

Supplementary File 1

S1.1 Obligatory criteria

Our differential expression analyses required non-normalised RNA-seq data for the hybrid and both parental species in each allopolyploid or homoploid hybrid complex. Only datasets that included at least two biological replicates of each species were considered. A genome or gene sequences for at least one of the parental species was needed for the utilisation of the HyLiTE pipeline (Duchemin et al., 2015) in the differential expression analyses. The implementation of GO for functional analyses required genome annotations for at least one parental species, however, both a genome and genome annotation were not required, therefore if a dataset only had gene annotations available it was still considered. The RNA-seq data for the parents and hybrid had to be extracted from the same tissue, or from cells grown in the same medium, where applicable, and extracted under the same conditions.

S1.2 Preferential criteria

We gave preference to datasets where the respective hybrid species from which RNA-seq data was obtained were naturally occurring (it is common in the literature to see synthetic hybrids; commonly formed via artificial crosses for homoploid hybrids or colchicine treatment to obtain allopolyploids), to mitigate the influence of synthetic formation on any observed gene expression patterns. We also gave preference to allopolyploid and homoploid hybrid complexes that were as taxonomically close as possible, to minimise taxon-specific differences in observed gene expression patterns. Moreover, we preferred that both parental species were extant, where possible, as opposed to extant relatives of the extinct parents.

A broad search of the literature and online databases was performed with the above criteria considered. These are the resulting options and their justifications for use, or omission, in differential gene expression analysis.

S1.3 Animals

Achondrostoma oligolepis x Pseudochondrostoma polylepis

Naturally-occurring homoploid hybrid of two Iberian Leuciscinae fish (Pereira et al., 2014). No comparative transcriptomic studies are available of this parent-hybrid complex.

Ambystoma

McElroy et al. (2017) studied an allotriploid *Ambystoma* (mole salamander) with three parental species. This would have complicated our analyses as the classes used in the categorisation of differential gene expression are based on a two parent system (Cox et al., 2014).

In other publications, it was unclear as to exactly how many species were parents (parental species could potentially range from 2-4) of a given hybrid, or if the hybrid had a duplicated genome (Bogart et al., 2007; Schmid et al., 2015).

We additionally searched NCBI BioProjects for *Ambystoma*. There were some hybrids amongst the results, but they did not specify polyploidy/homoploidy, and as no papers have given specific hybrid/parent complexes other than McElroy et al, *Ambystoma* were not used in the analyses.

Bacillus

Stick insect genus purportedly containing allopolyploid species (Mallet, 2007). Subsequent searches of Google to identify specific species were unsuccessful and no data could be found on NCBI SRA.

Bufo viridis

The *B. viridis* subgroup contains a complex of diploid, triploid and tetraploid green toad species from Central Asia. The parental species of the triploid and tetraploid species are unclear (Stöck et al., 2005; Betto-Colliard et al., 2015).

Bulinus truncates

Allopolyploid freshwater snail briefly mentioned in (Mallet, 2007). Searches of NCBI SRA found no data.

Carassius auratus x *Cyprinus carpio*

Both parental species of this allopolyploid fish (carp) had genome sequences and annotations; the issue was a lack of homoploid hybrid complex from within the carp or carp-like fishes. Due to the lack of an accompanying publication, it was also unclear if this allopolyploid (NCBI BioProject PRJNA86641) was naturally formed.

Carassius auratus gibelio

Naturally-occurring allopolyploid fish (carp) formed from *Carassius auratus* x *Cyprinus carpio* pairing (Li et al., 2014). Only an mtDNA genome was available and limited gene models (13), however, there were extensive genome annotations available for the parental species. The issue was a lack of homoploid hybrid complex from within the carp fishes.

Carassius auratus red var. x *Cyprinus carpio*

Allopolyploid fish (carp) formed via artificial cross (Wang et al., 2015).

Carassius auratus red var. x *Megalobrama amblycephala*

Allopolyploid fish (carp) with genome sequence, however, only the transcriptome sequence for one biological replicate (Qin et al., 2016).

Cichlids

Within the literature, there exist a number of studies on cichlids (fish, family: Cichlidae), e.g. (Stelkens et al., 2009; Genner & Turner, 2011; Selz et al., 2014; Santos et al., 2016), however, none produced RNA-seq data from a comparative analysis between hybrid and parents.

Cobitis taenia x *Colbitis elongatoides*

These two diploid fish hybridised to form both diploid and polyploid lineages. RNA-seq data was only available for one parental species (*C. taenia*) (Juchno et al., 2007; Juchno & Boroń, 2018).

Cottus gobio

Homoploid hybrid fish derived from *C. perifretum* x *C. rhenanum* (Mallet, 2007; Stemshorn et al., 2011). No RNA-seq data was available for the hybrid.

Ctenopharyngodon idellus x *Megalobrama amblycephala*

This interspecific diploid fish pairing can form both diploid and triploid hybrids (He et al., 2013), however, there is no transcriptomic study that encompasses both parental species and the hybrids in the literature.

Two transcriptome accessions for triploid *Ctenopharyngodon idellus* x *Megalobrama amblycephala* hybrids can be found under NCBI BioProject PRJNA240314.

1 *Danio rerio* x *Danio nigrofasciatus*

2 A homoploid hybrid zebrafish complex (Spiewak et al., 2018). Although extensive genomic
3 information is available for *D. rerio*, there are no comparative transcriptomic data available
4 for this complex.

5 Artificial triploid *D. rerio* can be generated, however these are not allopolyploid (Mizgireuv
6 et al., 2004).

7 *Daphnia*

8 The water flea genus *Daphnia* does contain hybrid species, such as *D. galeata* × *D. hyalina*
9 (Wolinska et al., 2006) and some allopolyploids within the *D. pulex* complex (Dufresne,
10 2011). Comparative RNA-seq data could not be found for either complex.

11 *Drosophila*

12 Interspecific homoploid hybrids are common in the fruit fly genus *Drosophila* (Goulielmos &
13 Alahiotis, 1989; Landry et al., 2005; Kelleher et al., 2012). Some *Drosophila* species do
14 exhibit mosaic polyploidy (Fox et al., 2010), but there are no entirely allopolyploid species.

15 *Epinephelus coioides* x *Epinephelus lanceolatus*

16 Under NCBI BioProject PRJNA431058 there are transcriptome accessions for diploid and
17 triploid hybrids from the *Epinephelus coioides* x *Epinephelus lanceolatus* (grouper fish)
18 pairing. However, there are no accompanying parental transcriptomes, and only one
19 biological replicate at each ploidy level with two different tissues sampled.

20 BioProject PRJNA497240 has transcriptomic sequences for *E. coioides*, however, there is
21 only one replicate subjected to different treatment condition. Likewise, BioProject
22 PRJNA413272 has transcriptomic sequences for a single replicate of *E. lanceolatus*, sampled
23 over a time series, post-hatch.

24 *Gasterosteus nipponicus* x *Gasterosteus aculeatus*

25 Parent-hybrid fish complex with 6 or 7 RNA-seq runs available for each species, found under
26 NCBI BioProject PRJDB7242. Genome with gene models also available for *G. aculeatus*
27 (three-spined stickleback fish). However, as data was unpublished, it was unclear if the
28 hybrid was homoploid and if it was naturally or synthetically formed.

1 *Gila seminuda*

2 Homoploid hybrid fish formed from the hybridisation of *Gila robusta* x *Gila elegans* (Mallet,
3 2007; Mavárez & Linares, 2008). Only an organellar genome is available for *G. robusta* on
4 NCBI, in addition to 13 gene models. Further, no comparative RNA-seq data is available for
5 this hybrid complex.

6 *Megalobrama amblycephala* x *Cyprinus carpio*

7 RNA-seq data for the hybrid was unavailable (Wang et al., 2017). The research group was
8 contacted but no response was obtained.

9 *Morone chrysops* x *Morone saxatilis*

10 Six transcriptome accessions of homoploid hybrid striped bass available under NCBI
11 BioProject PRJNA382266. There were no accompanying parental transcriptome accessions.
12 A single transcriptomic replicate for *M. chrysops* and *M. saxatilis* were found under
13 BioSample SRR1187194 and SRR1187193, respectively.

14 *Oncorhynchus*

15 This genus in the Salmonidae family contains a number of hybrid species, including
16 *Oncorhynchus keta* x *Oncorhynchus gorbuscha* (Zhivotovsky et al., 2016), and diploid and
17 triploid *Oncorhynchus kisutch* (Withler et al., 1995). No comparative transcriptomic analyses
18 were found for either an allopolyploid or homoploid *Oncorhynchus* complex.

19 *Pelophylax esculentus*

20 The hybrid water frog of *Pelophylax lessonae* x *Pelophylax ridibundus* (Doležálková-
21 Kaštánková et al., 2018). Searches of NCBI database and <https://amphibiaweb.org> did not
22 find any genome sequences or comparative RNA-seq analyses.

23 *Poecilia formosa*

24 Naturally-occurring allopolyploid fish (molly) formed from *Poecilia Mexicana* x *Poecilia*
25 *latipinna* (Schedina et al., 2014). Genome sequences and annotations were available for both
26 parental species and the allopolyploid. The issue was a lack of homoploid hybrid complex
27 within the mollies.

28 *Salmo salar*

Atlantic salmon can occur as natural diploid and artificial triploid hybrids (Refstie & Gjedrem, 1975; Vera et al., 2017; Murray et al., 2018). However, there are no comparative transcriptomic analyses of parental species and hybrids in the literature.

Squalius

A genus of Cyprinidae fish with allopolyploid and homoploid hybrids produced from the same parental pairing. *S. alburnoides* exists as natural populations of hybrid allotriploid PAA, homodiploid hybrid PA, and the parental-like diploid AA genotypes. The parental species of *S. alburnoides* are *S. pyrenaicus* (PP) and an extinct species related to *Anaocypris hispanica* (Pala et al., 2010; Matos et al., 2015).

There are genome sequences and annotations for *S. pyrenaicus* available at ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/403/095/GCA_001403095.1_pp_cds_nonRedundant, there is also a GenBank record (accession CVRK000000000) for the *S. pyrenaicus* whole genome shotgun sequencing project, but it contains no sequence data.

Pala et al. (2008) performed cDNA sequencing of allotriploid *S. alburnoides*, but only for 6 genes.

There is comparative small RNA data available for this complex under GEO Series GSE38691 (Inácio et al., 2012).

Comparative RNA-seq data for allopolyploid and homoploid *Squalius* complexes can be found under ArrayExpress E-MTAB-3174 (Matos et al., 2015, 2019). This genus is a strong candidate for our homoploid and allopolyploid animal representatives.

Takifugu rubripes x *Takifugu flavidus*

An artificially formed homoploid hybrid fish (pufferfish), with transcriptome accessions only available for one replicate each of the parental species and hybrid (Gao et al., 2013).

Tigriopus californicus

Copepod species whose hybridisations are limited to being inter-population only (Pritchard et al., 2013; Barreto et al., 2014).

Xenopus laevis

Allopolyploid African clawed frog with unknown parental species (Session et al., 2016).

SI.4 Fungi

Aspergillus flavus x *Aspergillus parasiticus*

These Ascomycete molds form interspecific hybrid strains through artificial crosses, some with evidence of allopolyploidisation (Olarie et al., 2015). Genome sequences and annotations for both parental species are available through the NCBI database. No comparative transcriptomic studies available.

Blumeria graminis f. sp. *triticea*

A homoploid species of powdery mildew formed from the hybridisation of *B. g. f. sp. tritici* and *B. g. f. sp. secalis*. There is an annotated genome available for *B. g. tritici* and RNA-seq data for all members of this complex available. However, these transcriptomic data did not originate from a single study, so the conditions around RNA extraction could not be guaranteed as controlled across all samples, therefore we would not use this as a first option dataset (Menardo et al., 2016; Praz et al., 2018).

Additional comparative transcriptomic analyses relating to this complex involve only *B. g. tritici* (Hu et al., 2018).

Epichloë canadensis

Allopolyploid endophyte hybrid of *E. elymi* x *E. amarillans* with RNA-seq data with replicates for all members of the complex, in addition to genomes and gene sequences for both the parental species (data unpublished). A strong candidate for our allopolyploid fungal complex.

Neotyphodium lolii x *Epichloë typhina* Lp1

Allopolyploid endophyte. RNA-seq data with replicates available for all members of the complex, in addition to gene sequences for both the parental species (Cox et al., 2014; Campbell et al., 2017).

Ophiostoma ulmi x *Ophiostoma novo-ulmi*

Transient hybrids of *Ophiostoma ulmi* x *Ophiostoma novo-ulmi* do occur in nature (Brasier, 2001). No comparative transcriptomic analyses of this homoploid hybrid complex are

available; only a single study in which the *O. novo-ulmi* transcriptome was compared with that of *Candida albicans* and *Histoplasma capsulatum* (Nigg et al., 2015).

Saccharomyces cerevisiae x *Saccharomyces bayanus*

Homoploid hybrid yeast. Genome annotations for both parental species are available at <http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current>, in addition to RNA-seq reads from a comparative transcriptomic analysis of this complex. The hybrids were generated synthetically through mating a single haploid individual of each parental species, growing a clonal population of the diploid, and checking it by PCR (Schraiber et al., 2013).

Saccharomyces cerevisiae x *Saccharomyces kudriavzevii*

There is a comparative transcriptomic study available that used two biological replicates of this homoploid hybrid yeast, however, it used a microarray and only compared the hybrids at varying temperatures (Tronchoni et al., 2017).

Saccharomyces cerevisiae x *Saccharomyces paradoxus*

Homoploid hybrid yeast. RNA-seq-based transcriptomic analyses of multiple replicates are available. The hybrids were generated synthetically through mating a single haploid individual of each parental species, growing a clonal population of the diploid, and checking it by PCR (Schraiber et al., 2013). Genome annotations for both parental species available at <http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current>. A strong candidate for our homoploid fungal complex.

Swain Lenz et al. (2014) also did a comparative transcriptomic analysis of this complex, however, due to the genetic manipulations performed during their synthetic crossing of the parental species, we have opted to use the data from Schraiber et al.

Saccharomyces cerevisiae x *Saccharomyces uvarum*

Synthetically formed homoploid hybrids (Pfliegler et al., 2012). Although genome annotations are available for both parental species on <http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current>, the only comparative transcriptomic studies

1 available relating to this complex are of a single hybrid replicate grown at varying
2 temperatures, available under NCBI BioProject PRJNA505697.

3 *Saccharomyces pastorianus* (syn. *Saccharomyces carlsbergensis*)

4 This allopolyploid yeast is formed from the mating of *S. cerevisiae* and *S. eubayanus*. The
5 allopolyploid does not have a genome sequence or annotations available, but both parental
6 species do through the NCBI database. A comparative transcriptomic analysis of this
7 complex was performed by (Gibson et al., 2010), however, they used a microarray. It was
8 unclear whether the *S. pastorianus* they used was a naturally occurring allopolyploid, so the
9 authors were emailed to clarify. Their response was that their experimental procedure
10 involved an industrial strain that had been in use for decades, thus its ancestry is not entirely
11 certain. However, the author did not think it had originated from a synthetic protocol. The
12 literature also suggests that *S. pastorianus* arose through instantaneous speciation during an
13 interspecific hybridisation event (Dunn & Sherlock, 2008).

14 *Zygosaccharomyces parabailii*

15 A homoploid hybrid species of *Z. bailii sensu stricto* and an unidentified *Zygosaccharomyces*
16 species. There is an RNA-seq study of the response to lactic acid stress in *Z. parabailii*, but it
17 does not involve comparisons to its parental species (Ortiz-Merino et al., 2018).

18 *Zygosaccharomyces rouxii*

19 Yeast with allopolyploid strains. *Zygosaccharomyces rouxii* NBRC 1876 draft genome
20 sequence is available (Sato et al., 2017). RNA-seq data for this species can be found under
21 NCBI BioProject PRJNA437612. However, no comparative transcriptomic studies were
22 found through NCBI SRA.

23 *Zymoseptoria pseudotritici*

24 *Zymoseptoria pseudotritici* is a fungal homoploid hybrid grass pathogen with unknown
25 parental species (Stukenbrock et al., 2012).

26 ***S1.5 Plants***

27 *Arabidopsis suecica*

1 Natural allopolyploid of *A. thaliana* x *A. arenosa* (Jeffrey Chen et al., 2004). Comparative
2 RNA-seq data of this complex is available under NCBI BioProject PRJNA393427 with two
3 biological replicates for each member, in addition to genome annotations available through
4 NCBI SRA. The main issue was no suitable *Arabidopsis* homoploid hybrid complex.

5 *Arabidopsis thaliana* x *Arabidopsis lyrata*

6 Artificial homoploid hybrid with two RNA-seq replicates available for the hybrid and *A.*
7 *lyrata* (Zhu et al., 2017). The issue was that this study did not perform RNA-seq for *A.*
8 *thaliana*, so there was no guarantee that the conditions under which extraction was performed
9 were held constant across all species.

10 *Arachis hypogaea*

11 Peanut is an allopolyploid of *A. ipaensis* and *A. duranensis*. RNA-seq data, genomes and
12 genome annotations for the parental species and the allopolyploid are available (Bertioli et
13 al., 2019).

14 Further RNA-seq data for allopolyploid *A. hypogaea* is also available, without biological
15 replicates (Han et al., 2017).

16 The major issue was a lack on a homoploid hybrid complex from within this genus.

17 *Brassica juncea*

18 Allotetraploid hybrid of *B. rapa* and *B. nigra*. (Yang et al., 2016) did RNA-seq analysis of *B.*
19 *juncea* only, in addition to a genome annotation of *B. juncea*. The genome annotation of *B.*
20 *rapa* is available through NCBI SRA.

21 *Brassica napus*

22 An allotetraploid hybrid of *B. rapa* x *B. oleracea*. RNA-seq data with three biological
23 replicates for each member of the complex is available under NCBI BioProject
24 PRJNA449400 (Wu et al., 2018). All members have genes and genomes available through
25 NCBI SRA. This is a possible option for an allopolyploid complex.

26 *Brassica napus* x *Brassica carinata*

27 Homoploid hybrid artificially produced via hand pollination and embryo rescue. Comparative
28 RNA-seq analysis of this homoploid hybrid complex with three biological replicates for each

member, and functional gene annotations is available (Chu et al., 2014). Extensive genome annotations are available for *B. napus* through NCBI SRA. Limited gene models are available for *B. carinata* through NCBI SRA and <http://brassicadb.org>. This is a possible option for a homoploid hybrid plant complex.

Brassica napus x *Brassica rapa*

Comparative RNA-seq analysis of this homoploid hybrid complex (Zhang et al., 2015), with no biological replicates.

Camellia

Camellia reticulata can exist as an allopolyploid (Gu & Xiao, 2003), but there are no comparative transcriptomic studies on the allopolyploid complex. The only related RNA-seq data on NCBI SRA is of five different *C. reticulata* tissues (Yao et al., 2016).

A homoploid hybrid complex exists in *Camellia azalea* x *Camellia amplexicaulis*, with RNA-seq data on each member available. There are no biological replicates; the RNA libraries were formed from pooled RNA of three individuals (Zhang et al., 2018).

Capsella bursa-pastoris

Natural allopolyploid of *C. orientalis* and *C. grandiflora*. Multiple replicates of RNA-seq data are available for the allopolyploid and parental species (Kryvokhyzha et al., 2019).

Capsella rubella x *Capsella grandiflora*

Reciprocal homoploid hybrids with RNA-seq data, however, no accompanying RNA-seq data is available for the parental species (Rebernig et al., 2015).

Chrysanthemum nankingense x *Tanacetum vulgare*

Homoploid hybrid with comparative RNA-seq data available for hybrid and parental species (Wang et al., 2013; Qi et al., 2018). Qi et al. also generated allopolyploids through colchicine treatment of homoploid hybrids in addition to performing functional annotations of genes, making this a possible option for our analyses.

Coffea arabica

1 Natural allopolyploid of *C. eugenoides* and *C. canephora*. Data from a microarray-based
2 comparative analysis of this complex are available (Bardil et al., 2011), as well as an RNA-
3 seq-based comparative analysis of *C. arabica* grown under different temperatures (Combes et
4 al., 2013).

5 *Glycine*

6 No records of an RNA-seq-based study of *Glycine* homoploid hybrids. However, an
7 intraspecific comparative transcriptome analysis of homoploid *G. max* hybrids has been done
8 (Zhang et al., 2017).

9 *Glycine dolichocarpa*

10 A naturally formed recent allopolyploid of *G. syndetika* and *G. tomentella*. RNA-seq data for
11 only the allopolyploid is available (Coate et al., 2014).

12 A comparative transcriptomic study of the allopolyploid and its parents is found here, with 3
13 biological replicates per member (Ilut et al., 2012). <https://soybase.org> only has *G. max* and
14 *G. soja* genome and gene sequences. NCBI SRA has 127 gene models available for each of
15 *G. syndetika*, *G. tomentella* and *G. dolichocarpa*.

16 Transcriptomic analyses of this complex can also be found here (Coate et al., 2012).

17 *Gossypium*

18 Microarray-based analysis of natural allopolyploid cotton (*G. hirsutum*) and synthetic
19 homoploid hybrid progeny of *G. arboreum* and *G. raimondii* (Flagel et al., 2008).

20 RNA-seq based analysis of natural allopolyploid (*G. hirsutum*) and synthetic homoploid
21 hybrid progeny of *G. arboreum* and *G. raimondii* (Yoo et al., 2013). There are 3 biological
22 replicates of RNA-seq data available for each member under NCBI BioProject
23 PRJNA171342. The synthetic hybrid was formed by emasculation of the A2 parent in the
24 evening and subsequent cross-pollination the following morning. They are a strong option for
25 our homoploid and allopolyploid plant representatives.

26 *Helianthus*

The sunflower genus *Helianthus* contains several homoploid hybrid species (Ungerer et al., 2006). RNA-seq data is available (Renaut et al., 2014), in addition to a reference genome for the parental species *H. annuus* (Badouin et al., 2017).

There are some purportedly allopolyploid *Helianthus* species (Espinasse et al., 1995), but data on these are very limited, especially RNA-seq.

Mimulus

Mimulus peregrinus is a naturally formed recent allopolyploid of *M. luteus* x *M. guttatus*. Genomes and genome annotations for both parents found at <https://datadryad.org/resource/doi:10.5061/dryad.d4vr0>. Edger et al. (2017) performed a comparative RNA-seq analysis of this complex, in addition to an artificially formed *M. x robertsii* of the same parent pairing. *Mimulus x robertsii* was formed by hand pollination via diallel cross. They also did GO and KEGG. The issue was there were no biological replicates for any of the RNA-seq data.

Oryza

Comparative RNA-seq analysis of intraspecific rice hybrids and their derived allopolyploids (Xu et al., 2014).

Comparative RNA-seq analysis of a synthetic interspecific rice hybrid and its two parental species (Wu et al., 2016). However, the hybrid is a triploid produced from a diploid and tetraploid, so its genome size relative to one parent has increased and to the other, decreased, and thus it would confound the interpretation of our analyses.

Saccharum

Modern allopolyploid and homoploid sugarcane cultivars are commonly formed from pairings between domesticated *S. officinarum* and wild *S. spontaneum* (Song et al., 2016). RNA-seq data for *S. officinarum*, *S. spontaneum*, and their F₁ hybrid are available under NCBI BioProject PRJNA335885. *Saccharum intermedium*, an allopolyploid of *S. angustifolium* and *S. villosum*, has recently been described (Welker et al., 2017), but the complex lacks accompanying RNA-seq data.

Senecio

Comparative transcriptomic analyses of both an allopolyploid (*S. cambrensis* = *S. vulgaris* x *S. squalidus*) and homoploid hybrid (*S. x baxteri* = *S. vulgaris* x *S. squalidus*) of this ragwort genus are available (Hegarty et al., 2006), however, they are microarray-based. Further microarray-based transcriptomic analyses of this genus are also available (Hegarty et al., 2005; Hegarty et al., 2008, 2009).

Spartina

The cordgrass genus contains a recently formed natural allopolyploid, *S. anglica* (Ainouche et al., 2004), two interspecific hybrids *S. x neyrautii* and *S. x townsendii*, and the parental species *S. maritima* and *S. alterniflora*. Non-normalised Illumina data is available for these complexes as assembled reference transcriptomes (Boutte et al., 2016), but comparative RNA-seq data is as yet unavailable.

Microarray data for allopolyploid, homoploid hybrid and parental *Spartina* are also available (Chelaifa et al., 2010).

Tragopogon

There is RNA-seq data with biological replicates for the allopolyploid species *T. mirus* and *T. miscellus* and their diploid parents available under NCBI BioProject PRJNA210897.

A study of *T. miscellus*, its parental species, and their synthetically produced homoploid hybrid has been done, but it was not RNA-seq based, rather surveying expression of 144 duplicated gene pairs derived from the parental species (Buggs et al., 2011).

Triticeae

Synthetic allopolyploid of *Aegilops sharonensis* and *Triticum monococcum* ssp. *aegilopoides* obtained through colchicine treatment of F₁ hybrids. Gene expression was analysed through cDNA-AFLP (Kashkush et al., 2002).

Synthetic allopolyploid of *Aegilops longissimi* and *Triticum urartu*. Gene expression of the allopolyploid and its diploid parental species was analysed through RNA-seq (Wang et al., 2016). The main issue was that the allopolyploid was synthetic, as well as the lack of RNA-seq data for a homoploid hybrid complex within these genera.

Vigna reflexo-pilosa var. *glabra*

1 Allopolyploid mungbean species with hypothetical parental species, one of which is thought
2 to be extinct. RNA-seq assemblies are available for the allopolyploid (Kang et al., 2014)

3 *Zea mays*

4 Maize is purportedly of allotetraploid origin that has subsequently undergone rediploidisation
5 (Gaut et al., 2000). Thus, it would not be suitable for investigating the impact of genome
6 doubling on gene expression.

7 *Zea mays* x *Tripsacum dactyloides*

8 Interspecific hybrid of maize and gamagrass (Shavrukov & Sokolov, 2015) with
9 transcriptomic studies of each parent available (Wu et al., 2017; Gault et al., 2018), albeit
10 none for the entire complex.

11

SI.6 References

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