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Selection of reference genes for flowering pathway analysis in the masting plants, *Celmisia lyallii* and *Chionochloa pallens*, under variable environmental conditions

Samarth & Paula E. Jameson 

Mast flowering is characterised by mass synchronised flowering at irregular intervals over a wide geographical area. An understanding of the molecular drivers of mast flowering requires expression analysis of key developmentally regulated gene(s). Reverse transcription-quantitative PCR is the gold standard technique used to assess expression of target gene(s) and to validate high-throughput sequencing data. Selection and validation of appropriate reference gene(s), used as normalisation factors in transcript abundance analysis, is an essential step to avoid ambiguous expression results. Eight candidate reference genes were assessed to select the best internal normalisation factors in naturally growing masting plants *Chionochloa pallens* and *Celmisia lyallii*. Statistical packages geNorm, Normfinder, BestKeeper, ΔC_t and RefFinder were used to determine the expression stability in plants translocated to different altitudes and sampled across the season. *GAPDH* and *PP2a* in *Celmisia* and *ExP* and *THP* in *Chionochloa* were found to be the best pairs of reference genes for normalisation of the gene expression data. Our study revealed environmentally-induced changes in reference gene expression, information that will be utilised as we investigate flowering phenology of masting plants under global climatic change.

Advances in sequencing have revolutionised the field of gene expression, particularly in non-model organisms^{1–4}. The onset of next-generation technologies and the rapid decrease in per-base sequencing costs has boosted the use of massively parallel cDNA sequencing (RNA-seq)^{5,6}. RNA-seq is now a cost-effective technique, enabling the acquisition of large amounts of transcriptomic data from different sources. RNA-seq can be used to determine the amount of differentially expressed transcripts, novel genes, transcription factors, alternatively spliced variants and Single Nucleotide Polymorphisms (SNPs), even in species that lack a reference genome⁷. *De novo* transcriptome assembly is particularly advantageous when studying ecological, biological, cellular and molecular processes in distantly related non-model plant species^{4,8–12}.

However, the data generated in RNA-seq or microarray analysis requires an authentic tool for validation^{13–16}. Reverse transcription quantitative polymerase chain reaction (RT-qPCR) is the gold-standard used by researchers to validate data obtained from protocols such as RNA-seq¹⁷. The sensitivity, precision, reproducibility and real-time progression of the PCR reaction allows it to be the most accurate and reliable resource for confirming expression analysis data obtained from sources such as microarrays and RNA-seq^{18,19}. It allows monitoring of expression profiles and mRNA abundance levels across different samples concurrently²⁰. Moreover, RT-qPCR can be used for the detection of low expressed transcripts which cannot be determined through high-throughput sequencing analysis²¹. It can provide either an absolute number of cDNA copies or a relative quantification of the desired transcript across samples^{22,23}. In the latter case, the amount of expression of the target gene is compared with the expression of an internal reference gene to normalise the copy numbers in different samples^{24,25}.

Strategies have been employed to accurately normalise the variation in different samples for reproducible and precise measurements including starting with an optimum amount of material, having an adequate number of biological replicates as well as appropriate technical replication. Good quality RNA, cDNA quality checks, no

School of Biological Sciences, University of Canterbury, Christchurch, New Zealand. Correspondence and requests for materials should be addressed to P.E.J. (email: paula.jameson@canterbury.ac.nz)

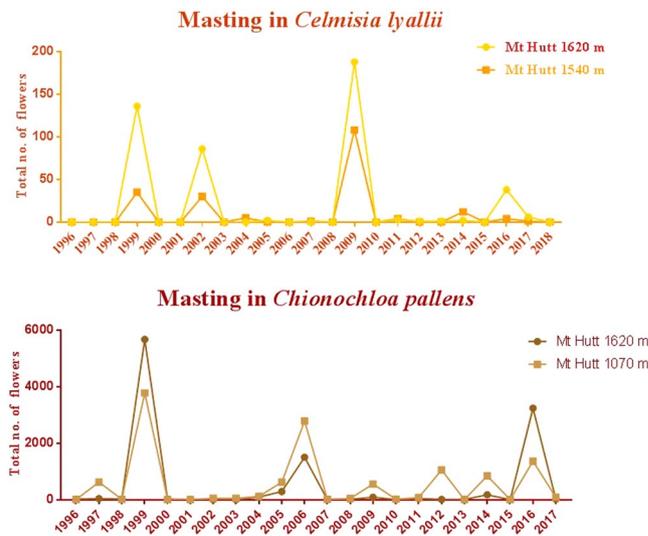


Figure 1. Mastings in *Celmisia lyallii* and *Chionochloa pallens* using data collected from the Mt Hutt field site over the past 26 years. The y-axis corresponds to the number of flowers per plant, and the x-axis corresponds to the timescale represented in years.

template and negative RT controls, an amplification factor of 2.0, qPCR efficiency ranging between 90–110%, proper controls for normalisation and statistical analysis are all also necessary²⁶. To date, normalisation of the target genes across different samples has been a key step in minimising the variations produced in qPCR^{27,28}. Normalisation involves the selection of appropriate control/reference genes, whose expression is compared to the gene of interest in the test and control samples. The reference genes, previously referred to as housekeeping genes, are genes selected because they are constitutively expressed among different tissues and cells in different conditions. The expression of an ideal reference gene is stable across tissues and remains unaffected by experimental treatments²⁹. Such genes generally belong to basic cellular processes, primary metabolism, or are cell structure determinants. Thus, many traditional reference genes used in plant-based research include *actin* (*ACT*), *elongation factor 1 α* (*EF1 α*), *glyceraldehyde-3-phosphate dehydrogenase* (*GAPDH*), *eukaryotic initiation factor 4 ϵ* (*eIF4 ϵ*), *ubiquitin* (*UBQ*), and *18S ribosomal RNA* (*U18S*).

There are numerous reports of selection and validation of reference genes in model plant species including *Arabidopsis thaliana*²⁰, *Oryza sativa*³⁰, *Helianthus annuus*³¹, *Triticum aestivum*^{32,33}, *Zea mays*³⁴ and *Glycine max*³⁵. The list also includes diverse non-model plant species including flax³⁶, white clover³⁷, bamboo³⁸, peach³⁹, *Mimulus*⁴⁰, watermelon⁴¹, grape vine⁴², and lettuce⁴³. However, in most of these cases the selection of suitable reference gene(s) was based on tightly controlled experimental conditions, whereas it has been reported that the expression of these gene(s) can vary in different tissues under different experimentally controlled conditions^{26,44–48}. Selection of such biased reference genes can result in misinterpretation of the qPCR data and, consequently, output of misleading expression data. In recent years, researchers have stressed the importance of selection and proper validation of reference genes under natural environmental conditions as a mandatory step before normalisation against the expression of the gene of interest^{27,42}. The necessity of proper validation increases in research involving non-model plant species where genomic data is unavailable.

This report deals with identification, selection and validation of suitable candidate reference genes for our study of the ecological phenomenon of masting in two non-model plant species, *Chionochloa pallens* (Poaceae) and *Celmisia lyallii* (Asteraceae)⁴⁹. Masting is synchronised intermittent flowering and production of seeds by a perennial plant population over a wide geographical area^{50,51}. *Chionochloa pallens* and *C. lyallii* are endemic to New Zealand and are the two strongest masting alpine plants (Fig. 1)⁵². Masting is a major problem in New Zealand. For example, *Nothofagus* sp. (beech) trees flower irregularly, typically once in every 2 to 6 years, resulting in the intermittent production of large quantities of seed. During the masting event, populations of seed predators, such as introduced rodents and stoats, increase dramatically. Due to the abundance of food, these invasive predators reproduce more frequently and their numbers rise rapidly. When the large populations of rodents and stoats have consumed the seeds, they turn to preying on indigenous species including kiwi, kaka, kakapo, kea and native bats. Rapid expansion of the rodent population can lead to an 80–90% decline in the population of mohua birds⁵³. Such attacks are threatening the survival of endangered birds. Moreover, climate change may have effects at both an individual and at a population level in terms of the masting phenomenon. Consequently, it is crucial to identify the molecular markers regulating flowering-time control, so they can be used as predictive markers of masting in order to launch pre-emptive conservation measures.

It has been shown that the temperature difference between the two previous summers (ΔT) can be used to predict a masting season. The ΔT model is based on the seed fall measured in 40 different masting species over 26 years⁵². To induce mast flowering, we carried out translocation experiments in the field to provide, or not, an appropriate ΔT . We gathered samples for analysis of gene expression in order to gain an understanding of the molecular controls of mast flowering. Consequently, it became crucial to identify highly stable reference genes

Gene	Gene name	Homolog identifier	GenBank ID	Protein ID	% Identity	E-value	Reference
Identification of candidate reference genes in <i>Celmisia</i>							
<i>C. lyallii</i> EF1 α	<i>Elongation factor 1α</i>	<i>Ha</i> EF1 α	XM_022150167	XP_022005859	87.21	1.43E – 52	⁶³
<i>C. lyallii</i> eIF4 ϵ	<i>Eukaryotic initiation factor 4ϵ</i>	<i>Ha</i> eIF4 ϵ	HQ430514	AEB36860	83.65	8.66E – 98	³⁴
<i>C. lyallii</i> GAPDH	<i>Glyceraldehyde-6-phosphate dehydrogenase</i>	<i>Ha</i> GAPDH	EU112608	ABW89100	89.29	0	¹⁸
<i>C. lyallii</i> SAND	<i>SAND family protein</i>	<i>Chs</i> SAND	KF752605	AHC13232	81.77	0	⁶⁴
<i>C. lyallii</i> MTP	<i>Metalloprotease</i>	<i>Chs</i> MTP	KJ524574	AJF20615	78.5	0	⁶⁴
<i>C. lyallii</i> PGK1	<i>Phosphoglyceratekinase1</i>	<i>Chs</i> PGK1	KJ524576	AJF20617	84.6	0	⁶⁴
<i>C. lyallii</i> PP2A	<i>Protein phosphatase 2A</i>	<i>Ha</i> PP2A	XM_022138979	XP_021994671	82.8	0	⁶⁴
Identification of candidate reference genes in <i>Chionochloa</i>							
<i>C. pallens</i> EF1 α	<i>Elongation factor 1α</i>	<i>Osa</i> <i>Elongation factor 1α</i>	AK061464	BAG87945	83.2	0.00E + 00	⁶³
<i>C. pallens</i> GAPDH	<i>Glyceraldehyde-6-phosphate dehydrogenase</i>	<i>Osa</i> <i>Glyceraldehyde-6-phosphate dehydrogenase</i>	AK064960	BAG89296	87.4	0.00E + 00	¹⁸
<i>C. pallens</i> NBP	<i>Nucleic acid binding protein</i>	<i>Osa</i> <i>Nucleic acid binding protein</i>	LOC_Os06g11170	XP_015644323	87.76	1.47E – 84	⁶⁶
<i>C. pallens</i> ExP	<i>Expressed protein</i>	<i>Osa</i> <i>Expressed protein</i>	LOC_Os07g02340.1	XP_015646888	85.71	6.24E – 37	⁶⁶
<i>C. pallens</i> THP	<i>Tumour homolog protein</i>	<i>Osa</i> <i>Tumour homolog protein</i>	XM_015761574	XP_015617060	77.31	3.56E – 46	⁶⁶
<i>C. pallens</i> ACT	<i>Actin 2</i>	<i>Zm</i> <i>ACT 2</i>	J01238	AAA33433.1	76.3	0.00E + 00	⁶⁵
<i>C. pallens</i> β -TUB	β -Tubulin	<i>Zm</i> <i>tubulin β-2</i>	NM_001111956	NP_001105426	97.71	0	³⁰

Table 1. Identification of the candidate reference genes from the *de novo* transcriptome assembly of *Celmisia* and *Chionochloa*.

which remained unaffected in the diverse environmental conditions of our experiment. Improper identification and validation of the reference genes would lead to errors and misinterpretation of the gene expression data. Thus, it was critical to test and validate various reference genes prior to determining the molecular basis of flowering in these non-model plant species.

In this study, novel and potentially stable genes were identified from the *de novo* transcriptome assembly⁵⁴ of *Chionochloa* and *Celmisia*. These genes were analysed based on the statistical programs geNorm⁵⁵, Normfinder⁵⁶, BestKeeper⁵⁷, ΔC_t ⁵⁸ and RefFinder⁵⁹ in order to identify and rank the best possible reference gene(s) or combination of genes for the normalisation of the qPCR data obtained from the field experiments. Potential reference genes were tested against altitudinal translocations, and changes over season and development in leaves from vegetative and flowering plants. These parameters acted as strong controls for an unbiased identification of appropriate reference genes for further gene expression analysis.

Results

A list of reference gene sequences was prepared based on previous reports of reference gene selection for plants in either the Asteraceae or Poaceae. Gene sequences encoding *elongation factor 1- α* (EF-1 α)⁶⁰, *glyceraldehyde-6-phosphate dehydrogenase* (GAPDH)²⁰, *eukaryotic initiation factor 4 ϵ* (eIF-4 ϵ)³⁴, *phosphoglycerate kinase 1* (PGK1)⁶¹, *protein phosphatase 2a* (PP2a)⁶¹, *metalloprotease* (MTP)⁶¹, *SAND*⁶¹, *actin* (ACT)⁶², β -*tubulin* (TUB)³⁰, *expressed protein* (ExP)⁶³, *nuclease-binding protein* (NBP)⁶³, and *tumour homolog protein* (THP)⁶³ were downloaded from the Genbank database and used to search for the corresponding homologous sequences in the *Celmisia* and *Chionochloa* transcriptomes (Table 1). Candidate reference gene sequences were identified from the transcriptomic data (unpublished) using TBLASTN⁶⁴. Since most of the gene sequences belonged to a protein family, the identified candidate reference gene sequences were subjected to a phylogenetic analysis using MEGA 7.0⁶⁵ to confirm their identity (Supplementary Data S1). All the putative reference gene sequences clustered with their corresponding protein family.

Primer specificity and amplification efficiency. All the designed primers for the corresponding selected reference genes with their abbreviations, primer melting temperature (T_m), amplicon length, amplification efficiency and correlation coefficient are provided in Table 2. For *18S ribosomal RNA* (*U18S*), universal primers were used for ribosomal gene quantification. All the primers were tested for amplification efficiency using the LinRegPCR software. The software allows estimation of amplification efficiencies for individual samples for a single gene primer pair. The mean amplification efficiency ranged from 95.4 to 110.6. The coefficient of correlation for the primers ranged from 0.998 to 0.9999. Additionally, the designed primers were validated for specificity from the melt curve analysis. All the primers showed a single peak in the dissociation curve indicating the presence of a single product (Supplementary Fig. S2a,b). The amplified PCR products showed single bands when run on 1.5% agarose gel (Supplementary Fig. S3). The sequences of the amplified PCR products confirmed the specificity of the primers.

Expression analysis of the candidate reference genes. The raw quantification cycle (C_q) values for each of the eight candidate reference genes in *Celmisia* and *Chionochloa* are shown in Fig. 2 (Supplementary Data S4). In *Celmisia*, the C_q values varied from 8.44 to 25.10 while the mean C_q value ranged from 10.63 to 22.44. *18S* showed the greatest variance amongst the eight candidate reference genes. In *Chionochloa*, the C_q values

Gene	Primer sequences	Length	Tm	E (amp)	Efficiency (%)	R2
Celmisia						
<i>EF</i>	5'-CCGCCACTTCCATCTCTACAATCTA-3' 5'-AGCAACACACTCATACCCTGACT-3'	244	60	1.995	99.5	0.9999
<i>eIF</i>	5'-TCCTACTTATGTTGTTGGTGTCAATGC 5'-CAGTGTAAGAGTGAGTGGTGGTCAT	164	60	2.087	108.7	0.9995
<i>GAPDH</i>	5'-ATACTTTGTCTGTCATCGTCATCTTCAC-3' 5'-CCTGGTCGGTGGATATTGTTGTAGA-3'	202	58	2.055	105.5	0.99983
<i>U18S</i>	5'-GCTGAAACTTAAAGGAATTGACGGAAG-3' 5'-TTGAAGACCAACAATTGCAATGATCTATC-3'	320	60	1.954	95.4	0.9998
<i>SAND</i>	5'-GACATGACACCATTGCTTGG-3' 5'-GAGTCAGCAACATCCTGCAA-3'	161	58	1.972	97.2	0.99998
<i>MTP</i>	5'-GCCAAGGGAAATAGATGCAA-3' 5'-TCAAGCACCAGATCAGCATC-3'	162	58	1.977	97.7	0.9999
<i>PGK1</i>	5'-GCTTCCGCTTCTGTACTCCAA-3' 5'-GGTTCCTGTCTACCCTTGATCT-3'	182	60	1.99	99	0.99996
<i>PP2A</i>	5'-CCAACGCTGCATGGTTCCTCT-3' 5'-GGTTCAGTGAGCCTGAATGTTTC-3'	191	60	2.116	110.6	0.9964
Chionochloa						
<i>EF</i>	5'-CATGCTCTCCTTGCTTTCACCTT-3' 5'-CTTGACCAGTCAAGGTGGTGGAC-3'	228	60	2.077	107.7	0.9992
<i>GAPDH</i>	5'-CTTCCTGCCCCTTAATGGAAAGTTG-3' 5'-GTCACCCTGGAAGTCAGTGGAAAC-3'	210	58	2.073	107.3	0.9991
<i>U18S</i>	5'-GCTGAAACTTAAAGGAATTGACGGAAG-3' 5'-TTGAAGACCAACAATTGCAATGATCTATC-3'	320	60	1.965	96.5	0.9999
<i>NBP</i>	5'-GGTTAGTCAAGAAGAGGCATACAAGTC-3' 5'-ACAGCAGCAGCAGATGGAGTG-3'	198	60	1.984	98.4	0.99988
<i>Exp</i>	5'-GCACCACCTCTGAAGCCAAG-3' 5'-CCACATATAAGACAACCAGTCATCG-3'	213	58	1.968	96.8	0.99998
<i>THP</i>	5'-AGAAGGAACTTGGTGGCAGACTC-3' 5'-TCCGTGAAGGTGGTTGACATTGT-3'	176	60	2.045	104.5	0.99998
<i>Actin</i>	5'-TGAGCATGGAATTGTGAGCAACTG-3' 5'-TGGATGGCAACATACATAGCAGGA-3'	198	60	2.003	100.3	0.99997
<i>B-Tubulin</i>	5'-GAGTGGAGTCATGCTGCCTAA-3' 5'-GACCTCCTTCGTGCTCATCTTCC-3'	100	60	1.974	97.4	0.9998

Table 2. Primer efficiency for housekeeping genes in *Celmisia* and *Chionochloa*.

ranged from 8.15 to 23.15 with an average C_q value ranging from 10.02 to 22.87. In *Chionochloa*, *U18S* had the highest variability amongst the eight candidate reference genes. The stability was analysed in comparison with developmental stage (vegetative and flowering), time-course (January, May, September, and March), and altitudinal changes (1520, 1350, 1070 m at Mt Hutt and near sea level at the University of Canterbury).

Stability of the candidate reference genes in *Celmisia*. A potential reference gene should have a stable expression across the developmental, altitudinal and seasonal changes. GeNorm analysis showed that *eIF* and *PP2a* were the more stable genes across all the different comparisons (Fig. 3). The optimal number of reference gene(s) required for normalisation in all the experimental manipulations was calculated using geNorm. The calculated pairwise variation for all the different experimental groups indicated two genes were sufficient for normalisation as the cut-off value was below 0.15 even when additional reference genes were added ($V2/3 = 0.000$ and $V3/4 = 0.000$). NormFinder analysis showed *SAND* and *PP2a* as the higher stability genes compared to other genes in the collected samples (Table 3), whereas Bestkeeper analysis pointed to *PP2a* as the most stable gene (Fig. 4). A similar ranking was seen when all the reference genes were analysed by the ΔC_q method (Table 4).

RefFinder generated a comprehensive list of ranking order of the candidate reference genes. In the comparative analysis for leaves from vegetative and flowering samples, *PP2a* and *GAPDH* were found to be the two most stable reference genes. Under altitudinal translocations, *PP2a*, *eIF* and *GAPDH* were the most stable candidate reference genes. However, the time-course analysis of the candidate reference genes showed *eIF*, *SAND* and *GAPDH* as the better reference genes for data normalisation. From the analysed data, *PP2a* and *GAPDH* were found to be best for gene expression data normalisation in *Celmisia* (Table 5).

Stability of reference genes in *Chionochloa*. The geNorm analysis showed *Exp* and *THP* to be the most stable reference genes in most of the experimental groups (Fig. 5). *TUB* and *GAPDH* were found to be more stable in the January samples collected from the University of Canterbury and 1070 m base of Mt Hutt, while *EF* was also found to be an equally stable reference gene in the samples collected in March and September. Similar to *Celmisia*, the pairwise variation for an optimal number of reference genes was found to be less than 0.15 for adding additional genes more than two. This suggests that two reference genes are sufficient to normalise the gene expression data from *Chionochloa* samples. NormFinder identified *EF* as the most stable gene across all the samples followed by *TUB* except for samples collected from 1070 and January time point. *Exp* and *ACT* were more stable in the

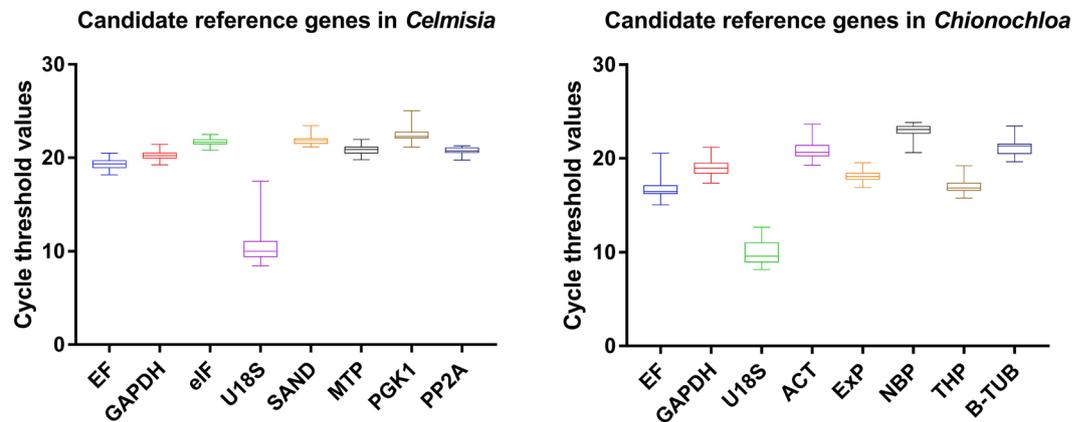


Figure 2. Cycle threshold values for candidate reference genes in *Celmisia* and *Chionochloa* are shown in box and whisker plots. The bars represent maximum and minimum C_q value.

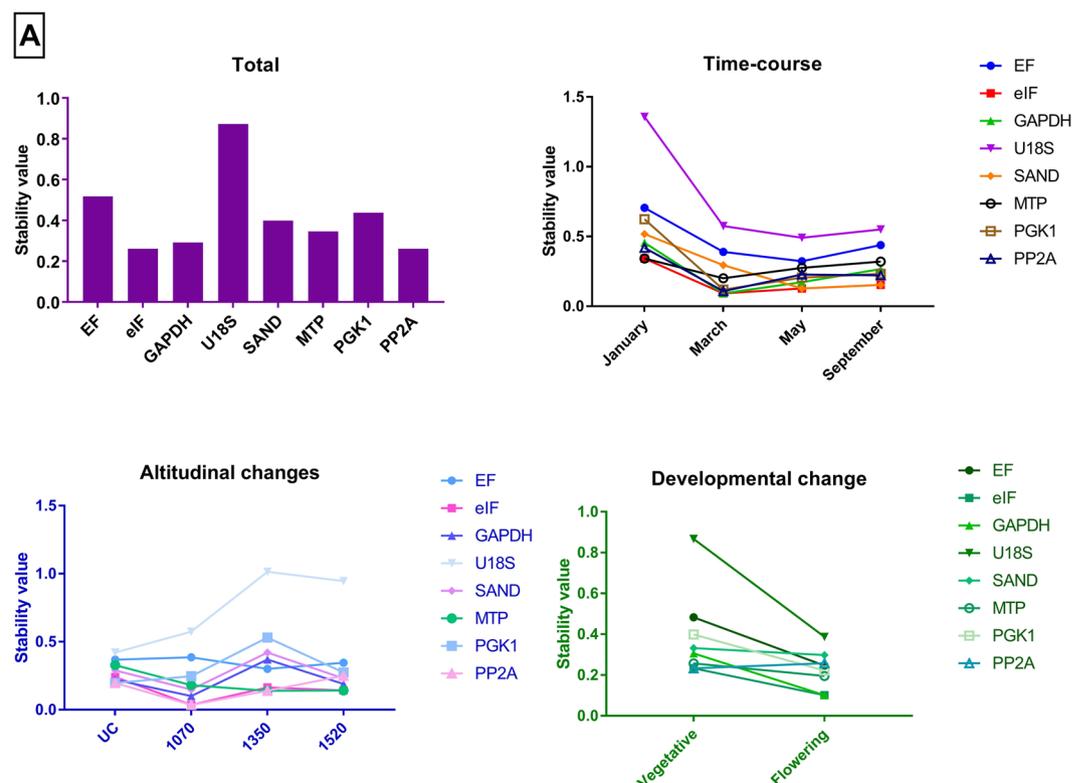


Figure 3. GeNorm analysis of the candidate reference genes in 48 collected *Celmisia* samples across different experimental groups (Total, time-course, altitude and developmental stage). The gene with the lowest stability value is the most stable gene.

January and February samples, respectively (Table 3). According to the Best Keeper analysis based on standard deviation (std dev) values, *Exp* was the most stable gene for all the samples (Fig. 6). The coefficient of variation was lowest for *NBP* in most of the samples across different experimental groups. However, the ranking of *NBP* was different in vegetative and flowering samples. Interestingly, *U18S* was ranked highest for samples collected from 1520 m base of Mt Hutt.

During the time course experimental group, *THP*, *EF*, and *GAPDH* were found to be more stable in the March, September, and May samples. The ranking for the candidate reference genes using the ΔC_t method was variable in different experimental groups as shown in Table 4. *EF* was consistently a stable gene in most of the experimental groups. Similar variability can be seen in the comprehensive ranking order generated by RefFinder across all the different experimental groups. *Exp* and *THP*, or either of them were always present in the top two positions in terms of expression stability. Based on the relative fold change in the expression levels and outputs from the statistical analysis, *Exp* and *THP* were selected as the best gene combination for normalisation of the gene expression analysis (Table 5).

Ranking	Total		1520		1350		1070		UC		January		March		May		September		Vegetative		Flowering	
	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value
Celmisia																						
1	GAPDH	0.101	PGK1	0.053	MTP	0.101	eIF	0.038	U18S	0.068	PGK1	0.100	EF	0.012	eIF	0.057	SAND	0.050	GAPDH	0.089	eIF	0.038
2	SAND	0.102	SAND	0.053	GAPDH	0.101	MTP	0.046	MTP	0.109	EF	0.124	SAND	0.032	PP2A	0.063	GAPDH	0.053	PP2A	0.089	MTP	0.092
3	PP2A	0.163	MTP	0.073	PP2A	0.191	PGK1	0.053	SAND	0.128	SAND	0.139	PP2A	0.039	SAND	0.066	U18S	0.122	PGK1	0.146	PP2A	0.118
4	eIF	0.237	U18S	0.077	EF	0.265	SAND	0.081	PP2A	0.158	GAPDH	0.145	U18S	0.079	PGK1	0.169	MTP	0.158	U18S	0.261	SAND	0.127
5	PGK1	0.330	GAPDH	0.272	PGK1	0.295	GAPDH	0.180	PGK1	0.242	MTP	0.465	eIF	0.295	GAPDH	0.187	PP2A	0.243	EF	0.311	GAPDH	0.141
6	EF	0.372	eIF	0.343	eIF	0.348	EF	0.322	GAPDH	0.259	eIF	0.599	MTP	0.325	EF	0.218	EF	0.353	eIF	0.360	PGK1	0.144
7	MTP	0.400	PP2A	0.372	U18S	0.561	U18S	0.474	EF	0.263	PP2A	0.651	PGK1	0.366	MTP	0.316	eIF	0.441	SAND	0.380	EF	0.294
8	U18S	1.319	EF	1.901	SAND	1.692	PP2A	0.757	eIF	0.355	U18S	2.281	GAPDH	0.753	U18S	0.673	PGK1	0.568	MTP	1.378	U18S	0.433
Chionochloa																						
Ranking	Total		1520		1070		UC		January		February		March		May		September		Vegetative		Flowering	
	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value
1	TUB	0.309	TUB	0.208	THP	0.078	TUB	0.201	NBP	0.037	ExP	0.050	ExP	0.096	ExP	0.041	ExP	0.206	THP	0.194	THP	0.296
2	ExP	0.325	THP	0.210	ACT	0.128	NBP	0.239	THP	0.068	EF	0.143	THP	0.197	TUB	0.041	U18S	0.303	TUB	0.209	ExP	0.363
3	THP	0.365	GAPDH	0.211	EF	0.168	U18S	0.251	EF	0.152	U18S	0.143	EF	0.262	THP	0.291	NBP	0.304	ACT	0.353	TUB	0.372
4	EF	0.370	ACT	0.264	NBP	0.326	GAPDH	0.278	ExP	0.167	NBP	0.161	GAPDH	0.410	GAPDH	0.307	EF	0.386	U18S	0.411	NBP	0.387
5	GAPDH	0.384	NBP	0.299	GAPDH	0.480	ACT	0.401	U18S	0.288	GAPDH	0.183	NBP	0.412	NBP	0.351	TUB	0.458	GAPDH	0.432	GAPDH	0.411
6	NBP	0.432	U18S	0.364	ExP	0.514	ExP	0.482	ACT	0.585	ACT	0.195	ACT	0.435	ACT	0.439	GAPDH	0.462	EF	0.433	EF	0.449
7	ACT	0.479	ExP	0.588	TUB	0.788	EF	0.484	TUB	0.820	THP	0.431	U18S	0.496	U18S	0.446	ACT	0.543	ExP	0.437	U18S	0.534
8	U18S	0.887	EF	0.734	U18S	1.064	THP	0.726	GAPDH	1.539	TUB	0.495	TUB	0.528	EF	0.805	THP	0.589	NBP	0.833	ACT	0.966

Table 3. NormFinder analysis for selection of candidate reference gene(s) in *Celmisia* and *Chionochloa*.

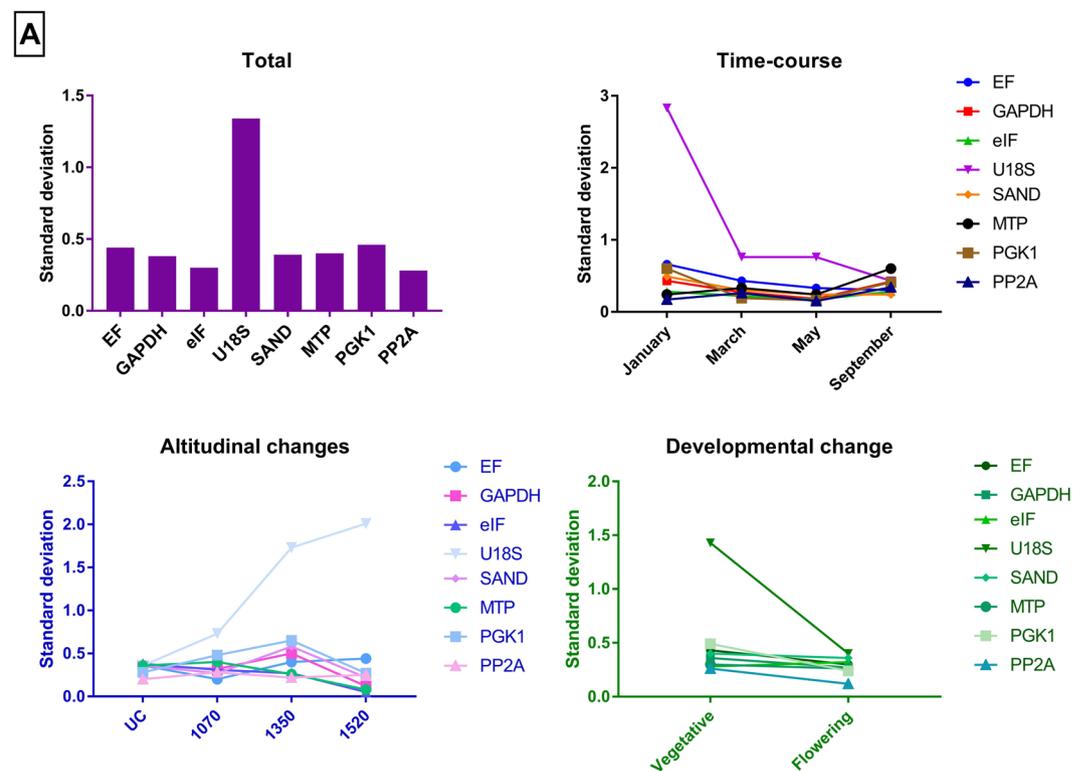


Figure 4. BestKeeper analysis of the candidate reference genes in 48 *Celmisia* samples tested across different experimental groups (Total, time-course, altitude and developmental stage). The gene with the lowest standard deviation value is the most stable gene.

Validation of the selected reference gene. The reliability of the selected reference genes was further verified by analysing the expression profile of *CONSTANS* (*CO*) and *Heading date 1* (*Hd1*). *Heading date 1* is an orthologue of *CO* present in monocots⁶⁶. Relative expression levels of *CO* and *Hd1* were normalised using the

Ranking	Total		1520		1350		1070		UC		January		March		May		September		Vegetative		Flowering	
	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev						
Celmisia																						
1	GAPDH	0.63	SAND	0.61	PP2A	0.71	PP2A	0.4	PP2A	0.32	GAPDH	0.95	eIF	0.39	GAPDH	0.36	SAND	0.4	GAPDH	0.62	MTP	0.29
2	PP2A	0.64	PP2A	0.63	GAPDH	0.73	SAND	0.4	PGK1	0.34	PP2A	0.96	PGK1	0.4	eIF	0.36	PP2A	0.41	PP2A	0.62	GAPDH	0.33
3	eIF	0.66	GAPDH	0.66	MTP	0.74	eIF	0.4	GAPDH	0.35	SAND	1	PP2A	0.4	SAND	0.38	eIF	0.42	SAND	0.64	PGK1	0.33
4	SAND	0.69	PGK1	0.66	eIF	0.74	GAPDH	0.42	eIF	0.38	eIF	1.03	GAPDH	0.4	PGK1	0.4	PGK1	0.43	eIF	0.65	PP2A	0.33
5	PGK1	0.77	MTP	0.71	SAND	0.8	MTP	0.45	SAND	0.45	MTP	1.15	MTP	0.57	PP2A	0.41	GAPDH	0.5	MTP	0.7	eIF	0.35
6	MTP	0.78	eIF	0.74	EF	0.87	PGK1	0.59	MTP	0.46	EF	1.18	SAND	0.61	EF	0.5	MTP	0.6	PGK1	0.8	EF	0.35
7	EF	0.87	EF	0.81	PGK1	1.07	EF	0.8	EF	0.48	PGK1	1.27	EF	0.69	MTP	0.53	EF	0.74	EF	0.87	SAND	0.47
8	U18S	1.94	U18S	2.75	U18S	2.47	U18S	1.14	U18S	0.57	U18S	3.32	U18S	1.13	U18S	0.99	U18S	0.88	U18S	2.02	U18S	0.65
Chionochloa																						
Ranking	Total		1520		1070		UC		January		February		March		May		September		Vegetative		Flowering	
	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev	Gene	Std dev						
1	ExP	0.8	GAPDH	0.78	TUB	0.75	EF	0.66	GAPDH	0.78	ACT	0.36	EF	0.53	TUB	0.57	EF	0.64	TUB	0.71	EF	0.81
2	TUB	0.83	TUB	0.84	ExP	0.8	NBP	0.69	TUB	0.84	ExP	0.39	THP	0.59	EF	0.57	ExP	0.68	ExP	0.72	THP	0.86
3	THP	0.83	ExP	0.86	THP	0.82	TUB	0.7	ExP	0.86	U18S	0.4	GAPDH	0.63	GAPDH	0.65	THP	0.7	THP	0.79	ExP	0.87
4	EF	0.83	THP	0.89	GAPDH	0.86	ExP	0.7	THP	0.89	EF	0.42	ExP	0.73	ExP	0.68	TUB	0.81	EF	0.85	GAPDH	0.89
5	GAPDH	0.87	NBP	1	ACT	0.94	THP	0.8	NBP	1	NBP	0.42	ACT	0.78	ACT	0.72	ACT	0.86	ACT	0.86	TUB	0.93
6	NBP	0.92	ACT	1.06	NBP	1.02	ACT	0.88	ACT	1.06	TUB	0.47	NBP	0.81	THP	0.76	GAPDH	0.88	GAPDH	0.86	NBP	0.98
7	ACT	0.93	EF	1.29	EF	1.22	GAPDH	0.9	EF	1.29	GAPDH	0.67	U18S	0.86	NBP	0.83	NBP	0.94	NBP	0.88	ACT	1.01
8	U18S	1.39	U18S	2.26	U18S	1.6	U18S	1.16	U18S	2.26	THP	0.76	TUB	0.9	U18S	1.22	U18S	1.02	U18S	1.3	U18S	1.5

Table 4. ΔCt analysis for selection of candidate reference gene(s) in *Celmisia* and *Chionochloa*.

Ranking	Total		1520		1350		1070		UC		January		March		May		September		Vegetative		Flowering	
	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value
Celmisia																						
1	PP2A	1.57	SAND	2	PP2A	1.32	PP2A	1.32	PP2A	1	PP2A	1.86	eIF	1.41	SAND	1.86	eIF	1.19	PP2A	1.565	MTP	1.73
2	GAPDH	1.73	eIF	2.55	MTP	2.21	eIF	2.63	PGK1	1.68	GAPDH	2.63	SAND	2	eIF	2.06	GAPDH	1.57	GAPDH	2.378	GAPDH	2.21
3	eIF	2.21	MTP	2.78	GAPDH	3.16	SAND	2.63	GAPDH	3.57	MTP	2.78	GAPDH	2.21	PP2A	2.45	PGK1	2.91	eIF	2.378	PP2A	2.63
4	SAND	3.56	PP2A	3.16	SAND	3.66	GAPDH	3.31	SAND	4.4	eIF	2.78	PP2A	3.22	PGK1	3.34	PP2A	4.23	SAND	2.943	PGK1	3.13
5	MTP	5.38	GAPDH	3.41	eIF	3.66	EF	4.3	eIF	4.76	EF	4.14	PGK1	5.23	GAPDH	3.36	MTP	5.23	MTP	3.873	eIF	3.66
6	PGK1	5.69	PGK1	4.9	EF	4.9	MTP	5.23	MTP	5.96	SAND	4.16	MTP	5.73	EF	6.19	SAND	5.66	PGK1	6.236	EF	5.23
7	EF	6.48	EF	5.66	PGK1	7	PGK1	6.24	U18S	6.73	PGK1	6.48	EF	7	MTP	6.48	EF	6.45	EF	6.735	SAND	7
8	U18S	8	U18S	8	U18S	8	U18S	8	EF	6.74	U18S	8	U18S	8	U18S	8	U18S	7.74	U18S	8	U18S	8
Chionochloa																						
Ranking	Total		1520		1070		UC		January		February		March		May		September		Vegetative		Flowering	
	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value	Gene	M-value
1	ExP	1.19	THP	1.5	TUB	1.57	EF	0.201	GAPDH	1.57	ACT	1.73	EF	1.19	GAPDH	2.28	EF	1	ExP	1.41	THP	1.68
2	THP	2.06	ExP	2.45	ExP	2.63	GAPDH	0.482	ExP	2.06	ExP	1.86	THP	1.41	ExP	2.51	ExP	2.21	THP	2.06	ExP	1.97
3	TUB	2.78	EF	2.91	GAPDH	2.99	U18S	0.726	TUB	2.34	NBP	2.34	GAPDH	3.41	TUB	2.63	THP	3.22	TUB	2.24	EF	1.97
4	EF	3.72	ACT	3.98	THP	3.22	ACT	0.484	NBP	3.34	U18S	3.13	ExP	3.72	EF	2.66	TUB	3.72	ACT	4.36	GAPDH	3.46
5	NBP	5.24	U18S	4.76	NBP	3.83	ExP	0.278	THP	4	EF	4.47	ACT	5.23	THP	3.35	ACT	4.95	EF	5.09	TUB	5.38
6	ACT	5.6	GAPDH	4.76	ACT	5.44	NBP	0.239	ACT	6	TUB	5.73	NBP	5.42	ACT	4.68	GAPDH	5.89	NBP	5.21	NBP	5.63
7	GAPDH	5.69	TUB	5.05	U18S	5.66	THP	0.401	EF	7.24	GAPDH	7.24	U18S	7.24	NBP	6.74	U18S	6.26	GAPDH	5.83	ACT	6.19
8	U18S	8	NBP	7	EF	7.24	TUB	0.251	U18S	7.74	THP	7.74	TUB	7.74	U18S	8	NBP	7	U18S	7.74	U18S	8

Table 5. Comprehensive ranking of candidate reference genes in *Celmisia* and *Chionochloa*.

normalisation factor derived from the two most stable reference genes (*PP2a* and *GAPDH* in *Celmisia*, and *ExP* and *THP* in *Chionochloa*) (Fig. 7), and the least stable-reference gene (*U18S*) (Fig. 8).

The expression pattern of *CO* in *Celmisia* was generally found to be similar to its ortholog of *Hd1* in *Chionochloa* when normalised with selected reference genes in the respective species (Fig. 7). The expression

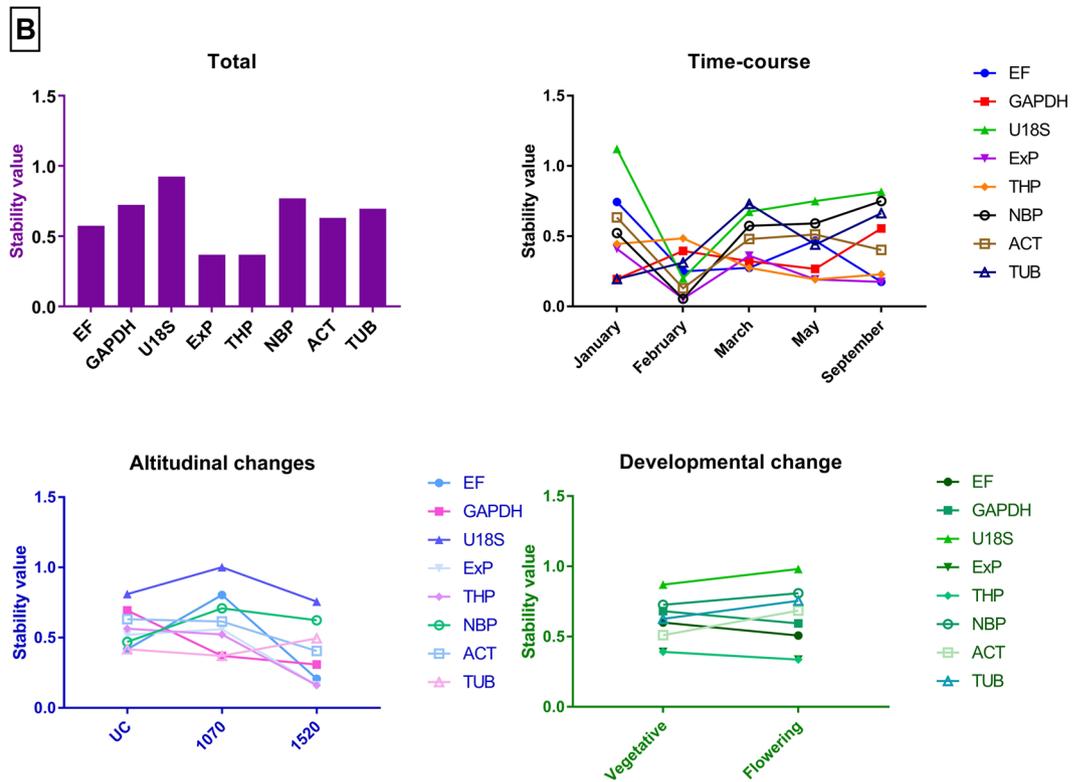


Figure 5. GeNorm analysis of the candidate reference genes in 54 collected *Chionochloa* samples across different experimental groups (Total, time-course, altitude and developmental stage). The gene with the lowest stability value is the most stable gene.

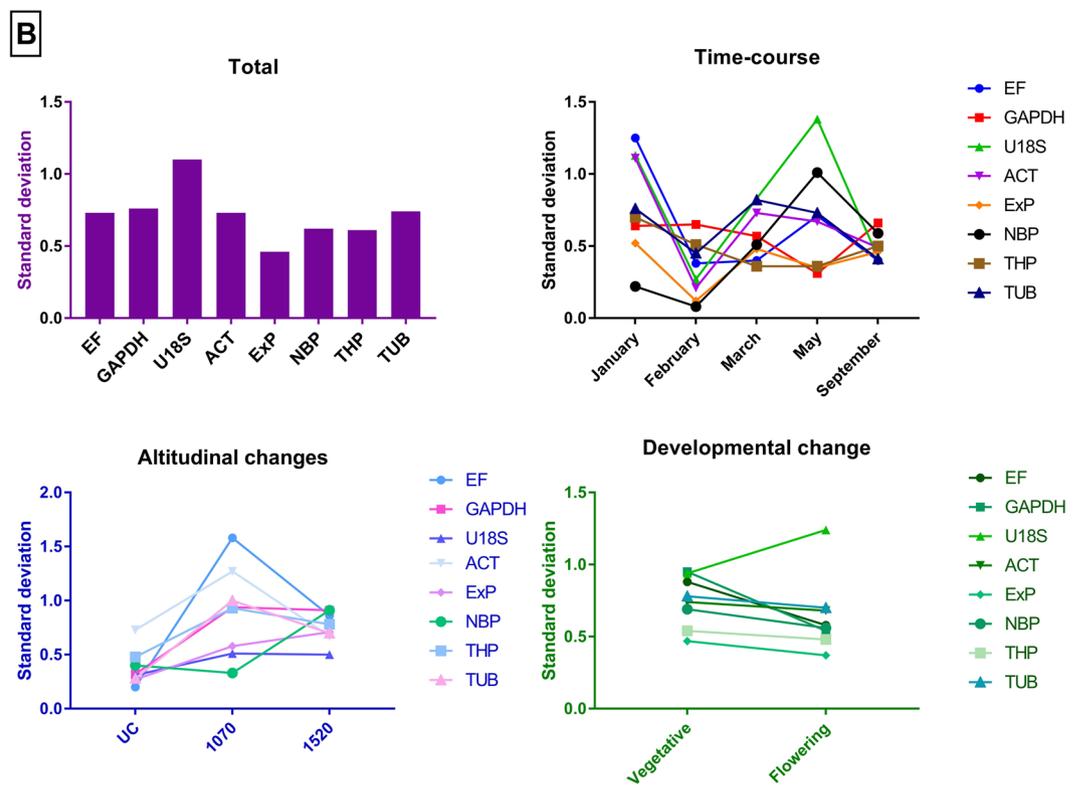


Figure 6. BestKeeper analysis of the candidate reference genes in 54 *Chionochloa* samples tested across different experimental groups (Total, time-course, altitude and developmental stage). The gene with the lowest standard deviation value is the most stable gene.

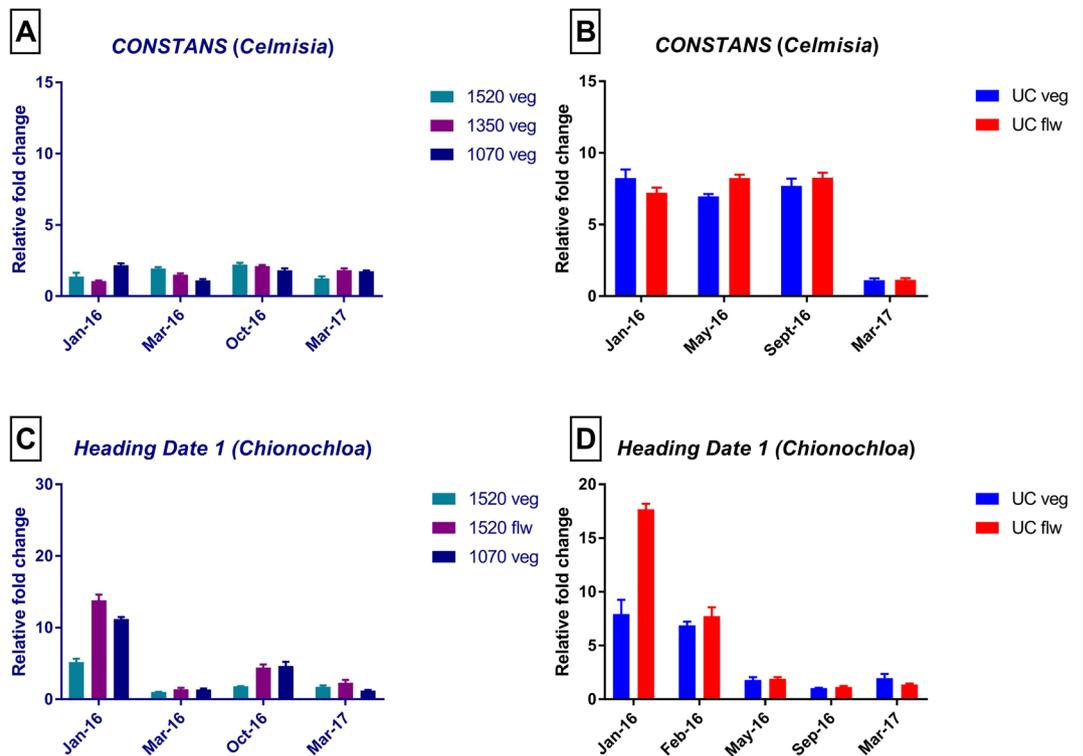


Figure 7. Validation of the selected reference genes in *Celmisia* and *Chionochloa*. (A) Expression analysis of *CO* in samples collected from Mt Hutt using *PP2a* and *GAPDH*. (B) Expression analysis of *CO* in vegetative and flowering samples collected from the University of Canterbury using *PP2a* and *GAPDH*. (C) Expression analysis of *Hd1* in vegetative and flowering samples collected from Mt Hutt using *ExP* and *THP*. (D) Expression analysis of *Hd1* in vegetative and flowering samples collected from the University of Canterbury using *ExP* and *THP*. The data represent the mean \pm S.D. of two independent biological replicates, each with three technical replicates. Legends ending with flw or veg corresponds to the fate of the leaves used in the analysis as flowering or vegetative respectively.

patterns of *CO* and *Hd1* varied across the season (Fig. 7B,D) (P -value < 0.0001). The expression of *Hd1* was significantly greater in the samples collected in January compared to other time points from the plants at the University of Canterbury (UC) and Mt Hutt (P -value < 0.0001) (Fig. 7C and D). Irrespective of whether the plants subsequently flowered or not, the patterns for *CO* and *Hd1* expression were the same in the leaves collected over time from UC in *Celmisia* (Fig. 7B) (P -value < 0.0001 , $F = 349.6$). Expression of *Hd1* was much greater in leaves from the *Chionochloa* plants that flowered in the next season compared to leaves from plants that remained vegetative.

The expression data was also normalised using *U18S*, the least stable candidate gene in *Chionochloa* and *Celmisia*. Because the expression of *U18S* was itself highly variable, this is reflected in the variable expression of *CO* and *Hd1* in both the species in all the experimental groups as seen in the relative fold changes when comparing the y-axes in Figs 7 and 8. There were no significant differences in the expression of *CO* or *Hd1* at different time points in either species. Consequently, normalising the data using *U18S* would lead to inaccurate conclusions.

Discussion

RT-qPCR is a widely used technique to study transcript abundance of a particular gene in distinct biological samples. Due to its high sensitivity and reliability, it is considered to be the gold standard for detecting and quantifying the expression pattern of gene(s) of interest. The choice of an appropriate normalisation factor is a key step in the RT-qPCR analysis to obtain accurate interpretation of the results. The normalisation factor is based on reference gene(s). Reference gene(s) are selected based on the prerequisite that they will be stably expressed in all the tissues/cells, and unaffected by experimental manipulation. Thus, the majority of the traditionally used reference genes are metabolic genes involved with basal cellular activities such as carbon metabolism, cellular structure maintenance and protein translation. *Actin*, *elongation factor 1 α* , *β -tubulin*, *glyceraldehyde-3-phosphate dehydrogenase* and *ubiquitin* have been repeatedly used for RT-qPCR analysis in plants, as they are expected to be uniformly expressed in different tissues and organs. Consequently, variability in the expression of a reference gene can demonstrate the variability introduced to samples due to imperfections of the technology and sample preparation steps.

There are several steps during an RT-qPCR analysis where it is possible to introduce variations in the final results including mRNA extractions, cDNA synthesis, the PCR procedure, and design of primers⁶⁷. Most researchers would agree that these potential variations can be reduced through the use of appropriate reference

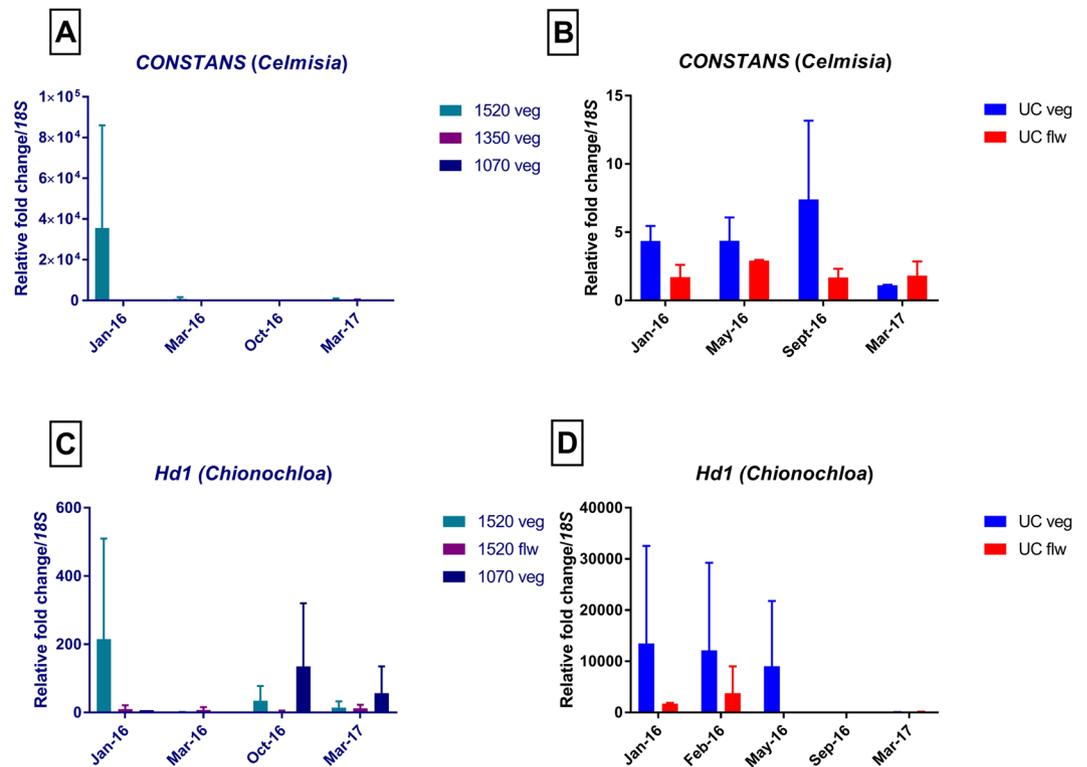


Figure 8. Expression analysis of *CO* and *Hd1* in *Celmisia* and *Chionochloa* using the least stable reference gene, *18S ribosomal gene*. **(A)** *CO* expression in samples collected from Mt Hutt. **(B)** *CO* expression in vegetative and flowering samples collected from the University of Canterbury. **(C)** *Hd1* expression in vegetative and flowering samples collected from Mt Hutt. **(D)** *Hd1* expression in vegetative and flowering samples collected from the University of Canterbury. The data represent the mean \pm S.D. of two independent biological replicates, each with three technical replicates. Legends ending with flw or veg corresponds to the fate of the leaves used in the analysis as flowering or vegetative respectively.

genes. These reference genes, with proper validation, can be used to correct such methodological errors in an effective and convenient manner. This ensures that any variation is covered to a similar extent in controls and experimental treatments.

However, there is no single gene known that remains stable in diverse experimental conditions, and use of a single reference gene as the normalisation factor can lead to accumulation of relatively large errors in the interpretation of the gene expression data⁴⁷. Unfortunately, an awareness of the importance of systematic validation of appropriate reference genes has still not completely permeated the scientific community. In one study in 2008, only 3.2% of 188 papers published in plant science journals from July 2007 to December 2007 used a validated reference gene²⁷. Even today, many of the RT-qPCR analyses published in *Plant Physiology* and *The Plant Cell* in the past six months have used only a single reference gene, many of which were not reported to have been validated (Supplementary Fig. S5).

There are already reports of traditional reference genes that, while shown to be stably expressed under various biotic and abiotic stresses, have differential expression under other experimental conditions^{35,43,47}. Studies using *Arabidopsis* have demonstrated variations in reference gene stability under different experimental conditions²⁰. Similar studies have also been published in rice³⁰, citrus⁶⁸, pea⁶⁹, ryegrass⁷⁰, carrot⁷¹, soybean^{45,46} and maize³⁴ suggesting variation in the ranking of the reference gene stability can be attributed to different stresses applied to the plants of interest. In one such study in citrus, different pairs of reference genes provided better normalisation factors under different biotic stresses⁶⁸. Such studies show that the use of non-statistically validated reference genes can negatively impact the normalisation procedure and introduce errors in the expression patterns of the genes of interest. The most appropriate reference gene(s) should be properly identified and validated in all biological samples across the different experimental groups.

However, field conditions differ from controlled environment conditions, and this adds another level of complexity to the selection of appropriate reference genes. Systematic validation of the reference genes in real-time PCR analyses in non-model plant species in the field is required as pointed out in Tashiro *et al.*⁴². Tashiro *et al.*, identified stably expressed genes in different grapevine cultivars emphasising the importance of validation of ranking stability of reference genes in a heterologous plant population. There are limited reports of selection of reference genes for normalisation in experimentally manipulated plants in the field^{42,70,72}, and no such study has been published for masting plants.

We aimed to identify stably expressed genes to avoid the limitations imposed by (a) inappropriate selection, (b) improper validation, and (c) field conditions in order to study gene expression in the non-model masting

plants under prevailing environmental conditions. Plants used in this study, *Chionochloa* and *Celmisia*, were translocated to different altitudes to provide conditions predicted to promote flowering⁵². It was interesting to note that only the *Celmisia* and *Chionochloa* plants translocated to sea level flowered heavily, along with a few of the *Chionochloa* plants translocated to the 1520 m site at Mt Hutt. Candidate reference genes were selected and analysed in different temporal-spatial manipulations for both of the species using four different statistical algorithms - geNorm, NormFinder, BestKeeper, and ΔC_t . Since the ranking of stably expressed genes can differ across these four algorithms due to varied strengths and application conditions of each of the software^{55,58}, it is often difficult for researchers to identify the most stable reference genes. In cases where multiple algorithms are used, a comprehensive ranking is required for the selection of appropriate reference genes. RefFinder is a web-based analysis tool that generates a final comprehensive ranking of reference genes based on their stability output as evaluated by the four independent algorithms. The global ranking is based on the integration of the geometric mean (GM) of the ranking values obtained from the four statistical tools. Importantly, RefFinder evaluates the ranking independent of the unrelated cut-offs and appropriate weights of the GM of the ranking values^{28,73}.

The candidate reference genes were selected based on their previous validation in related species specifically in response to temperature shifts. Even then, the stability ranking of the candidate reference genes in *Celmisia* and *Chionochloa*, as determined by geNorm, NormFinder, BestKeeper and ΔC_t , was found to be variable in different experimental groups. This variation may arise due to the different limitations of the statistical algorithms used in each program.

In *Chionochloa*, the geNorm analysis suggests that all the selected reference genes could be used as a potential normalisation factor as they have stability values of less than 1.5, an indicator of stably expressed reference genes. Reference genes showed a similar range of stability values during altitudinal and developmental shifts (Fig. 3). During the time-course analysis, an increase in the stability of reference genes was observed from January to February. Such change can be attributed to post-translocation effects. Since most of the selected reference genes regulate internal metabolism of the plants, the increase in the stability of the reference genes may then correspond to a plant's ability to adapt to the new environment. Furthermore, either *Exp* or *THP* regularly showed up as the best normalisation factor for all the collected *Chionochloa* samples with other statistical tests as well. Two reference genes, *Exp* and *THP*, were found to be the most stably transcribed among all the samples, as previously reported for rice as well⁶³ – both rice and *Chionochloa* are in the Poaceae. Since the pairwise variation for V3/4 was less than 0.15, *Exp* and *THP* were selected as the best candidate reference genes to be used as the normalisation factor for gene expression analysis in *Chionochloa*. *Exp* and *THP* code for an esterase and a mercury-dependent metal transporter, respectively. Esterases are generally associated with fatty acid degradation and modification. *THP*, a metal transporter protein, should have a stable expression under our experimental conditions. In our study, neither of these factors changed significantly in response to temperature changes.

In *Celmisia*, ranking of the candidate genes in all the experimental groups (Total) was found to be similar when analysed by the four algorithms. GeNorm identified *eIF* as the most stable gene in all the experimental samples. The stability ranking was found to be more variable in the NormFinder analysis. *PP2a* and *SAND* showed more stable expression across altitudinal and time-course change experiments. The BestKeeper and ΔC_t analysis identified *PP2A* and *GAPDH* as having the most stable expression pattern. Moreover, either *GAPDH* and/or *PP2a* always showed up in the top three positions in the comprehensive ranking, as the most stable reference genes across all the experimental groups. Based on the calculated pairwise variation output, *PP2a* and *GAPDH* were selected to validate the gene expression data of the flowering promoter *CONSTANS*. *PP2a* has already been established and validated to be one of the best candidate reference genes for normalisation in many plant species^{74–76}. The protein is an essential component of cellular signalling pathways to achieve coordinated functioning between different cell types against oxidative stress. On the other hand, *GAPDH* is a classical reference gene used by many researchers, although its expression has been shown to vary under different environmental conditions⁷⁷. Expression of *GAPDH* in coffee was found to be the most stable among all the tested candidates between different tissues⁷⁸. In flax, *GAPDH* was found to be highly stable during different stages of plant development³⁶. Expression of *GAPDH* may increase in conditions of abiotic and biotic stress where a plant requires more sugar utilisation and energy to stabilise its growth condition⁷⁹. Since the sequence of *GAPDH* is highly conserved, it may be considered a good reference gene in many non-model plant species⁸⁰. However, we highly recommend that *GAPDH* also be validated under experimental conditions in the field, as it was not the most stable gene in *Chionochloa*.

CONSTANS, was selected as a target gene to validate the credibility of the selected reference genes. *CONSTANS* is a CAAT-box transcription factor that has been shown to regulate photoperiodic control of flowering in Arabidopsis and in many other plant species⁵⁶. The expression analysis of *CO* in *Celmisia* and *Chionochloa* was found to be similar to that in published reports when normalised using the two pairs of reference genes⁸¹. The two-way anova analysis suggests that the expression of *CO* was significantly different in all the seasons in distinct altitudes (P-value < 0.0001, F = 20.5). This is as expected as the transcription of the *CO* gene is regulated by photoperiodic signals. The expression was not significantly different between distinct altitudes of Mt Hutt. But the interaction between different seasons and altitude showed a positive response to the relative expression of *CO* in both species. The flowering genetic network is different between monocots and dicots even though the core genes remain the same⁸². This could explain the variation in the expression pattern of *Hd1* in the January leaf samples with different fates in *Chionochloa*, compared to *Celmisia* (Fig. 7D).

Even though the ranking order of the candidate reference genes may have differed, all the statistical programs consistently excluded *U18S*, ranking it as the most unstable gene among all the candidates. Expression analysis using the least stable gene (*U18S*) as the normalisation factor for both *Celmisia* and *Chionochloa*, showed significantly different results to the expression pattern using the selected reference gene pairs described above (comparing Figs 7 and 8). The expression values differed up to 14 log₂ fold change in *Celmisia* and 12 log₂ fold change in *Chionochloa* when analysed with *U18S* as the normalisation factor (Supplementary Fig. S7). These results clearly suggest that inappropriate selection of reference genes can introduce significant bias in the expression analysis

and lead to misinterpretation of results. The use of *U18S* has also been discouraged among plant scientists due to its greater abundance in a sample compared to the target gene which can introduce greater errors in the analysis²⁶.

Conclusion: A Systematic Validation for Plants in Field Experiments

RT-qPCR is an extremely sensitive and important technique for real time amplification of transcripts. The selection of appropriate reference genes to use as the normalisation factor is equally as important as the technique. Since conditions in the field add a layer of complexity over those in controlled environments, it is crucial to verify the reliability of all potential reference genes in order to avoid misinterpretation of the genetic analysis. Discrepancies in the ranking order of candidate reference genes emphasises how crucial it is to validate every reference gene for any gene expression output in the natural environment. This work constitutes the first systematic analysis to identify, select and validate appropriate reference genes for genetic analysis in masting plants growing under prevailing environmental conditions. We have identified stably expressed reference genes from the draft transcriptomes of two masting plants, *Chionochloa* and *Celmisia*. These genes showed constant expression levels across seasonal, altitudinal and developmental changes and can be used to validate gene expression analysis. Our study will benefit both molecular and ecological research towards forecasting mast flowering in non-model plants under global climate change. Additionally, it will enable the New Zealand government to design efficient conservation measures aimed at the protection of endangered, endemic species.

Methods

Experimental design and plant material. Experiments were set up at the field site at Mt Hutt (43°32'S, 171°33'E). The control plots for *Celmisia* and *Chionochloa* were present at the 1350 m and 1070 m base of Mt Hutt, respectively. A set of 20 plants, randomly selected from the control plots, were moved to sea level (University of Canterbury, 43°31'S, 172°35'E). A similar set of *Chionochloa* was also translocated to an altitude of 1520 m on Mt Hutt, and a set of *Celmisia* plants was translocated to 1070 m and 1520 m. Leaf samples were collected four times throughout the year from each of the plants that were then segregated into two sets depending on whether the plants subsequently flowered (flowering sample) or remained vegetative (vegetative sample). Furthermore, an additional set of samples were also collected in the late summer for *Chionochloa* plants translocated to sea level to study the effect of a complete summer season on the flowering response. All of the samples were harvested and frozen using dry ice. The collected material was stored in -80°C until subsequent analysis. Two independent biological replicates were used in the study, each consisting of a pool of three independent plants.

Total RNA extraction. All the independent replicates were ground in mortar and pestle using liquid nitrogen. RNazap was sprayed to clean the desk and types of equipment prior to use to inactivate the RNases present in the surroundings. Total RNA was extracted using the Trizol-chloroform method: 1 ml of Trizol along with 60 μl of 20% (w/v) Sarkosyl was added to the ground sample (~100 mg). The sample was centrifuged at 12000 g for 5 mins. The supernatant was transferred to a clean tube followed by addition of 200 μl of chloroform for phase separation. The mixture was allowed to stand for 3–4 mins followed by centrifugation at 12000 g for 15 mins. The aqueous phase from the above step was collected into a new tube and 500 μl of isopropanol was added to precipitate the RNA. The mixture was again centrifuged for 5 mins at 12000 g. The supernatant was discarded and the pellet was washed twice with 80% ethanol at 12000 rpm for 2 min. The clean, translucent pellet was air dried for 5–6 minutes. The RNA pellet was dissolved in RNase-free water in a dry bath at 65°C and stored at -80°C . The concentration and purity of the extracted RNA was assessed using a Nanodrop 2000c Spectrophotometer (Thermo Scientific, US). The absorbance ratios of A260/280 and A260/230 were the parameter used to check the quality of the extracted RNA. The values are required to be in between 2.0–2.1 for A260/280 and 2.0–2.2 for A260/230 for a pure RNA sample. The integrity of RNA was assessed using 1.2% (w/v) agarose gel electrophoresis.

Reverse transcription-quantitative PCR (RT-qPCR). Purified RNA (1 μg) was treated with DNase I to remove any genomic traces from the sample. 1 μl of 25 mM EDTA was added to the treated RNA followed by an incubation of 10 min at 65°C to inactivate the DNase I. For reverse transcription, 1 μl of 50 μM oligodT, 1 μl of 50 μM random hexamers and 10 mM dNTPs were added to the treated RNA⁸³. The sample was incubated at 65°C for 5 min and then on ice for 2 min. 7 μl of reverse transcription master mix, comprising 5X first strand buffer, 0.1 M DTT, 40 U/ μl RNaseOUT, and 200 U/ μl Superscript III reverse transcriptase were added to the above RNA mix. The sample was then incubated for the following conditions to synthesize the first strand of cDNA: 50°C for 60 min followed by 70°C for 15 min. The cDNA product was diluted five-fold and stored at -20°C until quantitative PCR (qPCR).

RT-qPCR reactions were performed in a 15- μl final volume with 7.5 μl of a SYBR master mix (Kappa, Sigma), 4.5 μl of water, 10 μM of each forward and reverse primer. Cycling conditions were 95°C for 10 min hold, followed by 40 cycles of 95°C for 10 s, 60°C for 15 s and 72°C for 20 s. A melt curve analysis was performed to determine the primer specificity with the following conditions: Ramping of temperature from 72 – 95°C by one degree Celsius at each step, with a waiting time of 5 s after each ramping step. All the RT-qPCR reactions were run in triplicate for all the samples across the eight candidate reference genes with negative water and reverse transcriptase control using the RotorGene-Q (Qiagen, Germany).

In silico identification, gene sequence search and primer design. Based on a literature search, eight candidate reference genes for each of *Chionochloa* and *Celmisia* were selected for the study. Reference gene sequences present in sunflower, *Chrysanthemum*, rice, and maize were used as query sequences to search for the orthologous sequences in *Celmisia* and *Chionochloa*. These query sequences were blasted against the transcriptome assembly of *Celmisia* and *Chionochloa* (unpublished data) to identify the candidate reference genes. The putative sequences were further analysed using multiple sequence alignment and phylogenetic analysis.

Both the forward and reverse primers for each of the candidate reference genes were designed using Primer premier 6.0⁸⁴ with the following conditions: Tm values ranging between 58–62 °C, GC content between 40–60%, primer lengths of 18–30 base-pair (bp), and product length of 100–300 bp. The primers were synthesized by the Macrogen Company (South Korea). All the primers were tested for amplification efficiency and coefficient of determination across all the samples using LinReg PCR software⁸⁵. This software calculates the amplification efficiency based on the data points measured from the amplification curve when plotted against the log-fluorescence axis. The amplified products were run on 1.5% (w/v) agarose gel to verify the specificity of the primers along with dissociation curve analysis. The amplified products were cleaned up using a DNA agarose extraction kits (New England Biolabs) as per the manufacturer's instructions for sequencing. These products were again sequenced using Sanger sequencing⁸⁶ at the University of Canterbury, to confirm the identity of the amplified PCR product. The sequences have been lodged in GenBank. The Accession numbers are provided in Supplementary File 6.

Determination of reference gene expression stability. The stability of expression of the reference genes across distinct temporal-spatially collected samples was assessed using five different statistical packages: geNorm, Normfinder, BestKeeper, ΔC_t and RefFinder. All the packages were used according to the manufacturer's instructions. Averaged C_q values from the triplicate reactions for each sample and for each gene combination were used for the analysis. For geNorm and Normfinder, the raw C_q values were transformed to relative quantities (RQ) using the formula $RQ = 2^{(C_{q \text{ min}} - C_{q \text{ sample}})}$, where $C_{q \text{ min}}$ is the lowest C_q value across the sample pool. The geNorm algorithm calculates the expression stability value (M) and pairwise variation (V). All the genes across different conditions were ranked by their stability value, the lower the value of M, the more stable the gene expression. The computed pairwise variation, based on the normalisation factor, allows for the determination of the minimum number of reference genes required for normalisation of the data. A value of V less than 0.15 indicates the appropriate number of reference genes required for analysis⁵⁵. Normfinder evaluates the expression stability of candidate reference genes at inter-group and intra-group levels. Ideally, the two genes with the lowest stability values are the most appropriate genes to be used for normalisation⁵⁶. BestKeeper analyses the candidate genes based on the standard deviation and coefficient of variation (CV) of the C_q values in a sample pool. The smaller the standard deviation and CV, and the higher the coefficient of regression, the more stable is the gene⁵⁷. The ΔC_t method compares the relative expression of the pair of genes in a sample pool, suggesting a correlation between the variations in the C_q values of a candidate reference gene across the samples with their stability. RefFinder is another tool that determines a comprehensive ranking of the stability of the candidate reference genes based on the inputs from geNorm, Normfinder, Bestkeeper and ΔC_t methods. The tool analyses the output from all the statistical software and generates a comprehensive ranking list of reference genes based on their stability⁵⁹.

Validation of the reference gene analysis. *Cp Heading Date1 (Hd1)* and *Cl CONSTANS (CO)* were used as the targets to validate the selected reference genes for data normalisation in *Chionochloa* and *Celmisia*, respectively. *CO* and *Hd1* are two orthologous proteins found in *Arabidopsis* and rice, respectively^{66,87}. These proteins belong to the zinc-finger transcription factor family that upregulates the expression of florigen (*FT*) that codes for the flowering hormone⁵⁶. These genes physically bind to the promoter of *FT* to induce flowering in plants. The expression analysis was done as described above and the results statistically tested using two-way analysis of variance (ANOVA).

Ethics approval and consent to participate. All plant material was collected with appropriate permissions and consultation. Department of Conservation permit number 40225-FLO.

Data Availability

The data generated and analysed is provided in the article and Supplementary Files. The accession numbers of the sequences are in Supplementary File 6.

References

- Okubo, K. *et al.* Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression. *Nat Genet* **2**, 173–179 (1992).
- Giorgi, F. M., Del Fabbro, C. & Liccausi, F. Comparative study of RNA-seq- and Microarray-derived coexpression networks in *Arabidopsis thaliana*. *Bioinformatics* **29**, 717–724 (2013).
- Pavey, S. A., Collin, H., Nosil, P. & Rogers, S. M. The role of gene expression in ecological speciation. *Ann Ny Acad Sci* **1206**, 110–129 (2010).
- Deng, Y. *et al.* Molecular ecological network analyses. *Bmc Bioinformatics* **13** (2012).
- Stranneheim, H. & Lundeberg, J. Stepping stones in DNA sequencing. *Biotechnol J* **7** (2012).
- Wang, Z., Gerstein, M. & Snyder, M. RNA-Seq: a revolutionary tool for transcriptomics. *Nat Rev Genet* **10**, 57–63 (2009).
- Martin, L. B., Fei, Z., Giovannoni, J. J. & Rose, J. K. Catalyzing plant science research with RNA-seq. *Front Plant Sci* **4**, 66 (2013).
- Eklom, R. & Galindo, J. Applications of next generation sequencing in molecular ecology of non-model organisms. *Heredity (Edinb)* **107**, 1–15 (2011).
- Duan, J. L., Xia, C., Zhao, G. Y., Jia, J. Z. & Kong, X. Y. Optimizing de novo common wheat transcriptome assembly using short-read RNA-Seq data. *Bmc Genomics* **13** (2012).
- Garg, R., Patel, R. K., Tyagi, A. K. & Jain, M. De Novo Assembly of Chickpea Transcriptome Using Short Reads for Gene Discovery and Marker Identification. *DNA Res* **18**, 53–63 (2011).
- Iorizzo, M. *et al.* De novo assembly and characterization of the carrot transcriptome reveals novel genes, new markers, and genetic diversity. *Bmc Genomics* **12** (2011).
- Kerr, S. C., Gaiti, F., Beveridge, C. A. & Tanurdzic, M. De novo transcriptome assembly reveals high transcriptional complexity in *Pisum sativum* axillary buds and shows rapid changes in expression of diurnally regulated genes. *Bmc Genomics* **18** (2017).
- Kakumanu, A. *et al.* Effects of Drought on Gene Expression in Maize Reproductive and Leaf Meristem Tissue Revealed by RNA-Seq. *Plant Physiol* **160**, 846–867 (2012).

14. Chakraborty, S., Britton, M., Martinez-Garcia, P. J. & Dandekar, A. M. Deep RNA-Seq profile reveals biodiversity, plant-microbe interactions and a large family of NBS-LRR resistance genes in walnut (*Juglans regia*) tissues. *Amb Express* **6** (2016).
15. Li, Y. *et al.* An RNA-Seq transcriptome analysis revealing novel insights into aluminum tolerance and accumulation in tea plant. *Planta* **246**, 91–103 (2017).
16. Taniguchi, M., Miura, K., Iwao, H. & Yamanaka, S. Quantitative assessment of DNA microarrays - Comparison with Northern blot analyses. *Genomics* **71**, 34–39 (2001).
17. VanGuilder, H. D., Vrana, K. E. & Freeman, W. M. Twenty-five years of quantitative PCR for gene expression analysis. *Biotechniques* **44**, 619–626 (2008).
18. Czechowski, T., Bari, R. P., Stitt, M., Scheible, W. R. & Udvardi, M. K. Real-time RT-PCR profiling of over 1400 Arabidopsis transcription factors: unprecedented sensitivity reveals novel root- and shoot-specific genes. *Plant J* **38**, 366–379 (2004).
19. Nolan, T., Hands, R. E. & Bustin, S. A. Quantification of mRNA using real-time RT-PCR. *Nat Protoc* **1**, 1559–1582 (2006).
20. Czechowski, T., Stitt, M., Altmann, T., Udvardi, M. K. & Scheible, W. R. Genome-wide identification and testing of superior reference genes for transcript normalization in Arabidopsis. *Plant Physiol* **139**, 5–17 (2005).
21. Malgouyre, A., Banzet, S., Mouret, C., Bigard, A. X. & Peinnequin, A. Quantification of low-expressed mRNA using 5' LNA-containing real-time PCR primers. *Biochem Bioph Res Co* **354**, 246–252 (2007).
22. Leong, D. T. *et al.* Absolute quantification of gene expression in biomaterials research using real-time PCR. *Biomaterials* **28**, 203–210 (2007).
23. Bustin, S. A. Absolute quantification of mRNA using real-time reverse transcription polymerase chain reaction assays. *J Mol Endocrinol* **25**, 169–193 (2000).
24. Chini, V., Foka, A., Dimitracopoulos, G. & Spiliopoulou, I. Absolute and relative real-time PCR in the quantification of *tst* gene expression among methicillin-resistant *Staphylococcus aureus*: evaluation by two mathematical models. *Lett Appl Microbiol* **45**, 479–484 (2007).
25. Cikos, S., Bukovska, A. & Koppel, J. Relative quantification of mRNA: comparison of methods currently used for real-time PCR data analysis. *Bmc Mol Biol* **8** (2007).
26. Kozera, B. & Rapacz, M. Reference genes in real-time PCR. *J Appl Genet* **54**, 391–406 (2013).
27. Guenin, S. *et al.* Normalization of qRT-PCR data: the necessity of adopting a systematic, experimental conditions-specific, validation of references. *J Exp Bot* **60**, 487–493 (2009).
28. Bustin, S. A. *et al.* The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments. *Clin Chem* **55**, 611–622 (2009).
29. Thellin, O. *et al.* Housekeeping genes as internal standards: use and limits. *J Biotechnol* **75**, 291–295 (1999).
30. Jain, M., Nijhawan, A., Tyagi, A. K. & Khurana, J. P. Validation of housekeeping genes as internal control for studying gene expression in rice by quantitative real-time PCR. *Biochem Bioph Res Co* **345**, 646–651 (2006).
31. Fernandez, P. *et al.* Comparison of predictive methods and biological validation for qPCR reference genes in sunflower leaf senescence transcript analysis. *Plant Cell Rep* **30**, 63–74 (2011).
32. Sinha, D. K. & Smith, C. M. Selection of Reference Genes for Expression Analysis in *Diuraphis noxia* (Hemiptera: Aphididae) Fed on Resistant and Susceptible Wheat Plants. *Sci Rep-Uk* **4** (2014).
33. Paolacci, A. R., Tanzarella, O. A., Porceddu, E. & Ciaffi, M. Identification and validation of reference genes for quantitative RT-PCR normalization in wheat. *Bmc Mol Biol* **10** (2009).
34. Lin, Y. A. *et al.* Validation of Potential Reference Genes for qPCR in Maize across Abiotic Stresses, Hormone Treatments, and Tissue Types. *Plos One* **9** (2014).
35. Wan, Q. *et al.* Stability evaluation of reference genes for gene expression analysis by RT-qPCR in soybean under different conditions. *Plos One* **12** (2017).
36. Huis, R., Hawkins, S. & Neutelings, G. Selection of reference genes for quantitative gene expression normalization in flax (*Linum usitatissimum* L.). *Bmc Plant Biol* **10** (2010).
37. Narancio, R., John, U., Mason, J. & Spangenberg, G. Selection of optimal reference genes for quantitative RT-PCR transcript abundance analysis in white clover (*Trifolium repens* L.). *Funct Plant Biol* **45**, 737–744 (2018).
38. Fan, C. J. *et al.* Selection of Reference Genes for Quantitative Real-Time PCR in Bamboo (*Phyllostachys edulis*). *Plos One* **8** (2013).
39. Luo, X. Y. *et al.* Selection of suitable inner reference genes for normalisation of microRNA expression response to abiotic stresses by RT-qPCR in leaves, flowers and young stems of peach. *Sci Hortic-Amsterdam* **165**, 281–287 (2014).
40. Stanton, K. A. *et al.* A Whole-Transcriptome Approach to Evaluating Reference Genes for Quantitative Gene Expression Studies: A Case Study in *Mimulus*. *G3-Genes Genom Genet* **7**, 1085–1095 (2017).
41. Kong, Q. S. *et al.* Identification of Suitable Reference Genes for Gene Expression Normalization in qRT-PCR Analysis in Watermelon. *Plos One* **9** (2014).
42. Tashiro, R. M., Philips, J. G. & Winefield, C. S. Identification of suitable grapevine reference genes for qRT-PCR derived from heterologous species. *Mol Genet Genomics* **291**, 483–492 (2016).
43. Sgama, T., Pape, J., Massiah, A. & Jackson, S. Selection of reference genes for diurnal and developmental time-course real-time PCR expression analyses in lettuce. *Plant Methods* **12** (2016).
44. Borowski, J. M. *et al.* Selection of candidate reference genes for real-time PCR studies in lettuce under abiotic stresses. *Planta* **239**, 1187–1200 (2014).
45. Ma, S. H. *et al.* Expression Stabilities of Candidate Reference Genes for RT-qPCR under Different Stress Conditions in Soybean. *Plos One* **8** (2013).
46. Gao, M. M. *et al.* Evaluation of Reference Genes for Normalization of Gene Expression Using Quantitative RT-PCR under Aluminum, Cadmium, and Heat Stresses in Soybean. *Plos One* **12** (2017).
47. Gutierrez, L. *et al.* The lack of a systematic validation of reference genes: a serious pitfall undervalued in reverse transcription-polymerase chain reaction (RT-PCR) analysis in plants. *Plant Biotechnol J* **6**, 609–618 (2008).
48. Schmittgen, T. D. & Zakrajsek, B. A. Effect of experimental treatment on housekeeping gene expression: validation by real-time, quantitative RT-PCR. *J Biochem Bioph Meth* **46**, 69–81 (2000).
49. Schauber, E. M. *et al.* Masting by eighteen New Zealand plant species: The role of temperature as a synchronizing cue. *Ecology* **83**, 1214–1225 (2002).
50. Kelly, D. The Evolutionary Ecology of Mast Seeding. *Trends Ecol Evol* **9**, 465–470 (1994).
51. Kelly, D. & Sork, V. L. Mast seeding in perennial plants: Why, how, where? *Annu Rev Ecol Syst* **33**, 427–447 (2002).
52. Kelly, D. *et al.* Of mast and mean: differential-temperature cue makes mast seeding insensitive to climate change. *Ecol Lett* **16**, 90–98 (2013).
53. O'Donnell, C. F. J. Predators and the decline of New Zealand forest birds: An introduction to the hole-nesting bird and predator programme. *New Zeal J Zool* **23**, 213–219 (1996).
54. Grabherr, M. G. *et al.* Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nat Biotechnol* **29**, 644–U130 (2011).
55. Vandesompele, J. *et al.* Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. *Genome Biol* **3** (2002).

56. Andersen, C. L., Jensen, J. L. & Orntoft, T. F. Normalization of real-time quantitative reverse transcription-PCR data: a model-based variance estimation approach to identify genes suited for normalization, applied to bladder and colon cancer data sets. *Cancer Res* **64**, 5245–5250 (2004).
57. Pfaffl, M. W., Tichopad, A., Prgomet, C. & Neuvians, T. P. Determination of stable housekeeping genes, differentially regulated target genes and sample integrity: BestKeeper - Excel-based tool using pair-wise correlations. *Biotechnol Lett* **26**, 509–515 (2004).
58. Silver, N., Best, S., Jiang, J. & Thein, S. L. Selection of housekeeping genes for gene expression studies in human reticulocytes using real-time PCR. *Bmc Mol Biol* **7** (2006).
59. Xie, F. L., Xiao, P., Chen, D. L., Xu, L. & Zhang, B. H. miRDeepFinder: a miRNA analysis tool for deep sequencing of plant small RNAs. *Plant Mol Biol* **80**, 75–84 (2012).
60. Zhang, L. *et al.* In-depth analysis of the endogenous reference genes used in the quantitative PCR detection systems for rice. *Eur Food Res Technol* **234**, 981–993 (2012).
61. Qi, S. *et al.* Reference Gene Selection for RT-qPCR Analysis of Flower Development in *Chrysanthemum morifolium* and *Chrysanthemum lavandulifolium*. *Frontiers in Plant Science* **7** (2016).
62. Li, X. Y. *et al.* Validation of Reference Genes for Accurate Normalization of Gene Expression in *Lilium davidii* var. unicolor for Real Time Quantitative PCR. *Plos One* **10** (2015).
63. Narsai, R., Ivanova, A., Ng, S. & Whelan, J. Defining reference genes in *Oryza sativa* using organ, development, biotic and abiotic transcriptome datasets. *Bmc Plant Biol* **10** (2010).
64. Gertz, E. M., Yu, Y. K., Agarwala, R., Schaffer, A. A. & Altschul, S. F. Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. *Bmc Biol* **4** (2006).
65. Kumar, S., Stecher, G. & Tamura, K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Mol Biol Evol* **33**, 1870–1874 (2016).
66. Yano, M. *et al.* Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the arabidopsis flowering time gene CONSTANS. *Plant Cell* **12**, 2473–2483 (2000).
67. Udvardi, M. K., Czechowski, T. & Scheible, W. R. Eleven golden rules of quantitative RT-PCR. *Plant Cell* **20**, 1736–1737 (2008).
68. Mafra, V. *et al.* Reference Genes for Accurate Transcript Normalization in Citrus Genotypes under Different Experimental Conditions. *Plos One* **7** (2012).
69. Die, J. V., Roman, B., Nadal, S. & Gonzalez-Verdejo, C. I. Evaluation of candidate reference genes for expression studies in *Pisum sativum* under different experimental conditions. *Planta* **232**, 145–153 (2010).
70. Lee, J. M., Roche, J. R., Donaghy, D. J., Thrush, A. & Sathish, P. Validation of reference genes for quantitative RT-PCR studies of gene expression in perennial ryegrass (*Lolium perenne* L.). *Bmc Mol Biol* **11** (2010).
71. Tian, C. *et al.* Selection of Suitable Reference Genes for qPCR Normalization under Abiotic Stresses and Hormone Stimuli in Carrot Leaves. *Plos One* **10** (2015).
72. Chao, W. S., Dogramaci, M., Foley, M. E., Horvath, D. P. & Anderson, J. V. Selection and Validation of Endogenous Reference Genes for qRT-PCR Analysis in Leafy Spurge (*Euphorbia esula*). *Plos One* **7** (2012).
73. Tricarico, C. *et al.* Quantitative real-time reverse transcription polymerase chain reaction: normalization to rRNA or single housekeeping genes is inappropriate for human tissue biopsies. *Anal Biochem* **309**, 293–300 (2002).
74. Zhu, J. *et al.* Reference gene selection for quantitative real-time PCR normalization in *Caragana intermedia* under different abiotic stress conditions. *Plos One* **8**, e53196 (2013).
75. Klie, M. & Debener, T. Identification of superior reference genes for data normalisation of expression studies via quantitative PCR in hybrid roses (*Rosa hybrida*). *BMC Res Notes* **4**, 518 (2011).
76. Jiang, Q. *et al.* Selection of suitable reference genes for qPCR normalization under abiotic stresses in *Oenanthe javanica* (BL.) DC. *Plos One* **9**, e92262 (2014).
77. de Jonge, H. J. M. *et al.* Evidence Based Selection of Housekeeping Genes. *Plos One* **2** (2007).
78. Barsalobres-Cavallari, C. F., Severino, F. E., Maluf, M. P. & Maia, I. G. Identification of suitable internal control genes for expression studies in *Coffea arabica* under different experimental conditions. *Bmc Mol Biol* **10** (2009).
79. Thanonkeo, P., Monkeang, R., Saksirirat, W., Thanonkeo, S. & Akiyama, K. Cloning and molecular characterization of glyceraldehyde-3-phosphate dehydrogenase gene from thermotolerant mushroom, *Lentinus polychrous*. *Afr J Biotechnol* **9**, 3242–3251 (2010).
80. Joseph, J. T., Poolakkalody, N. J. & Shah, J. M. Plant reference genes for development and stress response studies. *J Biosciences* **43**, 173–187 (2018).
81. Shim, J. S., Kubota, A. & Imaizumi, T. Circadian Clock and Photoperiodic Flowering in Arabidopsis: Constans Is a Hub for Signal Integration. *Plant Physiol* **173**, 5–15 (2017).
82. Song, Y. H., Shim, J. S., Kinmonth-Schultz, H. A. & Imaizumi, T. Photoperiodic Flowering: Time Measurement Mechanisms in Leaves. *Annu Rev Plant Biol* **66**, 441–464 (2015).
83. Lee, R., Baldwin, S., Kenel, F., McCallum, J. & Macknight, R. Flowering Locus T genes control onion bulb formation and flowering. *Nat Commun* **4**, 2884 (2013).
84. Singh, V. K., Mangalam, A. K., Dwivedi, S. & Naik, S. Primer premier: program for design of degenerate primers from a protein sequence. *Biotechniques* **24**, 318–319 (1998).
85. Ruijter, J. M. *et al.* Amplification efficiency: linking baseline and bias in the analysis of quantitative PCR data. *Nucleic Acids Res* **37** (2009).
86. Zimmermann, J., Voss, H., Schwager, C., Stegemann, J. & Ansoerge, W. Automated Sanger dideoxy sequencing reaction protocol. *FEBS Lett* **233**, 432–436 (1988).
87. Song, N. N. *et al.* Genome-wide analysis of maize Constans-Like gene family and expression profiling under light/dark and abscisic acid treatment. *Gene* **673**, 1–11 (2018).

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Author Contributions

P.E.J. provided overall supervision of the project. Samarth initiated the analysis of the reference genes and carried out the sample analyses; Samarth wrote the paper with substantial input and guidance from P.E.J.

Additional Information

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