes. The alignment identify conserved amino acid sequences (green color). The multi-alignment is done in MUSCLE pair-alignment using neighbor joining cluster method and CLUSTALW sequencing scheme (Geneious®).

Table 2. The identity of amino acid sequences and number (%) of two *UFC* proteins (*GhUFC-A*, *GhUFC-B*) in two Gladiolus (genotypes 1 and 15) in relation to other species (Gene locus/ID) through pair alignment, using MUSCLE alignment for the neighbor joining clustering method and the CLUSTALW sequencing scheme (Geneious®).

Species (Gene locus/ID)	*Gladiolus* ×*hybridus* genotype			
	Genotype 1		Genotype 15	
	GhUFC-A (%)	*GhUFC-B* (%)	*GhUFC-A* (%)	*GhUFC-B* (%)
Ananas comosus (Aco009327)	189 (33.51)	249 (53.21)	191 (34.35)	231 (52.98)
Musa acuminata (GSMUA_Achr5T28540_001)	251 (54.09)	170 (39.35)	250 (57.74)	148 (31.36)
Elaeis guineensis (p5.00_sc00099_p0095)	254 (52.05)	172 (40.86)	250 (51.23)	155 (39.85)
Asparagus officinalis (evm.model.AsparagusV1_08.3493)	213 (46.61)	148 (35.58)	213 (50.0)	135 (29.87)
Arabidopsis thaliana (AT5G10150)	137 (28.54)	129 (29.79)	138 (31.72)	117 (29.32)
Glycine max (Glyma.11G193000.1)	181 (33.64)	226 (52.19)	188 (35.67)	207 (52.01)

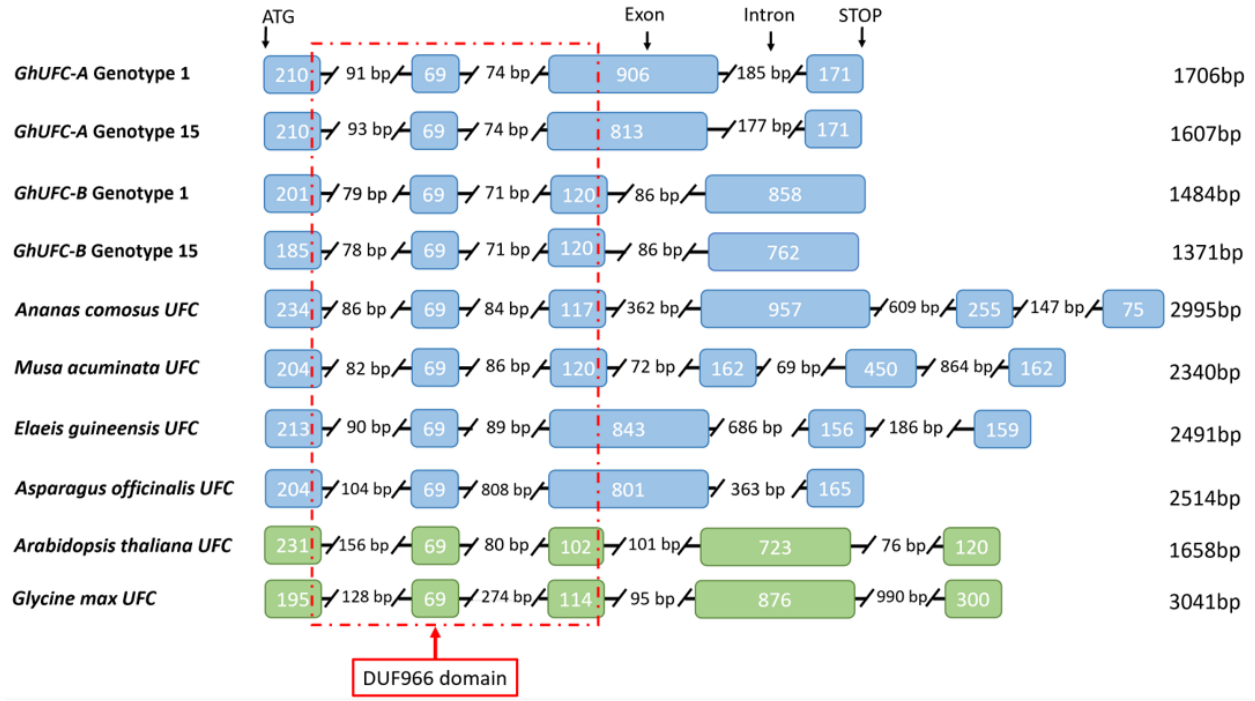

Fig. 4 Intron-exon configuration of the *UFC* genes in *Gladiolus ×hybridus* of genotypes 1 and 15 in relation to several species. Monocot species are highlighted in blue: *Ananas comosus, Musa acuminata, Elaeis guineensis* and *Asparagus officinalis*. Dicot species highlighted in green for *Arabidopsis thaliana* and *Glycine max*. Sequences were aligned based on first exon sequences. Total length of the gene's coding region is listed on the right of each respected species. The red line represents the conserved domain *DUF966* in relation to the location of the domain with exon configuration.

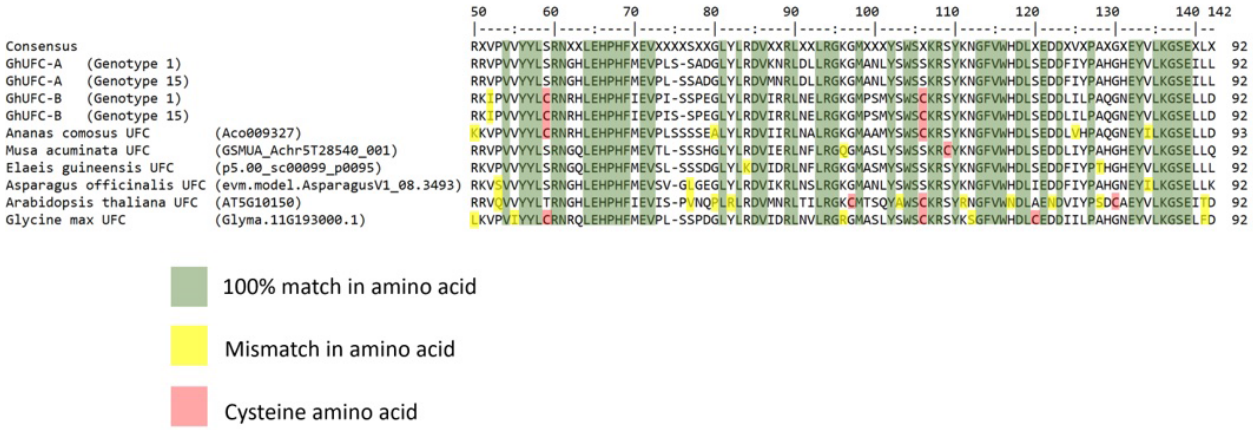

Fig. 5 Alignment of the globular region containing *DUF966* domain of *UFC* proteins from *Gladiolus ×hybridus* of genotypes 1 and 15, *Ananas comosus, Musa acuminata, Elaeis guineensis, Asparagus officinalis, Arabidopsis thaliana* and *Glycine max*. Green coloration shows identical amino acid sequence; yellow color highlights the polymorphisms while red color shows the cytosine amino acid. The conserved domain *DUF966* is 92 amino acids.

Table 3. Identity of amino acid sequences, number (%) of *UFC* proteins in the conserved domain *DUF966* in *Gladiolus* genotypes 1 and 15 in relation to other species (Gene locus/ID) through pair alignment.

Species (Gene locus/ID)	*Gladiolus* × *hybridus* genotype			
	Genotype 1		Genotype 15	
	GhUFC-A (%)	*GhUFC-B* (%)	*GhUFC-A* (%)	*GhUFC-B* (%)
Ananas comosus (Aco009327)	70 (76.09)	79 (84.95)	79 (84.95)	79 (84.95)
Musa acuminata (GSMUA_Achr5T28540_001)	78 (84.78)	71 (78.02)	78 (84.78)	71 (78.02)
Elaeis guineensis (p5.00_sc00099_p0095)	79 (85.87)	72 (79.12)	79 (85.87)	72 (79.12)
Asparagus officinalis (evm.model.AsparagusV1_08.3493)	75 (82.42)	70 (76.09)	75 (82.42)	70 (76.09)
Arabidopsis thaliana (AT5G10150)	61 (66.30)	61 (64.89)	62 (67.39)	61 (64.89)
Glycine max (Glyma.11G193000.1)	70 (76.92)	75 (82.42)	70 (76.92)	75 (81.52)

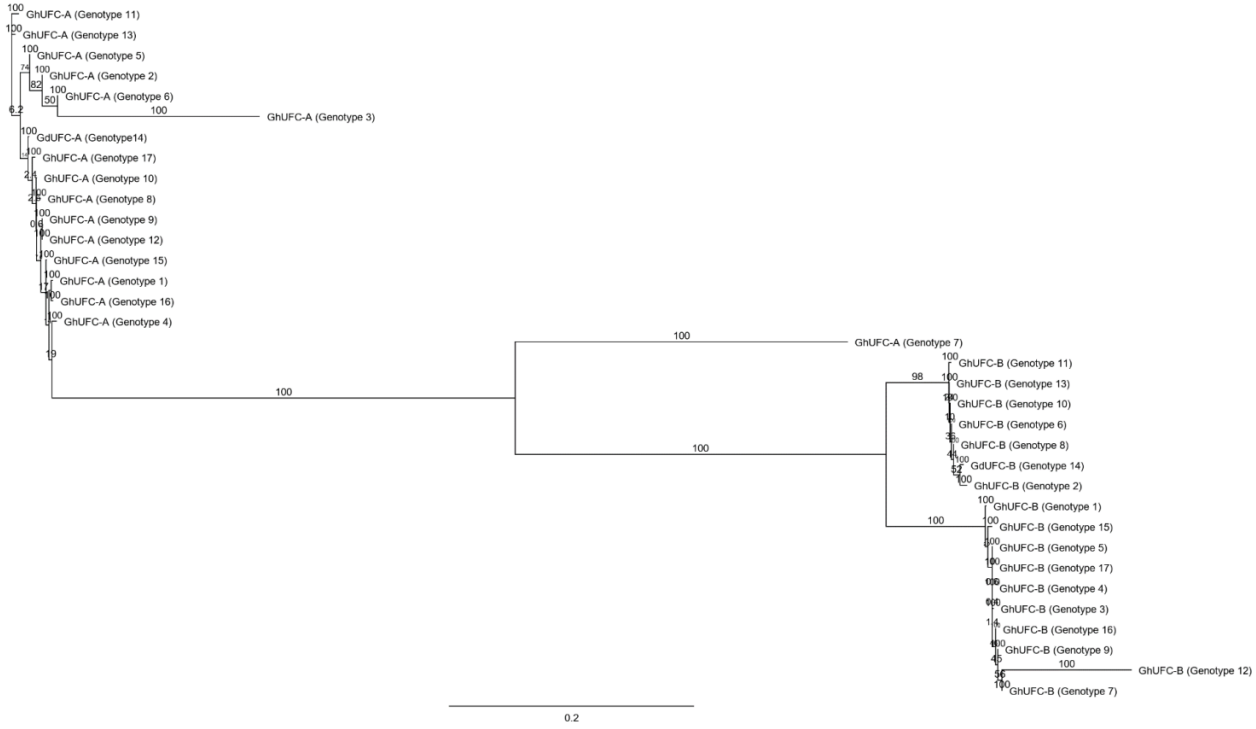

Fig. 6 The phylogenetic tree of all *UFC* genotypes in *Gladiolus*; genetic distances were computed using the Tamura-Nei method and are in the units of the number of base substitutions per site. The tree build using the Neighbor-Joining method and the bootstrap test was performed for each tree (500 replicates) and the tree format is organized and ordered with a scale bar of 0.2 (Geneious®).

Table 4. Number (%) of amino acid sequences of *GhFLX* protein in *Gladiolus* genotypes 3 and 6 (genotype 16 is identical to genotype 6) in relation to the other species through pair alignment; similarities of sequences in identity of gladiolus genotypes ranged from ~26% to ~65% across all investigated species of the whole *FLX* protein; alignment is done in MUSCLE, using the neighbor joining clustering method and the CLUSTALW sequencing scheme (Geneious®).

Species (Accession no.)	*Gladiolus* × *hybridus* genotype	
	GhFLX Genotype 3 (%)	*GhFLX* Genotype 6 and 16 (%)
Ananas comosus (XP_020095672.1)	180 (64.98%)	177 (64.60%)
Musa acuminata (XP_009420070.1)	122 (48.03%)	122 (48.03%)
Elaeis guineensis (XP_010922618.1)	132 (50.00%)	131 (49.62%)
Arabidopsis thaliana – *FLX* (NP_001154541.1)	82 (30.48%)	82 (30.48%)
Arabidopsis thaliana – *FLL1* (NP_566492.1)	135 (50.00%)	135 (50.00%)
Arabidopsis thaliana – *FLL2* (NP_001320766.1)	96 (36.09%)	94 (35.34%)
Arabidopsis thaliana – *FLL3* (NP_564678.1)	104 (34.67%)	104 (34.67%)
Arabidopsis thaliana – *FLL4* (NP_001119474.1)	67 (26.38%)	68 (26.77%)
Glycine max (Glyma.15g269300)	156 (57.14%)	155 (56.78%)

EXPRESSOR-LIKE 1 (FLL1), (FLL2), (FLL3) and (*FLL4*)[33]. Based on the pair-alignment, *GhFLX* and *GdFLX* match *FLL1* with as high as 50% amino acid identity (Table 4). The similarities of sequences in identity of gladiolus genotypes range from ~26% to ~65% across all investigated species of the entire *FLX* protein; the highest identity is the *Ananas comosus* match with ~65%. The multi-alignment for all *FLX* indicates that the tested gladiolus genotypes with the longest amino acid sequences lack exons (Fig. 7). A pair-alignment test with *Ananas comosus* – *FLX* reveals that *GhFLX G.* ×*hybridus* 'Glamini'® (genotype 16; Table 1) lacks two exons and a stop codon (Fig. 8).

DISCUSSION

The presence of a putative *UFC* gene in gladiolus is confirmed with two alleles, *GhUFC*-A and *GhUFC*-B. It is highly possible that allelic number is due to tetraploidy in cultivated gladioli ($2n = 4x = 60$)[46–48]; ploidy levels of *G. dalenii* have not been reported[46]. The cultivated *G.* ×*hybridus* are interspecific hybrids[49]. Therefore, the presence of different alleles would be expected in the diverse array of genotypes included in this study: 13 are from University of Minnesota gladiolus breeding program (interspecific hybrids) and four are commercial gladiolus cultivars with unknown ancestry and relatedness (Table 1). The *GhUFC*-A gene has ~50% identity with *Musa acuminata, Elaeis guineensis* and *Asparagus officinalis* (Table 2). The splicing of *Elaeis guineensis* and *Asparagus officinalis* exons is similar to *GhUFC*-A (Fig. 4). *GhUFC*-B gene splicing in the first 4 exons is similar to *Ananas comosus, Arabidopsis thaliana* and *Glycine max UFC* gene splicing (Fig. 4). These divergences in splicing of the *UFC* gene support *UFC* presence in gladiolus with two alleles[46]. Further tests should be done to identify

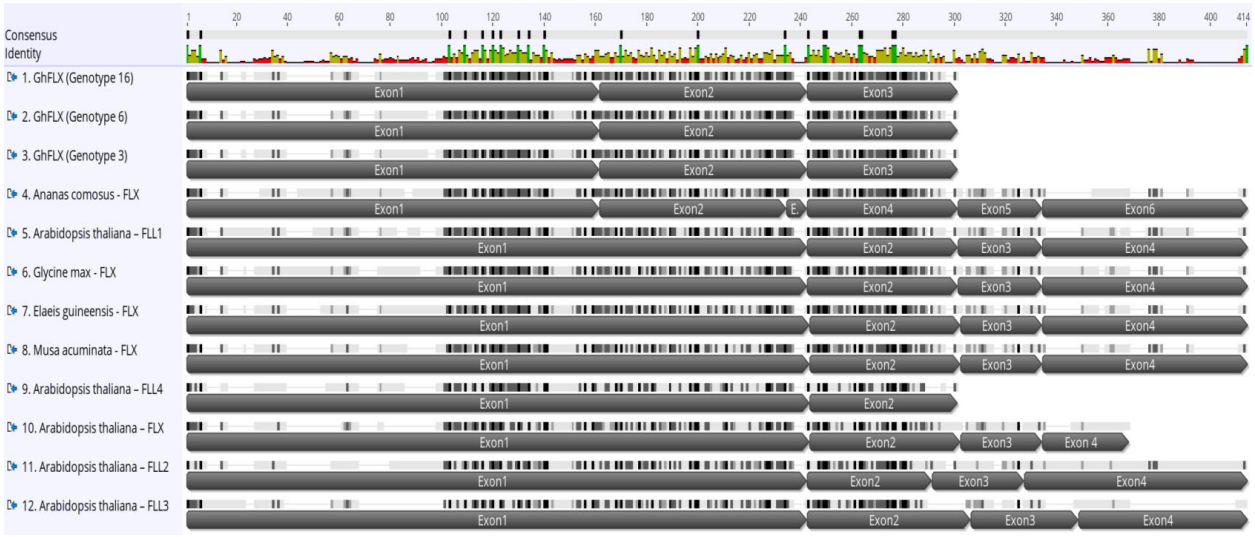

Fig. 7 Multi-alignment of *FLX* amino acid sequence in *Gladiolus* ×*hybridus* (*GhFLX*) with other species; *Arabidopsis thaliana, Ananas comosus, Elaeis guineensis, Musa acuminata* and *Glycine max*. The alignment is for the three gladiolus genotypes (3, 6 and 16) each genotype has 3 exons. The alignment shows missing amino acid sequences in gladiolus genotypes 3, 6 and 16 as amino acid sequences does not have a stop codon. The alignment identifies conserved amino acid sequences (green color). Note: *Arabidopsis thaliana – FLL4* is a functional protein which has two exons only (Lee and Amasino, 2013). The multi-alignment is done in MUSCLE pair-alignment using neighbor joining cluster method and CLUSTALW sequencing scheme (Geneious®).

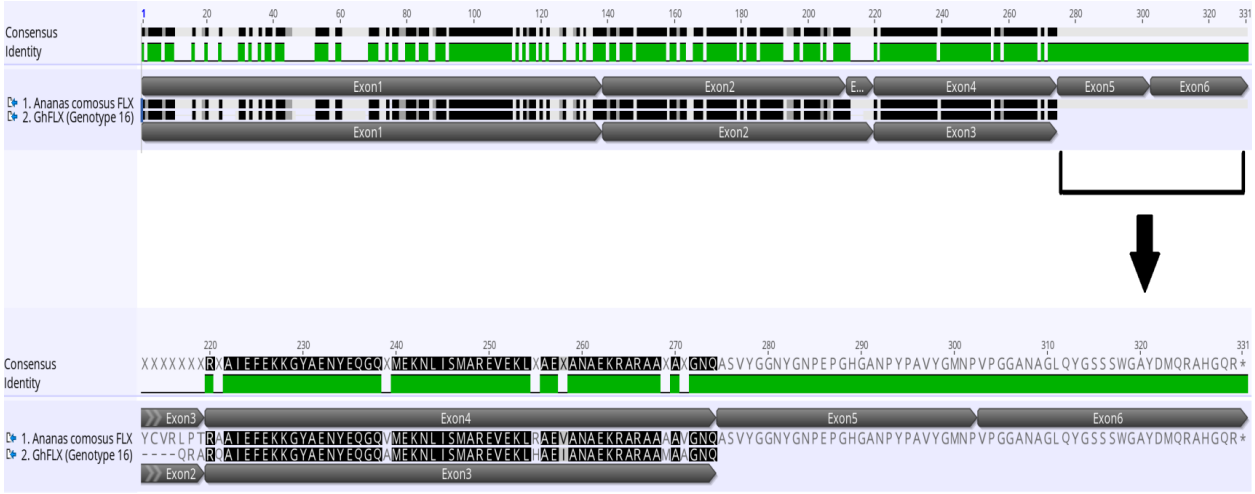

Fig. 8 Pair alignment of *FLX* protein in *Ananas comosus* and *Gladiolus* ×*hybridus* genotype 16 showing the complete *FLX* protein in *Ananas comosus* with five exons while incomplete *FLX* protein in *Gladiolus* ×*hybridus* (*GhFLX*) which lacks the remaining two exons and stop codon. The alignment is done in MUSCLE pair-alignment using neighbor joining cluster method and CLUSTALW sequencing scheme (Geneious®).

whether or not *UFC* is also present in diploid gladiolus species, such as *G. murielae, G. tristis* and *G. carneus*[50].

The *UFC* gene is responsive to vernalization by lowering expression alongside *FLC* and *DFC* in *Arabidopsis thaliana*, as all these genes are in the cluster of vernalization stimulus region[37]. *FLC* is a floral repressor, the overexpression of *FLC* results in a delay in flowering[51], while overexpression of *UFC* does not result in altering the flowering time[37]. Thus, *UFC* is adjacent to *FLC*, both are repressed by vernalization, yet *UFC* does not show any influence on flowering time. This was observed herein since the genotypes in this study include both RGC-1, which are early flowering gladiolus able to reach flowering in the first year from seed and the classical later-flowering gladiolus which requires 3-5+ years to flower from seed. The multi-alignment of *UFC* protein in RGC-1 genotypes does not show any difference from non-RGC-1 genotypes. Thus, the *UFC* gene most likely isn't involved in flowering, at least directly, which was proven in a *UFC* study in *A. thaliana*[38]. The main differences represent the differences between alleles of *UFC*-A and *UFC*-B, regardless of the gladiolus genotypes tested herein (Fig. 6).

During the winter cold period, vernalization suppress both *FLC* and *UFC* expression[37], which allows floral gene integrators to promote flowering. The hypothesis would be that, after vernalization and flowering, *UFC* protein involvement is in embryogenesis and root initiation such that growth and branching occur in the spring season (since it doesn't occur in the winter season). This could explain how *FLC* and *UFC* are

both negatively responsive to vernalization stimuli in the cluster genes area, while upstream of *UFC* is not responsive to vernalization[37].

The identification of *FLX* in gladiolus raises the question whether gladiolus follows the *Arabidopsis* dicot model of the flowering pathway. In the winter annual, *A. thaliana*, flowering is promoted after vernalization, which suppresses the floral suppressor *FLC* that is upregulated by *FRI* through activation of *FRI* complex of (*FRI, FRL1, FRL2, FES1* and *SUF4*) proteins in addition to *FLX* protein. *FLX* was proven to provide transcriptional activity for the *FRI* complex[11]. A loss of function of *FLX* in *A. thaliana* resulted in early flowering phenotypes[42], which indicates the clear role of *FLX* in flowering. The role of *FLX* in gladiolus has not been tested, particularly in RGC-1 genotypes and pedigrees. Thus, *FLX* upregulation of *FRI* in gladiolus would be a rational approach. However, *FRI* was not detected in gladiolus, using the primer design of *A. thaliana FRI* (*At4g00650*) because the *FRI* gene has not been previously detected in any monocotyledon species. Thus, the primer used from *A. thaliana* did not detect *FRI* in any of the 17 gladiolus genotypes[45]. Our results with gladiolus provide additional data in support of these previous results for *FRI* in monocots. In addition, *VRN2*, the repressor of flowering in cereals and *A. thaliana* was not detected in gladiolus, using the primer design of *Triticum monococum, T. durum* and *Hordeum vulgare* (Aljaser[45]; Supplemental Table S1, Supplemental Fig. S1 & S2). This is not conclusive evidence as the genetic similarities between *A. thaliana* and *Gladiolus* are low, given that *GhUFC*-A is ~32% and *GhFLX* is 50% identical to *A. thaliana* genes. Therefore, there could be an *FRI* gene in gladiolus but this would require better primer design to locate the gene because the presence of *GhFLX* might indicate in the presence of other flowering repressor genes as *FRI* protein upregulates *FLX* in *A. thaliana* and is part of the flowering pathway[11]. In addition, *Musa acuminata, Elaeis guineensis* and *Ananas comosus* are all monocots and tropical species which have *FLX* and *SUF4* genes as part of the *FRI* complex[51]. This indicates the presence of some of the *FRI* complex components while a lack of identification of *FRI* gene itself creates divergent possibilities: a) either there are *FRI* and *FLC* genes in these species or b) a lack of these genes and the presence of *SUF4* and *FLX* genes have other unknown flowering pathway purposes. Since *GhFLX* and *GdFLX* have similarities to *FLL1*, reaching up to 50% identity in amino acids, *FLX* gene is part of the gene family, *FLL1-FLL4*[11,33]. While the role of *FLL1* in flowering pathway is not proven, *FLX* and *FLL4* are the most crucial genes in control of flowering time in *Arabidopsis*[33]. Additionally, the relationship between *UFC* and *FLX* indicates that a mutation in *FLX* influences *UFC* expression, e.g., the *flx* mutant in *A. thaliana*[42].

The next step in this research would be to identify the *UFC* gene in diploid gladiolus species to determine if the allele is similar to *GhUFC*-A, *GhUFC*-B or a third allele. Use of diploids would simplify the study to determine the function of *UFC* protein in gladiolus by silencing and knocking out the gene. Locating the physical location of the *UFC* gene in *Gladiolus* will help in testing if there are other *UFC* genes in gladiolus as part of a *UFC* gene family, since the first discovered *UFC* gene (At5g10150) in *A. thaliana* is located in the cluster genes *UFC*, *FLC* and *DFC* on chromosome 5[37]. *UFC* is also designated *SOK2* and the other *UFC* genes are grouped in *SOK* gene family such as *SOK1* (At1g05577), *SOK3* (At2g28150), SOK4 (At3g46110) and SOK5 (At5g59790)[39].

Identifying the *FLX* gene in Eurasian species of *Gladiolus*, particularly *G. italicus, G. imbricatus* and *G. communis*, would be informative since these winter-hardy, perennial species grow in temperate habitats that require vernalization to break corm dormancy in the winter season[29,52,53]. Conversely, identifying *FLX* in subtropical gladiolus species, such as *G. crassifolius, G. laxiflorus* and *G. atropurpureus*[54], would allow comparison of *FLX* among these different habitats to further support the influence in *FLX* in the gladiolus flowering pathway. Furthermore, the use of transgene silencing of *FLX* in gladiolus would determine whether or not *FLX* influences the production of a rapid flowering phenotype gladiolus (RGC-1), as was reported in the loss of *flx* function in *A. thaliana*[42]. In conclusion, the discovery of *UFC* and *FLX* genes in gladiolus provides insight into understanding flowering and vernalization responses in ornamental, monocot geophytes.

CONCLUSIONS

Rapid generation cycling is a powerful tool that can be implemented to reduce the juvenility period in perennial crops such as gladioli and are being applied in the breeding program crop ideotype. Although it is possible to annualize a perennial crop through genetically modifying the flowering pathway by overexpression a positive flowering regulator or inserting blocker of flowering suppressor, such biotechnological methods require regulatory approval. Therefore, conventional breeding methods for early flowering are widely accepted and do not require regulation for cultivar release.

The search for *FLC* and its regulatory genes in gladiolus is a step to uncover the flowering pathway in geophytes. To uncover if *FLC* is present in *Gladiolus*, we searched for linked genes with *FLC*. In *Arabidopsis*, FLC is adjacent to two genes, *UFC* and *DFC*, both of which are downregulated by vernalization. The discovery of *UFC* in gladiolus, as well *FLX* (which upregulates *FRI*), is crucial to establish the flowering pathway. These may be early indicators of the presence of *FLC* homologue in gladiolus. Discovery of both genes are important to understand the flowering mechanism and genes in the flowering pathway to aid in breeding and selection of early flowering gladioli from seed or corms.

MATERIALS AND METHODS

Germplasm

The 17 gladiolus genotypes used in this study (Table 1) were chosen to represent a range of diversity within cultivated gladioli (*Gladiolus* ×*hybridus*, *G. dalenii*) which includes nine genotypes of Rapid Generation Cycling-1 (RGC-1; ones that flower in < 1 year from seed; [43–45]) and eight genotypes Non-RGC genotypes (that require 2 to 5 years to flower from seed). Fourteen of these genotypes are interspecific parents and hybrids created by the University of Minnesota Gladiolus Breeding Program, while three additional genotypes are commercial cultivars. Originally, 'Carolina Primrose' was introduced as *G. primulinus*. All gladiolus pedigrees used in this experiment are published[43–45] and commercial cultivars 'Beatrice' (an open-pollinated seedlings of unknown origin, occurring in a private garden, Brookfield, Vermont, in 2003). 'Beatrice' was selected for its winter hardiness, surviving in USDA Z3). 'Glamini'® a series of shorter in height than tall summer

gladiolus which blooms early and has a range of flowering colors[55]. One genotype 'Carolina Primrose' is an heirloom gladiolus, bred in 1908, with yellow flowers, collected at an old homesite in North Carolina and derived from *G. dalenii* (Table 1)[56].

Greenhouse environment

Mature gladiolus corms (competent to flower) were planted into 1,679.776 cm^2 square, deep pots (Belden Plastics, St. Paul. MN, USA) in week 23 (2017) and grown for 18 weeks. Containers were filled with SS#8-F2-RSi potting soil, 'SunGrow' (Sun Gro Horticulture, Agawam. MA, USA). The corms were grown in a long day photoperiod (0800 – 1600 HR supplied by 400-W high-pressure sodium lamps + 2200 to 0200 h night interruption, > 150 µmol m^{-2} sec^{-1}) at a minimum setpoint of 18 ºC (day/night), 70%–80% relative humidity, with irrigation accomplished using constant liquid feed (CLF) of 125 ppm N from water-soluble 20N–4.4P–16.6K (Scotts, Marysville, OH, USA) and deionized water on weekends. Standard fungicide drenches and insecticides were applied either monthly or as needed, respectively.

DNA extraction and probe design

Newly expanded gladiolus leaves were harvested, placed in an ice box and sent to RAPiD Genomics® LLC (Gainesville, FL, USA; http://rapid-genomics.com/home/) for DNA extraction, probe design, sequencing and computable analysis. Probe designs for the *UFC* gene were based on banana, *Musa acuminata* subsp. *malaccensis* accession XM_009383889, from the GenBank Nucleotide Core[57] and oil palm, *Elaeis guineensis* accession XM_010920607.2[58]. Probe design for *FLX* gene were based on oil palm, *Elaeis guineensis* accession XM_010924316.2[59] and date palm, *Phoenix dactylifera* accession XM_008801571.2[60]. The designed probe for *UFC* able to capture the locus in *Musa acuminata* and *Elaeis guineensis* by capturing the 2x coverage of the *UFC* exons in *Musa acuminata* and *Elaeis guineensis*, while the *FLX* probe captures the locus in *Elaeis guineensis* and *Phoenix dactylifera*. Probes are amplified in short reads of *UFC* and *FLX* genes in gladiolus. The reads are sequenced through the Illumina dye sequencing technique, the raw data is demultiplexed using Illuminas BCLtofastq and then assembled using MaSuRCA® software[61], creating full assembly sequence scaffolds. Afterwards, read mapping using the reference genome and blasting to filter all assembled sequences for hits to the sequences, provided the probes design (*UFC* and *FLX*). Then, count read numbers for each assembled sequence passed the filtering, accruing the final sequences for genetic analysis. Gene sequences are currently being deposited into GenBank.

Genetic analysis

The sequence data for the *UFC* and *FLX* genes used in this study were found in the genetic sequence database under the following accession/ID numbers: *Ananas comosus* (Aco009327) *UFC* gene is from the Pineapple Genomics Database[62]; *Musa acuminata* (GSMUA_Achr5T28540_001) *UFC* from the Banana Genome Hub[63]; *Elaeis guineensis* (p5.00_sc00099_p0095) *UFC* from the Malaysian Oil Palm Genome Programme[64]; *Asparagus officinalis* (evm.model.AsparagusV1_08.3493) *UFC* from the Asparagus Genome Project[65]; *Arabidopsis thaliana* (At5g10150) *UFC* from The Arabidopsis Information Resource (TAIR)[66]; *Glycine max* (Glyma.11G193000.1) *UFC* from the SoyBase[67]. The *FLX* protein was from the GenBank Nucleotide Core with accession numbers as follows: *Ananas comosus* (XP_020095672.1)[68], *Musa acuminata* (XP_009420070.1)[69], *Elaeis guineensis* (XP_010922618.1)[70], *Arabidopsis thaliana – FLX* (NP_001154541.1)[71], *Arabidopsis thaliana – FLL1* (NP_566492.1)[72], *Arabidopsis thaliana – FLL2* (NP_001320766.1)[73], *Arabidopsis thaliana – FLL3* (NP_564678.1)[74], *Arabidopsis thaliana – FLL4* (NP_001119474.1)[75] and *Glycine max* (Glyma.15g269300) *FLX* from the SoyBase[67].

Generated sequences were analyzed for gene prediction using the HMM-based gene structure prediction of FGENESH with *Arabidopsis thaliana* (Generic) as the specific gene-finding parameter. The predicted genes for *UFC* and *FLX* were analyzed in multi-alignment using Geneious© software (Biomatters Ltd, Auckland, NZ). The *UFC* protein sequences of gladiolus were analyzed for conserved domains using the Protein Homology/analogy Recognition Engine V 2.0 (Phyre2) browser[76]. Then the alignment of conserved domain was formed to compare the matching and differences in each amino acid in the sequences of gladiolus and the other comparison species. A phylogenetic tree of all *UFC* genotypes of *Gladiolus* was formed by computing the distances using the Tamura-Nei method and were in the units of the number of base substitutions per site. The tree building used the Neighbor-Joining method and a bootstrap test was performed for each tree (500 replicates).

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Conflict of interest

The authors declare that they have no conflict of interest.

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