RESEARCH ARTICLE



Evolution and diversity of *PAPhy_a* phytase in the genepool of wheat (*Triticum aestivum* L., Poaceae)

Claus Krogh Madsen · Gitte Petersen · Ole Seberg · Henrik Brinch-Pedersen

Received: 23 September 2016/Accepted: 15 February 2017/Published online: 1 March 2017 © Springer Science+Business Media Dordrecht 2017

Abstract Higher phytase activity in food and feedstuffs is desirable in order to counter the antinutritional effects of phytate. The most promising platform where this might be achieved through plant breeding is wheat and its Triticeae relatives. They already accumulate notable amounts of phytase in the grains and higher expression of the responsible *PAPhy_a* gene can increase the activity further. Here we provide a survey of the genetic diversity of PAPhy_a in wild and extant relatives of wheat. Fifty sequences of the structural gene were obtained from 34 samples representing 21 species or subspecies. A phylogenetic tree is presented, demonstrating that the three gene copies in hexaploid wheat have been inherited from its diploid ancestors. This finding is not only relevant for applied research, it also provides further evidence regarding the origin of the genomes in polyploid wheat. T. urartu Tumanian ex Gandilyan

Electronic supplementary material The online version of this article (doi:10.1007/s10722-017-0501-9) contains supplementary material, which is available to authorized users.

C. K. Madsen (⊠) · H. Brinch-Pedersen Department of Molecular Biology and Genetics, Section for Crop Genetics and Biotechnology, Aarhus University, Forsøgsvej, 1, 4200 Slagelse, Denmark e-mail: ClausKrogh.Madsen@mbg.au.dk

G. Petersen · O. Seberg Faculty of Science, Natural History Museum of Denmark, University of Copenhagen, Sølvgade 83, 1307 Copenhagen K, Denmark and *Ae. tauschii* Coss. are confirmed as donors of the **A** and **D** genomes, respectively, and the hypothesis of a common origin (*Ae. speltoides* Tausch) of the **B** and **G** genomes is supported. The survey suggests that the allele variation available for breeding is increased by the inclusion of the closest relatives of wheat. This effort should benefit greatly from molecular methods because specimens of the same species may have either novel- or alleles-identical to those of wheat.

Keywords Evolution $\cdot PAPhy_a \cdot Phytase \cdot$ Triticeae \cdot Triticum \cdot Wheat

Introduction

The *PAPhy_a* gene expresses a purple acid phosphatase phytase during grain filling and is the main source of mature grain phytase activity (MGPA) in cereals belonging to the Triticeae tribe (Brinch-Pedersen et al. 2013). Phytate represents the largest pool of phosphorus in cereal seeds and it chelates nutritionally important metals including calcium, iron and zinc. Monogastric animals excrete the majority of phytate bound phosphorus and metals unless the feed has sufficient phytase activity to degrade the phytate (Brinch-Pedersen et al. 2002). PAPhy enzyme activity therefore exerts a positive influence on the nutritional value of cereals as well as the environmental impact of farming. Accordingly, it is of major interest to find

ways of increasing the activity in elite cultivars (Brinch-Pedersen et al. 2013). A transformation mediated gene duplication of PAPhy_a resulted in approximately doubled phytase activity in barley (Hordeum vulgare L.) (Holme et al. 2012). This demonstrated that there is no physiological barrier against a significantly higher expression of the PAPhy_a gene. Increased levels of activity will be within reach through conventional breeding, providing that more transcriptionally active PAPhy_a alleles are available. One potential strategy is to utilize the genetic diversity among wild and extant relatives of the major crop species wheat (Triticum aestivum L.) and barley. In cases where donor and recipient species are sexually compatible, favourable alleles can be introduced into elite cultivars by crossbreeding. Alleles from more distant relatives may be introduced by transformation or serve as templates for genome editing. However, there is very little background information available to guide the effort to increase MGPA. The *PAPhy_a* gene was only recently described and its sequence is only known for a handful of species (Madsen et al. 2013). Isolated PAPhy_a genes were mapped to chromosome 5H in H. vulgare and chromosomes 5A, 5B and 5D in T. aestivum using aneuploid lines. A single PAPhy_a gene was also identified in the diploid species einkorn (T. monococcum L. subsp. monococcum) and Aegilops tauschii Coss. whereas two copies were identified in rye (Secale cereale L.) (Madsen et al. 2013). This suggests that *PAPhy* a existed as single gene on chromosome 5 in the diploid common ancestor of Hordeum L., Triticum L. and Aegilops L. and further that the PAPhy_a complement in modern wheat is directly inherited from its diploid ancestors. The search for more favourable PAPhy_a alleles and the study of wheat genome evolution may therefore be mutually informative.

The Triticeae cereals include diploids such as einkorn, barley and rye. However, the economically most important Triticeae cereals are the allopolyploid wheats. The allopolyploid wheats belong either to the 'emmer' group or the 'timopheevii' group. The 'emmer group' is derived from wild emmer (*T. turgidum* subsp. *dicoccoides* (Körn. ex Asch. et Graebn.) Thell.) and include among others, the domesticated, tetraploids emmer (*T. turgidum* subsp. *dicoccon* (Schrank) Thell.), durum (*T. turgidum* subsp. *durum* (Desf.) Husn.) and the hexaploid bread wheat (T. aestivum). Similarly, the 'timopheevii' group is derived from the wild T. timopheevii subsp. armeniacum (Jakubz.) van Slageren (syn. T. araraticum Jakubz.) and includes the domesticated forms sanduri (T. timopheevii Zhuk. (Zhuk.) subsp. timopheevii) and Zhukowskys wheat (T. zhukovskyi Menabde et Ericz.) (Salamini et al. 2002; Wagenaar 1966). The 'emmer' group became crops of global importance whereas the 'timopheevii' group remained restricted to the Transcaucasus region. Nevertheless, the 'timopheevii' group represent an important genepool for the improvement of wheat and has been the donor of e.g., disease resistance genes (Perugini et al. 2008). The genomes included in the 'emmer' group are denoted A, B and D and in the 'timophevii' group A and G (Kilian et al. 2007).

The evolution of the Triticeae cereals, in particular the identity of the donors of the *T. aestivum* genomes, has been studied for almost a century and the literature on the subject is immense [see reviews by Peng et al. (2011) and Haider (2013)]. Briefly, the **D** genome has been assigned to Aegilops tauschii (Kihara 1944; McFadden and Sears 1944, 1946). The A genome was initially assigned to wild einkorn (T. monococcum spp. aegilopoides (Link) Thell.), but the recognition of T. urartu Tumanian ex Gandilyan as a separate species prompted new investigations. Strong evidence now supports the later species as the A genome donor (Dvorak et al. 1993). The superscripts A^{u} and A^{m} are used to distinguish between the genomes from T. urartu and T. monococcum, respectively. The potential donor of the B genome remains controversial. Based on morphology, the search has focused on the Sitopsis section of Aegilops consisting of Ae. speltoides Tausch, Ae. sharonensis Eig, Ae. longissimi Schweinf. et Muschl., Ae. bicornis (Forssk.) Jaub. et Spach and Ae. searsii Feldman et Kislev ex Hammer (Sarkar and Stebbins 1956; van Slageren 1994). Each of these species has been suggested as donors of the **B** genome, but the most compelling evidence has been accumulated for Ae. speltoides (Haider 2013), though this is not universally accepted (Fernández-Calvín and Orellana 1994; Huang et al. 2002; Salse et al. 2008). The hybridization which created T. turgidum subsp. dicoccoides (AB) happened approximately 3–500,000 years before present (yBP), whereas the hybridization that created T. aestivum (ABD) took place 10,000 yBP (Haider 2013). Whole genome sequencing provided more ancient estimates of 580,000-820,000 yBP for AB and 230,000–430,000 yBP for ABD (Marcussen et al. 2014). It is however likely that these estimates partially reflect population divergence prior to the hybridization events as discussed by the authors. The more recent estimate for the ABD hybridization event is supported by the evidence which connect the hybridization event to the spread of agriculture (Salamini et al. 2002). The origin of bread wheat is so recent that its genomes have not diverged much form the donors and favourable alleles can relatively easily be introduced in T. aestivum from Ae. tauschii and T. turgidum via synthetic hexaploids (Dreisigacker et al. 2008). The phylogenetic relationships of diploid Triticeae has received comparatively less attention since molecular methods were introduced. Indeed, most studies have a priori limited themselves to species that are Triticum or Aegilops by name. This is unfortunate, since Petersen et al. (2006) placed a number of less studied species within the Triticum/ Aegilops clade. Amblyopyrum (Boiss.) Eig and Thinopyrum (Saÿvul. et Rayss) A. Löve was for example found to be much closer relatives of the A genome group than any of the Aegilops. Recently, the availability of whole genome sequence data has prompted renewed interest in the phylogenetic relationships of the diploid Triticum and Aegilops. Marcussen et al. (2014) proposed that Ae. tauschii and by extension the D genome resulted from an ancient hybridization between ancestors of the A and **B** genomes. A more complex hybridization history was subsequently suggested (Li et al. 2015a, b). El Baidouri et al. (2017) expanded on this, suggesting a model in which both the **B** and **D** genome ancestors had undergone ancient hybridizations. Further, the concept of subgenome genome dominance was used to explain different mutation rates following polyploidization. While genomics is certainly providing intriguing new insights it is unfortunately still limited to a few taxa. Approaches which can be applied to many taxa, such as single gene phylogeny, are therefore still indispensable.

Here we provide a survey of the diversity of *PAPhy_a* alleles in the Triticeae with emphasis on the *Triticum/Aegilops* complex. The survey includes seven samples of *Ae. tauschii* and *T. turgidum* since these species are of special interest to the improvement of bread wheat. Also rye has been used in the improvement of wheat and for the generation of synthetic polyploids, triticale (X *Triticosecale* Witt.)

(Oettler 2005; Rabinovich 1998). We have therefore included four *Secale* L. accessions. A phylogenetic tree was constructed to visualize the evolution of the gene. The closest relatives of the wheat alleles were subjected to pairwise comparisons in order to assess the potential for finding useful genetic variation. To meet this end, we analysed approximately 2300 bp conserved gene sequence encompassing the core promoter, some 3'UTR and all introns and exons from the *PAPhy_a* gene. Fifty sequences from 34 samples of 21 species were included.

Materials and methods

The 34 samples used representing 21 species are listed in Table 1, which also include the authors of the taxa used. Note that two samples labelled as *T. urartu* by the IPK genebank (Tri 11494 and Tri 11495) have been re-identified as *T. monococcum* subsp. *aegilopoides*. This was done by morphology according to van Slageren (1994).

DNA was extracted for the current study as described by Møller et al. (2003). Some DNA samples were reused from Petersen et al. (2006), see Table 1. PCR was performed with Herculase II polymerase (Agilent Technologies) in 50 µL reaction mixture with 6% DMSO according to the manufacturer's instructions. The primers used are listed in Table 2. Primers 1, 2 and 3 were reused from (Madsen et al. 2013). Primer 4 was designed to overcome the poor performance of primer 3. It is shifted 9 bp in the upstream direction. I.e. amplicons of this primer are 9 bp shorter when excluding the primer sequences themselves. Most samples were amplified using primers 1 + 3 and/or 1 + 4. Combination 1 + 4produce stronger bands than combination 1 + 3 and requires no pre-annealing (see below). However combination 1 + 4 is not as universal as combination 1 + 3. Samples which failed to produce amplicons with these primer sets (i.e., Secale) were amplified using primers 2 + 3. Reactions with primer 3 required a pre-annealing step with this primer alone: 98 °C, 5 min; 30 °C, 20 s; heating to 72 °C at 2.0 °C/s; 72 °C, 5 min; 4 °C, ∞. The forward primer was subsequently added, whereafter the PCR proceeded using the same conditions for all primer combinations: 96 °C, 2 min; 38× (96 °C, 1 min; 59 °C, 20 s; 72 °C, 2 min 30 s; 72 °C, 3 min); 72 °C, 3 min; 4 °C ∞.

				-	•••		
Species	Sample accession no.	Country of origin	Source	PAPhy_a sequenced in this study	<i>PAPhy_a</i> sequenced in Madsen et al. (2013) or Holme et al. (2012)	PAPhy_a from genome database	Sequence accession no. NCBI genebank or ENA
Ae. bicornis (Forsskål) Jaub. et Spach	H 6602		*	Х			LT623930
Ae. searsii Feldman et Kislev ex K. Hammer	H 6605		*	Х			LT623931
Ae. sharonensis Eig			_			Х	
Ae. speltoides Tausch	AE 327	Turkey	IPK genebank	Х			LT623934
Ae. speltoides Tausch	AE 413	Israel	IPK genebank	Х			LT623933
Ae. speltoides Tausch	AE 1084	Syria	IPK genebank	Х			LT623932
Ae. tauschii Cosson	AE 229	Armenia	IPK genebank	Х			LT623929
Ae. tauschii Cosson	AE 231	Armenia	IPK genebank	Х			LT623944
Ae. tauschii Cosson	AE 245	Armenia	IPK genebank	Х			LT623950
Ae. tauschii Cosson	NGB 9855		NordGen		Х		JF838317.1
Amblyopyrum muticum (Boiss.) Eig	Н 5572		*	Х			LT623942
Crithopsis delileana (Schult.) Roshev	Н 5558		*	Х			LT623939
Henrardia persica (Boiss.) C.E. Hubb	Н 5556		*	Х			LT623941
Pseudoroegneria spicata (Pursh) Á. Löve	H 9082		*	Х			LT623940
<i>T. aestivum</i> L. cv. Chinese spring	NGB 20850	China	NordGen		XXX		JF838307.1 [A]
T. aestivum L. cv. Bob				XXX			JF838309.1 [B] JF838305.1 [D] LT623916 [A]
<i>T. aestivum</i> L. cv.				XXX			LT623951 [B] LT623949 [D] LT623915 [A]
Villa Jurez							LT623917 [B] LT623948 [D]
T. timopheevii subsp. armeniacum (Jakubz.) van Slageren	Tri 11358	Armenia	IPK genebank	XX			LT623924 [A]
							LT623953 [G]

Table 1 Investigated samples and accession numbers for new and previously published sequences

Species	Sample accession no.	Country of origin	Source	PAPhy_a sequenced in this study	<i>PAPhy_a</i> sequenced in Madsen et al. (2013) or Holme et al. (2012)	PAPhy_a from genome database	Sequence accession no. NCBI genebank or ENA
<i>T. timopheevii</i> subsp. <i>armeniacum</i> (Jakubz.) van Slageren	Tri 18518	Iraq	IPK genebank	XX			LT623925 [A]
T. turgidum subsp. dicoccoides (Körn. ex Asch. et Graebner) Thell.	Tri 18485	Turkey	IPK genebank	XX			LT623926 [G] LT623943 [A]
<i>T. turgidum subsp.</i> <i>dicoccoides</i> (Körn. ex Asch. et Graebner) Thell.	Tri 18508	Syria	IPK genebank	XX			LT623952 [B] LT623919 [A]
<i>T. turgidum subsp.</i> <i>dicoccoides</i> (Körn. ex Asch. et Graebner) Thell.	Tri 18523	Israel	IPK genebank	XX			LT623920 [B] LT623918 [A]
T. monococcum L.	NGB		NordGen		Х		LT623921 [B] JF838315.1
<i>T. timopheevii</i> (Zhuk.) Zhuk.	Tri 3433	Turkey	IPK genebank	XX			LT623923 [A]
<i>T. timopheevii</i> (Zhuk.) Zhuk.	Tri 13159	Georgia	IPK genebank	XX			LT623954 [G] LT623945 [A]
T. monococcum subsp. aegilopoides (Link) Thell.	Tri 11494	Turkey	IPK genebank	Х			LT623927 [G] LT623946
<i>T. monococcum</i> subsp. <i>aegilopoides</i> (Link)	Tri 11495	Turkey	IPK genebank	Х			LT623928
<i>T. urartu</i> Tumanian ex Gandilyan	Tri 11497	Lebanon	IPK genebank	Х			LT623922
<i>T. zhukovsky</i> Menabde et Ericzjan	Tri 7258	Georgia	IPK genebank	XX			LT623947 [A]
<i>S. cereale</i> L. cv. Picasso			KWS		XX		LT623955 [G] JF838319.1 [1]
S. cereale L. cv.	R1150		IPK	Х			JF838321.1 [2] LT623935 [2]
S. strictum (C. Presl)	NGB9846		NordGen	XX			LT623937 [1]
C. 11001							LT623938 [2]

Table 1 continued

D Springer

Species	Sample accession no.	Country of origin	Source	PAPhy_a sequenced in this study	<i>PAPhy_a</i> sequenced in Madsen et al. (2013) or Holme et al. (2012)	PAPhy_a from genome database	Sequence accession no. NCBI genebank or ENA
S. sylvestre Host	R1116		IPK genebank	Х			LT623936
H. vulgare L. cv. Igri			6		Х		FR851293.1

Table 1 continued

* Represents samples which were reused from Petersen et al. (2006). Letters in brackets after the accession numbers of sequences from polyploids indicate the genome from which the sequence originates. A number is given in the brackets in the case of diploids with multiple gene copies

Primer no.	Primer name	Primer sequence
1	TaPAPhy_a1-311cons Fw	5'TTTGGACGAGCCATAGCTGCATA3'
2	ScPAPhy_a1-277Fw	5'TGCTTGCGCTTTAGTTTCAA3'
3	TaPAPhy_a NUE anker uni Rv	5'ACCGGGGGGTTTTTATTTCCA3'
4	PAPhy_a easy Rv	5'TTTTTATTTCCACGCTTGGGC3'
5	M13 uni(-43)	5'AGG GTT TTC CCA GTC ACG ACG TT3'
6	M13 rev(-49)	5'GAG CGG ATA ACA ATT TCA CAC AGG3'
7	Internal seq. Fw	5'CTGGGTCTCCTGGATCAC3'
8	Internal seq. Rv	5'CCCACCGAGATGTGCAC3'

Table 2 Primers used to amplify and sequence PAPhy_a

Amplicons were cloned in the pCR 4Blunt-TOPO vector (Invitrogen) and examined with EcoRI digests. Clones with 2000-2500 bp inserts were selected for sequencing. The restriction pattern from internal EcoRI sites supported the identification of homeologous clones in samples from the polyploid species. Sequencing was performed with two vector specific primers and two internal primers (Table 2 primers 5-8) by Eurofins Genomics, Ebersberg, Germany. The reads were assembled in CLC Main Workbench and trimmed to remove vector and incorporated primer sequences and to standardize the length of amplicons produced by different primer combinations. At least two clones from independent PCR reactions were sequenced per locus until a consensus was reached. The PAPhy_a sequence of Ae. sharonensis was downloaded from the published genome sequence after blasting with the TaPAPhy_al full length genomic sequence at http://wheat-urgi.versailles.inra. fr/Seq-Repo<3sitory/BLAST. All new sequences are deposited in ENA. See Table 1 for accession numbers.

Sequences were aligned using the CLC Main Workbench with default settings (gap open cost 10 and gap extension cost 1) and subsequently adjusted manually (supplementary file 1). CLC Main Workbench uses a proprietary algorithm based on progressive alignment (CLCbio 2007; Feng and Doolittle 1987). A phylogenetic analysis was performed using the RAxML maximum likelihood algorithm (Stamatakis 2006) implemented in Geneious version 8.1.2 (Kearse et al. 2012). The analysis was done with data in four partitions (exons, introns, upstream and downstream regions) and using the GTR + GAM-MA + I nucleotide model and running 1000 bootstrap replicates. Pseudoroegneria (Nevski) A. Löve was used to root the tree in accordance with Petersen et al. (2006). The sequences from the taxa in the individual genome groups A, D and B/G/Ae. speltoides were realigned using above mentioned phylogenetic analysis (Fig. 3) as a guide tree. Again, the alignments were generated using CLC Main Workbench with the default settings, but without manual adjustment. The alignments were used for pairwise comparisons of the full length nucleotide sequences within the three genome groups. Subsequently, the alignments were shortened to include only the promotor and 5'UTR

sequences (5'flanking region). Separate pairwise comparisons were generated from this alignment. Finally, the encoded protein sequences were aligned and compared [excluding the signal peptide as defined in Dionisio et al. (2011)].

Results

A total of 50 PAPhy_a sequences were obtained. The sequences varied in length from 2239 to 2598 bp and the alignment had a length of 3253 bp. The conservation along the alignment is compared to the structure of the gene in Fig. 1. The gene structure was determined using the TaPAPhy_a1 coding sequence as scaffold. The exons are more conserved than nonconding promoter, intron and UTR sequences. Lengthy insertions in a single sequence cause the three stretches of only 2% conservation at 178-397 bp (insertion in S. cereale cv. Picasso 2), 1882-1995 bp [intron gain in S. strictum NGB9846.1 (2)] and 2656–2933 bp (elongated intron in H. vulgare cv. Igri). A pairwise comparison of similarity was generated from the alignment (Fig. 2). The lowest similarity of 71% (851 nucleotide differences and indels) was found between H. vulgare cv. Igri and S. cereale cv. Picasso. Seventeen sequences were identical with at least one other sequence. With a single exception, all identical sequences were from the same species or from homologous genome groups (e.g., the A^{u} genomes of tetraploid and hexaploid wheats). The maximum likelihood tree is shown in Fig. 3. Generally, there is no or only little bootstrap support (BS <50%) for the backbone of the tree whereas the various wheat genome groups and Secale are all strongly supported (BS = 100%). Accordingly, the data give only limited indication of relationships between the wheat genome groups. It does, however, allow us to infer the relationships within the groups including the relationships between polyploids and their diploid donor species. In the A genome group, sequences from T. monococcum and T. zhukovskyi are, with high support (BS = 100%), sister group to sequences from T. timopheevii, T. aestivum, T. turgidum and T. urartu. The highly supported **D** genome group (BS = 100%) consists only of sequences from Ae. tauschii and T. aestivum. The S' genome group consists of sequences from three Aegilops species (Ae. bicornis, Ae. sharonensis and searsii) and is also highly Ae. supported (BS = 100%); within this group Ae. bicornis and Ae. sharonensis are most closely related (BS = 99%). Full length nucleotide sequences in the A genome group were between 94 and 100% similar (Fig. 4 top panel left). The sequences can be divided in three groups: sequences A-G represent the A^u genome of the 'emmer' group and T. urartu. Sequences H-K represents the A^u genome of the 'timopheevii' group and sequences L–O represent the A^m genome. The full length nucleotide sequences within each group are



Fig. 1 Conservation along the *PAPhy_a* gene sequence. The *top bar* shows the gene structure. The 5'flanking region is *blue*, exons *green*, introns *red* and 3'UTR *yellow*. The hatch intron is

only found in one sequence (*S. cereale* cv. Picasso 2). The conservation is shown as a percent similarity graph below the *bar*. (Color figure online)

				_	-	2 6				2 11	- 17			15	16	1/		9					-12	- 19	1 1	2 29			11	1 H	12	- 10-			y	- 41	- 14-	-		- 42	<u>6</u> 6		- 42	
	T. austhum cv. Chinese spring IA1 NGB20850	2	0	4	17	9 9	10	172	85 8	15 115	24	73	73	73	231	73 13	72 17	2 172	176	176	192	149	174	204 24	15 18	14 300	301	292	203 20	0 310	625	257	295 2	96 23	2 232	209	430	218	245	350 27	1 27	292	292	292
Image: Note of the state of the st	T pareidos soban discossidor IAI Tribiant	2 100			17	o 0	10	172	85 8	20 21	8.4	73	73	73	231	73 12	72 17	2 173	176	176	182	1.62	174	104 34	15 18	14 300	301	292	303 30	0 210	635	257	205 2	96 22	2 232	209	430	210	2.45	350 27	1 22	292	292	292
A B D D D D D D D D D D D <																																												
Desc Desc Desc Desc Desc Desc Desc Desc Desc Desc Desc<	7. autouse ev. vita Jardz [A]	3 39,83	23,83		19 1	1 11	12	1/1	80 8	15 85	24	69	6.9	69	229	69 1.	/1 1/	1 1/1	1/5	105	181	247	1/1	102 24	и 18	12 298	299	290	301 2	a 308	0.14	130	295 4	96 23	2 28	207	428	210	244	348 25	9 20	290	290	290
Processe Processe Processe Processe Processe Processe Processe Processe Processe Processe Processe Process Process <t< td=""><td>T. antinum cv. llob White [A]</td><td>4 99,27</td><td>99,27 \$</td><td>19,18</td><td></td><td>4 14</td><td>15</td><td>177</td><td>90 9</td><td>10 90</td><td>19</td><td>78</td><td>28</td><td>78</td><td>235</td><td>78 13</td><td>77 17</td><td>7 173</td><td>181</td><td>181</td><td>187</td><td>154</td><td>179</td><td>189 15</td><td>20 19</td><td>1 306</td><td>307</td><td>299</td><td>309 31</td><td>6 315</td><td>630</td><td>263</td><td>304 3</td><td>05 24</td><td>1 236</td><td>213</td><td>434</td><td>224</td><td>252</td><td>356 23</td><td>8 27</td><td>299</td><td>299</td><td>299</td></t<>	T. antinum cv. llob White [A]	4 99,27	99,27 \$	19,18		4 14	15	177	90 9	10 90	19	78	28	78	235	78 13	77 17	7 173	181	181	187	154	179	189 15	20 19	1 306	307	299	309 31	6 315	630	263	304 3	05 24	1 236	213	434	224	252	356 23	8 27	299	299	299
I I I I I I I I I I I <	7. targidou subsp. dicaccoides [A] Tril8523	5 99,61	99,61 9	19,52 91	9,4	- 4	7	169	82 8	12 82	81	70	70	70	228	70 16	69 16	9 165	173	173	179	146	171	381 34	12 18	13 298	299	291	301 21	a 307	622	255	295 2	97 23	3 225	206	427	217	245	349 27	0 27	291	291	291
Image Image <th< td=""><td>7. tarridow subsp. dicaccoider IAI Tril 8508</td><td>6 99.61</td><td>99.61 9</td><td>9.52 91</td><td>9.4 99.8</td><td>3</td><td>7</td><td>169</td><td>82 8</td><td>2 82</td><td>81</td><td>70</td><td>70</td><td>70</td><td>228</td><td>70 10</td><td>69 16</td><td>9 165</td><td>173</td><td>173</td><td>179</td><td>145</td><td>171</td><td>381 34</td><td>2 18</td><td>13 298</td><td>299</td><td>291</td><td>301 21</td><td>8 327</td><td>622</td><td>255</td><td>295 2</td><td>97 23</td><td>3 225</td><td>205</td><td>427</td><td>217</td><td>245</td><td>349 27</td><td>0 27</td><td>291</td><td>291</td><td>291</td></th<>	7. tarridow subsp. dicaccoider IAI Tril 8508	6 99.61	99.61 9	9.52 91	9.4 99.8	3	7	169	82 8	2 82	81	70	70	70	228	70 10	69 16	9 165	173	173	179	145	171	381 34	2 18	13 298	299	291	301 21	8 327	622	255	295 2	97 23	3 225	205	427	217	245	349 27	0 27	291	291	291
A B C C C C C C C C C C C C C <	T unorth Tell 1497	2 00.57	0357 0	0.0 84.00	25 02	7 99 7		165	01 0	1 01	50	66	66	66	227	66 14	65 16	5 165	160	169	175	1.6.6	160	370 33	1 10	10 296	297	290	200 21	6 305	619	251	205 2	96 22	2 222	214	435	215	2.43	346 20	0 26	290	290	290
1 1 1 1 1 1 1 1 1 1 1	As smoothly APTER		03.73	3.74 43		4 03.04	03.03		101 00		110	167	147	167	310 1				10	10	20	134	100	348 34				333		3 300	6.30	100	347	44 33		31.0	430	310	234	347 34			337	277
Image Image <th< td=""><td>AR. ARRENT PARATE</td><td></td><td>22,72</td><td>12,10 52,</td><td></td><td></td><td>88,02</td><td></td><td>*** **</td><td></td><td></td><td>147</td><td></td><td>200</td><td></td><td></td><td></td><td></td><td></td><td></td><td>20</td><td></td><td>200</td><td></td><td></td><td></td><td></td><td>4//</td><td></td><td></td><td>378</td><td>200</td><td></td><td></td><td></td><td></td><td>100</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	AR. ARRENT PARATE		22,72	12,10 52,			88,02		*** **			147		200							20		200					4//			378	200					100							
And Anderse (1) And Anders	 Inspinitu (A) 10903 	3 30'11	99,32 5	6,12 36,	,12 90,4	5 99,45	36,49	90,61		0 2		11/	147	110	20/ 1	a 4	11 11	1 221	226	116	240	200	211	341 41		15 . 247	241	119	120 10	1 154	672	107	101 1	54 23	0 200	211	492	200	313	419 33	8 31	110	110	110
Departed system File File File File File File File F	T. rimphovii [A] Tril3159	20 96,32	96,32 5	16,32 96,	,12 96,4	5 96,45	\$6,49	90,61	100	2	9	137	137	137	297 1	28 22	21 22	1 221	226	226	230	200	211	241 41	1 22	15 347	241	229	350 2-	7 254	672	107	151 1	54 25	0 295	277	498	286	313	419 33	8 31	1 229	229	
	T. timophoviii subsp. armoniacum [A] Tril 1350	11 96,32	96,32 9	16,32 96,	,12 96,4	5 96,45	96,49	90,61	99,91 99,9	12	9	137	137	137	298 1	28 22	21 22	1 221	226	226	230	200	211	242 41	1 23	15 347	248	229	350 D	7 254	672	307	151 3	54 25	0 295	277	498	286	313	419 33	8 31	1 229	229	219
	T. rinophoviii subsp. armoniacum [A] Tril8518	12 96,37	95,37 9	16,37 96,	,16 96,4	9 96,49	96,54	90,7	22,6 29,	6 99,6		116	136	136	298 1	27 23	19 21	9 219	226	226	230	199	211	342 41	0 22	15 347	248	228	350 2-	7 354	671	307	353 3	54 25	0 296	276	497	285	312	418 33	7 31	228	228	238
	T. monococcam NGB10901	13 96.85	96.85 5	7.02 96.	64 96.5	8 96.98	97.15	92.92	94.08 94.0	94.08	94.13		0	0	230	2 10	67 16	7 167	171	171	176	150	174	377 24	16 10	16 304	205	294	307 36	4 313	631	263	291 2	99 23	237	216	437	225	254	356 27	3 27	294	294	294
A S A A A A A A A A A A A A A A A A A A	T. monococcum subsp. aerologoides Tril 1494	14 96.85	95.85 5	7.02 96.	64 96.5	8 96.98	97.15	92.92	94.08 94.0	94.08	94.13	100		0	230	2 10	67 16	7 167	171	171	176	150	174	377 34	6 19	16 304	205	224	307 3	4 313	631	263	291 2	99 23	8 237	216	417	225	254	356 27	3 27	294	294	294
1 1 1 1 1 1	T shadooda (a) ToTA	10 10.00	01.87	100 00	en 100 0	a 01.00	07.15	03.03	04.00 04.0		01.13	100	100		220	3 14		1 101	171		170	100	174	177 14		10 304	107	224	307 30		633	363	201 1			314	437	224	774	310 2		224	304	204
2 3 5 5 5 5 5 5 <	a semanting (ed) and an			17,02 00,				54,54	34,08 34,0			100			2.00						110						203	201	200 20			2.0.5					447						2.04	
	C. Internet H000	20 20,22		NU, 81 NU,			80,88		ar,4a ar,4			80,25	20,24	10,24	*	~							247										203 2		3 203		1.11	204						
Image Mark Mark Mark Mark Mark Mark Mark Mark	1. monococcum sallep, argroposars 1111495	27 30,85	99,85 5	17,02 96,	,64 96,3	a 99,98	30,15	92,92	94,04 94,0	94,04	94,08	99,91	39,91 1	10,91 9	10,24		67 16	/ 16/	1/1	1/1	1//	150	174	1/8 24	1/ 18	10 304	102	294	300 30	N 313	6.11	103	294 4	99 22	2.0	216	417	245	- 200	326 33	3 27	294	234	204
A B A B A B B B B B	T. austhum cv. Chinese spring [D] NGII20850	18 92,72	92,72 9	12,76 92,	,53 92,8	4 92,84	93,01	300	90,61 90,6	1 90,61	90,7	92,92	92,92 1	92,92 9	12,11 92,	92		0 0	10	30	20	136	160	348 25	10 16	ili 253	254	277	256 25	3 260	\$79	200	245 2	46 22	6 235	218	429	219	236	357 25	6 25	277	277	277
Image: Proper biase	T. austituse cv. Villa Jurez [D]	19 92,72	92,72 9	12,76 92,	53 92,8	4 92,84	93,01	300	90,61 90,6	1 90,61	90,7	92,92	92,92 1	2,92 9	11,11 92,	92 10	00	0	10	30	20	136	160	248 25	18 16	8 253	254	277	256 25	3 260	579	200	245 2	46 22	6 235	218	429	219	236	357 25	6 25	277	277	277
A B	T. antinen cv. lleb White (D)	20 92.72	92.72 9	2.76 92.	53 92.8	4 92.84	93.01	300	90.61 90.6	1 90.61	90.7	92.92	92.92 1	2.92 9	1.11 92.	92 10	00 10	0	10	30	20	136	160	248 25	10 16	8 253	254	277	256 25	3 260	579	200	245 2	46 22	6 235	218	429	219	235	357 25	6 25	277	277	277
A A A A A A A A A A	Ac. tanochii AE245	21 92.57	92.57 9	2.61 92	38 92.6	9 92.69	92.85	99.57	90.42 90.4	2 90.42	90.42	92.76	92,76 1	2,76 9	0.91 92	76 99.5	57 99.5	7 99.57		0	22	129	163	154 20	12 17	1 256	257	279	259 25	6 253	582	203	245 2	46 22	242	222	443	223	2.40	361 25	8 25	279	279	279
A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A <th< td=""><td>for second a better</td><td>22 02.67</td><td>03.57</td><td>0.63 60</td><td>38 03.6</td><td>0.03.00</td><td>03.85</td><td>00.57</td><td>00.43 00.4</td><td>0.43</td><td>00.43</td><td>03.76</td><td>03.36</td><td>10.76 0</td><td>0.01 03</td><td>37 . 60.1</td><td>17 00.0</td><td>7 00.57</td><td>100</td><td></td><td>22</td><td>130</td><td>101</td><td>14 14</td><td></td><td></td><td></td><td>333</td><td>100 10</td><td></td><td>643</td><td>303</td><td>347</td><td>44 33</td><td></td><td>333</td><td>443</td><td>222</td><td>242</td><td>363 34</td><td></td><td>133</td><td>330</td><td>220</td></th<>	for second a better	22 02.67	03.57	0.63 60	38 03.6	0.03.00	03.85	00.57	00.43 00.4	0.43	00.43	03.76	03.36	10.76 0	0.01 03	37 . 60.1	17 00.0	7 00.57	100		22	130	101	14 14				333	100 10		643	303	347	44 33		333	443	222	242	363 34		133	330	220
A A A A B	As small APPR	22 02.27	03.3	12,01 02,	11 02.4	0 02,00	03.00	00.14	00,02 00,0	12 00,12	00,72	03.54	03.54	10,70 0	0.01 02,	1 00.	14 00.1	4 00.14	00.07	00.05	**	147	170	101 2	4 17	200	202	287	100 1	3 3/0	633	20.3	203	F 11	r 244	222	473	120	240	360 34	: ::	207	200	207
A A A A B	Jac. And Land			12,04 52,			52,35	00,24	80,23 80,2		00,2.0	22,00	22,24		10,011 B.				88,03	89,03		2.44					203	287	203 21		37.8					2.00	424						287	
A A A A A B	Ar. Neurona 10002	24 33,62	94,62	93,7 93,	A2 90,5	4 33,74	\$1,81	54,21	91,6 91,	/4 91,4	91,44	91,56	93,55 1	N'2P 3	10,62 93,	39 34,.	21 94,2	1 94,21	94,09	94,09	94,78		21	114 11	10 V	4 238	2.89	252	241 2	a 252	610	2.04	245 4	36 13	1 200		409	230	239	341 23	0 23	252	121	- 202
Image Image <th< td=""><td>As. shavenessis (IWGC sequence)</td><td>25 92,57</td><td>92,57 9</td><td>12,66 92,</td><td>,38 92,6</td><td>8 92,69</td><td>92,78</td><td>93,21</td><td>90,93 90,9</td><td>13 90,93</td><td>90,93</td><td>92,56</td><td>92,56 1</td><td>22,56 1</td><td>19,55 92,</td><td>56 93,3</td><td>21 93,2</td><td>1 93,21</td><td>93,09</td><td>93,09</td><td>92,78</td><td>97,7</td><td></td><td>189 15</td><td>1 1</td><td>17 224</td><td>235</td><td>251</td><td>237 2</td><td>H 246</td><td>636</td><td>257</td><td>262 2</td><td>63 20</td><td>S 237</td><td>219</td><td>440</td><td>256</td><td>279</td><td>363 22</td><td>9 22</td><td>251</td><td>251</td><td>251</td></th<>	As. shavenessis (IWGC sequence)	25 92,57	92,57 9	12,66 92,	,38 92,6	8 92,69	92,78	93,21	90,93 90,9	13 90,93	90,93	92,56	92,56 1	22,56 1	19,55 92,	56 93,3	21 93,2	1 93,21	93,09	93,09	92,78	97,7		189 15	1 1	17 224	235	251	237 2	H 246	636	257	262 2	63 20	S 237	219	440	256	279	363 22	9 22	251	251	251
A A A A A A B	P. spicate 19002	25 84,09	\$4,09 \$	14,18 83,	,93 84,	2 84,2	\$4,32	85,54	85,54 85,5	4 85,5	85,5	\$4,34	\$4,34	64,34 8	16,52 \$	1,3 85,5	54 85,5	4 85,54	\$5,32	\$5,32	85,32	\$4,44 \$	3,85	33	1 22	13 421	422	421	424 43	1 434	721	371	426 4	27 35	9 415	282	604	407	412	512 43	G 41	421	421	421
A A B	II. persica 115556	27 85.88	85.88 8	5.92 #5.	71 85.9	9 85.99	86.15	87.74	83.17 83.1	7 83.17	83.21	85.8	15.1	15.1 1	5.84 85.	76 87.3	74 87.7	4 \$7.74	\$7.6	87.6	88.03	86.43 8	5.61 @	6.41	35	5 374	375	425	377 3	4 372	681	352	372 3	73 37	4 258	329	560	357	342	477 42	2 41	425	435	435
F and a 2 / 2 F and	Ac. searchi 19605	28 92.2	92.2 9	2.28 91	93 92.2	4 92.24	92.37	92.92	90 9	90 90	90	92.11	92.11 1	2.11	9.13 92.	11 92.1	92 92.9	2 92.92	92.81	92.81	92.58	96.82 9	6.26 B	1.77 115.3	2	247	248	257	250 2	7 254	627	254	245 2	46 20	0 243	229	450	249	280	359 27	4 23	257	257	257
Image: State Image: State<	T applying or Chinese string III NORNESS	22 87.48	0740 0	7.56 87	27 87.5	6 07.56	87.64	89.41	05.46 05.4	34.28 21	05.46	873	87.3	87.3 8	6.75 87	13 89.	41 02.4	1 00.41	89.31	89.31	89.04	80.97 Q	0.11 #	0.65 04 3	3 89.6	4		277	e .	0 63	678	240	211 2	12 20	6 343	328	540	319	335	453 20	5 25	277	277	277
Frame A D <thd< th=""> D <thd< th=""> <thd< th=""></thd<></thd<></thd<>	T and an an Alle have 180	33 87.44			22 82.8	3 4343	87.6	80.37	AT 41 AT 4		85.43	47.74	87.74			26 80.	17 00.1	1 00.33	80.34	00.36		#0.03 O	0.07 #		0.00	r 00.83		333			6.78	343				333	110	120	337	47.4 34		110	330	220
Properticie	2. antennet CV. Via Parts [in]	80 87,99	87,44 8			a ar, aa		22,27				87,40	87,88	.,	10,00 87,								0,00 #					4/1			478						220	220		101 10				
	7. avativuse cv. nos wane (n)	32 87,82	87,82	10,9 10,	,56 87,8	5 87,85	10,9	20,42	15,79 15,7	9 85,79	10,81	\$2,73	10,74	17,72	35,7 37,	7.4 88,7	42 23,4	8 35,45	38,42	38,42	10,07	29,29	29,4 2	1,63 B2,0	12 \$9,2	12 10,42	22,04		280 2	/ 285	610	100	2/1 4	12 1)		294	519	347	244 1	412 1	s 4		0	
P - P - P - P - P - P - P - P - P - P -	7. targidaw subsp. dicaccoider [A] Tril8508	32 87,35	87,35 1	17,44 117,	,24 87,4	3 17,43	\$7,52	89,28	45,33 45,3	13 115,33	\$5,11	87,18	17,18	17,18 8	16,62 17,	18 89,3	28 89,2	8 89,21	\$9,18	\$9,18	88,91	19,84 1	9,98 E	2,52 84,6	1 19,5	1 99,78	22,62	88,29		5 66	681	243	214 2	15 20	9 346	221	552	322	329	456 25	a 25	1 280	290	280
Desc Desc <thdesc< th=""> Desc Desc <thd< td=""><td>7. targishou subsp. dicoccoides [A] Tril \$485</td><td>33 \$7,48</td><td>87,48 1</td><td>17,56 117,</td><td>,27 87,5</td><td>6 17,56</td><td>\$7,64</td><td>89,41</td><td>15,46 15,4</td><td>16 15,46</td><td>85,46</td><td>87,3</td><td>£7,3</td><td>87,3 8</td><td>16,75 83</td><td>7,3 89,4</td><td>41 89,4</td><td>1 29,41</td><td>\$9,31</td><td>89,31</td><td>29,04</td><td>29,97 9</td><td>0,11 #</td><td>2,65 84,3</td><td>1 19,6</td><td>14 100</td><td>29,62</td><td>\$8,42 9</td><td>2,71</td><td>63</td><td>678</td><td>240</td><td>211 2</td><td>12 20</td><td>6 343</td><td>328</td><td>549</td><td>319</td><td>336</td><td>453 25</td><td>5 25</td><td>277</td><td>277</td><td>277</td></thd<></thdesc<>	7. targishou subsp. dicoccoides [A] Tril \$485	33 \$7,48	87,48 1	17,56 117,	,27 87,5	6 17,56	\$7,64	89,41	15,46 15,4	16 15,46	85,46	87,3	£7,3	87,3 8	16,75 83	7,3 89,4	41 89,4	1 29,41	\$9,31	89,31	29,04	29,97 9	0,11 #	2,65 84,3	1 19,6	14 100	29,62	\$8,42 9	2,71	63	678	240	211 2	12 20	6 343	328	549	319	336	453 25	5 25	277	277	277
Image Image <th< td=""><td>T. targidow subsp. disaccoides [A] Tril8523</td><td>34 \$7,07</td><td>87,07 8</td><td>17,16 \$1</td><td>6,9 87,3</td><td>9 \$7,19</td><td>\$7,27</td><td>89,11</td><td>85,16 85,1</td><td>16 \$5,16</td><td>85,16</td><td>86,93</td><td>\$6,93 1</td><td>86,93 8</td><td>16,99 86,</td><td>23 \$9,5</td><td>11 89,1</td><td>1 29,11</td><td>\$9,01</td><td>\$9,01</td><td>22,74</td><td>\$9,38</td><td>29,6 E</td><td>2,12 84,7</td><td>7 89,3</td><td>13 97,27</td><td>97,18</td><td>\$5,04 9</td><td>7,14 97,2</td><td>7</td><td>671</td><td>267</td><td>194 1</td><td>95 23</td><td>7 240</td><td>327</td><td>548</td><td>336</td><td>252</td><td>447 25</td><td>4 26</td><td>286</td><td>286</td><td>286</td></th<>	T. targidow subsp. disaccoides [A] Tril8523	34 \$7,07	87,07 8	17,16 \$1	6,9 87,3	9 \$7,19	\$7,27	89,11	85,16 85,1	16 \$5,16	85,16	86,93	\$6,93 1	86,93 8	16,99 86,	23 \$9,5	11 89,1	1 29,11	\$9,01	\$9,01	22,74	\$9,38	29,6 E	2,12 84,7	7 89,3	13 97,27	97,18	\$5,04 9	7,14 97,2	7	671	267	194 1	95 23	7 240	327	548	336	252	447 25	4 26	286	286	286
4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	II. usbrary cy. Inti	35 76.79	76.79 7	6.83 76.	66 76.8	9 76.89	76.99	78.36	74.96 74.9	6 74.96	75	76.52	76.52	76.52 7	5.34 76.	52 78.2	16 78.3	6 78.30	78.28	78.28	78.52	76.89 7	6.33 7.	1.38 75.0	13 76.7	74.94	74.94	75.25 7	183 74.5	4 74.88		608	662 0	ធ ធ	3 648	630	851	650	660	763 67	5 65	670	670	670
A relation of the state A relation of	A maticany 10572	36 \$9.21	89.21 8	9.29 88.	99 89.2	9 89.29	89.45	91.56	87.07 87.0	17 87.07	87.07	88.94	88.94 1	10.94 0	8.08 88.	94 91.5	56 91.5	6 91.50	91.45	91.45	91.06	90.14 8	9.21 #	154 15.3	6 19.2	9 89.86	89.81	87.51 8	2.72 89.1	6 \$8,76	77.25		247 2	49 24	7 284	251	472	265	281	382 27	1 27	300	300	200
A A A B	de moderides attract	22 82.28	0770 0		47 87.7	4 47.74	87.78		AT 37 AT 3		88.38	87.00	17.00		7.10					80.81				107 04	0 50.7	01.15	01.07	## 37 O		r 01.03	77.87	0.00		3 14	e 336	224	600	310	334	417 74	0 34		333	222
4 5	to mobile APAT	38 87,78	87,78 8	7.74 87	43 87	7 87.7	87.74	80.75	87,33 87,3	13 85,83	85,83	87,00	87.63	17,00 0	17.34 87	() (0)	76 80.7	e ao 74	80,77	80.77	10.46	00.13 0	0.03 #		a 20,7	01.11	01.07	88,79 9	100 01	1 01.75	70,00	10,000	0.01		7 334	201	104	120	317	410 24	0 20	272	272	272
A A B	AL APRILATE ADVES		87,74 8	17,14 87,			87,14	89,70					87,44	.,	17,24 87,			u			23,00	20,12 0					81,03				10,04						201	220					272	
La and La	Ar. Ipstoater ALS2/	29 90,29	90,19 5	10,19 19,	,84 90,3	5 90,15	90,29	50,48	17,71 17,7	1 17,71	11,71	29,94	29,94	19,94	11,4 19,	94 90,4	es 90/e	a 90,45	90,41	90,41	90,06	92,27 9	1,28 8	4,81 84,8	a 91,5	12 91,27	91,18	92,44 9	1,24 92,2	·/ 90,8	76,38	19,59 3	4,17 94	12	204	241	462	202	276	383 13	6 15	1/4	1/1	1/8
A A A A B	S. centale cv. Picasso [1]	40 90,22	90,22	90,3 90,	,08 90,3	4 90,24	90,42	90,03	17,56 17,5	6 17,56	87,52	90	90	- 90 B	18,92 89,	95 90,6	03 90,0	3 90,03	19,88	89,88	29,61	91,18	- 90	12,7 115,1	1 19,1	1 85,8	\$5,76	\$6,82 8	5,68 85	8 \$5,89	75,96	18,13	\$6,2 \$6	16 88,8	9	113	234	150	176	267 29	5 29	317	317	317
I wale A 1 A 1 A 1 B 1<	S. cereale cv. Imperial R1150	41 91,14	91,14 9	11,23 90,	,99 91,3	\$ 91,26	91,34	90,81	88,25 88,2	15 88,25	88,3	90,83	90,83 1	20,83	90,1 90,	\$3 \$0,5	81 90,8	1 90,81	90,66	33,02	90,31	91,99 9	0,71 \$	0,05 86,0	18 90,3	15 86,16	\$6,32	87,54 8	5,24 85,2	IG \$6,37	76,56	19,44 1	17,78 87	74 89,8	1 95,18		221	140	150	243 27	6 27	298	298	298
Constraining Star	S. cernale cv. Picasso [2]	42 \$3,33	83,33	83,4 83,	21 83,4	3 \$3,43	\$3,51	\$3,07	80,68 80,6	8 50,65	80,72	\$3,04	\$3,04 1	13,04 8	12,36 83,	04 \$3,0	07 83,0	7 \$3,07	\$2,95	\$2,95	\$2,61	\$4,07 \$	2,93 7	5,96 78,9	1 82,6	5 79,09	79,05	80,13 7	1,97 79,1	9 79,08	70,74	11,83 8	10,79 80	76 82,3	2 85,95	91,28		361	371	464 45	7 49	519	519	519
	S. sylvestre R1116	43 \$0.76	90.76 9	0.85 90.	54 90	8 90.8	90.89	90.75	87.88 87.8	8 87.88	87.92	90.46	90.45 1	20.46	88.1 90.	45 90.3	75 90.7	5 90.75	90.6	3.09	90.33	90.27 B	9.21 E	1.11 05.7	4 19.5	5 86.67	86.63	86.4 8	5.54 86.1	7 \$5.99	75.87	18.84 8	6.79 86	74 88.5	5 93.65	94.05	85.99		91	257 30	6 30	327	327	327
I ALL 2 ALL	S. etricture 111 NOD9645.1	44 89.67	09.67 0	971 8	0.4 00.6	z 03.66	89.75	90.06	05.0 05	0.050	05.04	89.78	89.28	19.70 0	7.05 89	24 901	nc 93.0	6 90.01	80.97	89.97	09.57	89.77 8	1.70 E	202 850		1 86.02	85.08	85.73 0		0 85.34	75.56	18.21	86.9 86	86 88 3	0 02.50	93.64	05.61	05.0		254 27	1 32	344	344	244
Templore days amounts (17410) = 8 10 100 10 11 10 10 10 10 10 10 10 10 10	S. michael [1] Milliona 1	45 85.03	0503 0	16.01 85	23 05.5	7 85.97	86.08	05.71	83.16 83.1	6 8316	83.2	05.67	15.67	15.67	84.2 85	67 85	71 057	1 05.71	85.58	82.28	05.24	86.26 0	541 2	2 73 01 3	5 85.6	2 82.04	82	83.09 8	1.92 82	4 82 23	72.03	84.7 0	13 49 83	45 04.0	2 09 22	90.13	82.71	89.57	89.68		0 40	425	435	425
amprovement of large control and and an experiment of large control and	T should all all a should be should be should be a should be a should be a sho	45 50.00	88,88 8	10,01 80,	44 88.7	3 88.73	86,08	80.36	84,10 84,4	3 86.63	84.71	88,61	88,97	10,00	100, A 80,	47 8.0,0 73 8.0,1	16 80.3	·	80,33	00.30	88,05	00.33	0.33	100 011	r 201	0 00.14		00.03	1.72 82,7	4 88.00	75.84		0.67 80	13 03.3		80,00	80.07	47.77	25.50 8	12.04		14.1	14.5	
	r. mequerre samp artentacian [G] IEESIS	10,00		a,ra 22,					30,07 35,5	* *0,07					10,00 EE,	- 19,1	- 29,5	29,00					0,00 I		50,2			**,42 8			14,84	10/12 I	19,07 23		47,71	-4,45	80,97	arjar 1					15	- 2
T mapping [17] [17] [17] [17] [17] [17] [17] [17]	2. tmopnovu sutsp. arminiacam [G] Tril 1350	47 \$9,60	88,69 S	18,78 BB,	/4 88,7	a sil,73	88,78	89,36	39,67 36,6	1/ 16,67	80,71	38,61	88,01 1	0,61 8	19,50 III,	oz \$9,3	10 29,3	o #9,36	89,29	89,29	10,95	90,81 9	0,22 E	4,89 83,3	is 90,2	w 19,14	m9,26	38,92 8	A.22 193,7	M \$8,95	10,84	18,42 1	19,67 89	as 93,3	/ 17,71	88,46	80,97	11,27 1	30,09 87	.4,95 20	0	25	25	- 25
7. desphave [171:041] #1/1 #1/2 #1/2 #1/2 #1/2 #1/2 #1/2 #1/2	7. timphovil [G] Tril3159	48 87,82	87,82	87,9 87,	56 87,8	5 \$7,85	\$7,9	\$2,45	85,79 85,7	9 \$5,79	85,83	\$7,73	\$7,73	17,73	86,7 87,	73 \$8,4	48 88,4	8 88,45	\$\$,42	88,42	88,07	\$9,29	29,4 E	2,63 82,4	2 89,2	12 88,42	\$\$,24	100 S	1,29 88,4	2 \$\$,04	75,25	17,51 1	18,76 88	72 92,4	4 95,93	\$7,54	80,13	35,4 1	\$5,73 \$2	3,09 93,5	2 98,9		0	0
7. abadwark (GT 177278 50 87.42 87.42 87.42 87.42 87.45 87.45 87.45 87.45 87.45 87.45 85.79 85.7	T. timphanti [G] Tri5433	49 87,82	87,82	87,9 87,	56 87,8	5 87,85	\$7,9	\$2,45	85,79 85,7	9 \$5,79	\$5,83	\$7,73	\$7,73 1	17,73	85,7 87,	73 \$8,4	48 88,4	8 88,45	\$5,42	\$8,42	88,07	\$9,23	29,4 X	2,63 82,4	12 \$9,2	12 88,42	88,34	100 S	1,29 88,4	2 \$5,04	75,25	17,51 0	18,76 88	72 92,4	4 85,82	\$7,54	80,13	35,4 2	45,73 87	3,09 98,9	2 98,9	100		0
	T. zkukovsky [G] Tzi7258	50 \$7,82	87,82	27,9 27,	56 17,5	5 87,85	\$7,9	\$2,42	85,79 85,7	9 \$5,79	\$5,83	\$7,73	\$7,73 1	17,72	\$5,7 \$7,	73 \$8,4	42 23,4	8 85,45	\$\$,42	\$8,42	22,07	\$9,22	29,4 X	2,63 82,4	12 \$9,2	2 88,42	\$1,24	100 8	1,29 88,4	2 \$5,04	75,25	17,51 8	18,76 88	72 92,4	4 \$5,83	\$7,54	\$0,13	35,4 /	45,73 87	3,09 93,5	2 98,9	1 100	100	1

Fig. 2 Pairwise comparison based on the alignment of all isolated sequences. Below the diagonal, percent similarity; above the diagonal, number of differences



Fig. 3 Maximum likelihood tree based on the four different partitions of the *PAPhy_a* gene. The *numbers* below or above the branches are bootstrap proportions

>99% similar (Fig. 4, top panel left). The 5'flanking sequences were 67-100% similar (Fig. 4, top panel center). As for the full length sequences, the **A** genome 5'flanking region are highly similar within the subgroups. The pairwise comparison can therefore be simplified: A–G is 74–75% similar to H–K and 91–92% similar to L–O. The groups H–K and L–O are 67-68% similar. At the protein level, the *T. aestivum* cv. Bob White allele stands out because of a frame shift insertion. The remaining proteins in the **A** genome group has 0–10 amino acid differences but no indels.

Three *T. aestivum* and four *Ae. tauschii* sequences belong to the **D** genome group (Fig. 4 bottom panel).

| |
 | | | C | D 1
 | 5 F. | G | н | I | · .
 | | L | м | N | 0 | Δ.
 | 8 | C | D I
 | | G | н | 1 | | K | L | м | N | 0 | | B | C | D | E | F | G | н | · . | 1 | ĸ | L | M N | 0 |

--
--

--

 | | 16 | 4 | 9 1
 | 8 8 | 1 | 56 | 34 | 54
 | \$3 | 72 | 72 | 72 | 72 |
 | 0 | 0 | 1 1
 | | 0 | 72 | 72 | 71 | 20 | 24 | 24 | 23 | 24 | | 250 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 0 | 0 |
| | T aratises cv. linb White [A] B
 | 99,21 | | 18 | 15 14
 | 14 | 54 | 90 | 90 | 90
 | 89 | 78 | 28 | 28 | 28 | 100
 | | 0 | 1
 | | | 72 | 22 | 71 | 70 | 24 | 24 | 23 | 24 | 306 | | 280 | 290 | 280 | 280 | 290 | 280 | 280 | 290 | 290 | 280 | 280 290 | 280 |
| | T. asstroam ev. Villa Juniz [A] C
 | 91,82 | 89,22 | | 11
 | 1 10 | 50 | 84 | 24 | 24
 | ** | 68 | - | 6.8 | - 64 | 100
 | 100 | | 1
 | | 0 | 22 | 22 | 71 | 70 | 24 | 24 | 23 | 24 | 0 | 206 | | 0 | 0 | 0 | | 0 | 0 | | 0 | 0 | 0 0 | 0 |
| | J. anarta 18110477 D
 | 99,61 | 99,35 | 99,52 |
 | 2 | | 81 | 85 | 85
 | 80 | 66 | 66 | 66 | 66 2 | 19,64 91
 | 9,64 5 | 98,64 |
 | | - 1 | 22 | 2.8 | 22 | 71 | 24 | 24 | 23 | 26 | 1 | 306 | | | 0 | 0 | | 0 | 0 | | | 0 | 0 0 | 0 |
| | I largahow opp. alconomies [A] InIHOS &
 | 500 | 99,85 | 99,81 9 | 0,45
 | | | 84 | | 84
 | | 72 | 72 | 72 | 72 | 100
 | 100 | 300 9 | 1,64
 | | | 72 | 72 | 71 | 70 | 24 | 24 | 21 | 24 | 0 | 206 | | | | 0 | | 0 | 0 | | | 0 | 0 0 | 0 |
| | They also a second seco
 | 99,65 | 99.4 | 99,52 | 99,7 99,40 |
 | | 82 | 82 | 82 | -
 | 70 | 70 | 20 | 70 | 100
 | 100 | 300 9 | 1,64 10 |
 | | 72 | 72 | 71 | 70 | | 24 | 21 | 24 | | 206 | | 0 | 1 | | | | | | | | | 0 |
| - | Transpane up announces (A) Transfer II
 | 64,65 | | 100,00
100,00 |
 | | 44.45 | ~ | ~ |
 | | - 22 | | - 22 | | 24.4
 | 200 | 200 0 |
 | | | | 14 | · · · | ~ | | | | | | 201 | | | | - 1 | | | | | | | | |
| | Z. dimensional (A) Tables 1
 | 56.16 | 96.11 | 10.16 | 6.43 96.10
 | 06.45 | 56.45 | 100 | × | - 1
 | | 127 | 122 | 122 | 127 | 24.5
 | 34.1 | 341 3 | 174 74
 | | 24.1 | 100 | | | | 61 | | 91 | 61 | : | 276 | | | | | - 1 | | | ž | | | | č |
| | T rimenhoosi one commission (A) Toi11350
 | 56.16 | 96.11 | 10.16 | 6.43 96.10
 | 06.45 | 56.45 | 99.91 | 99.91 |
 | | 127 | 122 | 122 | 127 2 | 4.46 2
 | 1.45 Y | 14.66 | 14.1 24.4
 | 74.4 | 34.46 | 99.53 | 00.52 | | | | | | | : | 200 | | ě | : | | - 5 - | | | | ő | | | ě |
| | T rimenheast one commission (A) Tol19519 K
 | 56.51 | 96.16 | 10.41 0 | 6.52 96.0
 | 10.43 | 56.03 | 99.6 | 99.6 | 88.6
 | | 126 | 116 | 122 | 126 2 | 4.63 2
 | 4.92 3 | 14.82 2 | 1.66 74.9
 | 74.91 | 34.92 | 99.04 | 99.04 | 99.57 | | | | | | | 207 | | | | | | | | | | | | |
| | 7. memoranam NGR1991 L
 | 15.89 | 96.64 | 97.66 5 | 0.15 96.81
 | 96.58 | 16.33 | 95.08 | 94.08 | 94.08
 | 94.52 | | | 2 | 0 8 | 1.32 9:
 | 137 8 | 15.37 9 | 1.37 91.3
 | 95.37 | 91.37 | 67.15 | 67.55 | 62.51 | 67.87 | | 0 | 1 | | ÷. | 308 | | - 2 | | 2 | | 2 | - 2 | - 2 | | | 0 0 | 0 |
| | Z menococcum snn. arrifeneider Trill#94 M
 | 96.89 | 96.64 | 97.06 5 | 0.25 96.81
 | 96.58 | 96.98 | 95.08 | 94.08 | 94.08
 | 96.52 | 100 | | 2 | 0 8 | 1.32 9:
 | 137 8 | 15.37 9 | 1.37 91.3
 | 95.33 | 91.37 | 67.15 | 67.55 | 62.51 | 67.82 | 100 | | 1 | | | 228 | | 7 | | 7 | | 2 | 7 | 2 | | 0 | | 0 |
| | 7. menoencom pp. aegilepeider Tril1095 N
 | 96.89 | 96.64 | 97.06 5 | 0.25 96.81
 | 96.58 | 96.98 | 95.05 | 94.04 | 94.05
 | 95.08 | 99.91 5 | 9.95 | | 2 8 | 1.72 8
 | 128 8 | 12.22 1 | 1.78 91.7
 | 91.27 | 91.72 | 67.15 | 67.55 | 67.51 | 67.82 | 99.63 | 99.63 | | | | 228 | | | | | 20 | | | | | 1 | 1 | 0 |
| | T abakevsky [A] Tii7258 O
 | \$6,89 | 96,64 | 97,06 8 | 0,25 96,87
 | 96,58 | \$6,98 | \$5,08 | 94,08 | 94,08
 | \$4,52 | 500 | 100 99 | | - 1 | 1,32 9.
 | uin s | 65,27 B | 1,27 91,3
 | 95,31 | 91,37 | 67,15 | 67,55 | 67,51 | 67,87 | 100 | 100 | 19,63 | | | 308 | 1 | 7 | | 7 | 1 | - 2 | 7 | 2 | | 0 | 0 1 | |
| |
 | _ | | | | | | | | | | | | | | | | | | | | | | | |
 | | | | |
 | | | | | |
 | | |
 | | | | | | | | | | | | | | | | | | | | | | | | |
| |
 | | | | | |
 | Full sade | olde (% sine | alarity \ diffe | sunces) |
 | | | | | |
 | | | 9 Flanki
 | gragion(% | similarly (a | Termon) | | | | | | | | | | | Protein | (difference) | (apple in | | | | | | | | |
| |
 | A | - 2 | c | D I
 | i 8 | G | ы | - | 3
 | x | L | м | N | A | 2
 | C | D | 1 3
 | 6 | | | 3 | x | L | М | N | A | - 2 | C | D | 3 | - 8 | G | н | _ | 3 | x | L | м | N | | |
| | 7. arstivem ev. Clause spring [8] M.620000 A
 | | 210 | | 0 1
 | | 247 | 210 | 210 | 215
 | 225 | 172 | 166 1 | 245 | | 76
 | 1 | 0 | 0
 | 24 | | 74 | 21 | 21 | | | | | | 0 | | | 0 | 0 | 0 | | 0 | 0 | | | 0 | | |
| | 7. arsthum cv. Ho Wide [1] H
 | 88,91 | | 228 | 217 24
 | 255 | 0 | 0 | | 20
 | 25 | 171 | 228 2 | 228 7. | 2,88 |
 | 11 | - 24 | 76 7
 | | 0 | | 24 | 24 | 11 | 71 | 29 | 16 | | 0 | | | 0 | 0 | 0 | | 0 | 0 | | | 0 | | |
| | A second of the second of the second of the
 | 99,82 | 89,82 | |
 | | 229 | 239 | 228 | 215
 | 217 | 174 | 148 1 | 267 9 | 4,57 | 72
 | | 1 | 1
 | | | <i>n</i> | | | | | | 0 | 14 | | 0 | | | | | | | | | | 0 | | |
| | r. organie pp. anternaie pij ritteto in
 | 200 | 40,04 | |
 | | 447 | 2.8.7 | 287 | ***
 | | | | | | u,m
 | 00,417 | |
 | | | | | | | | | | | | | ~ | | | | × . | | | × . | | | | |
| |
 | | | | | | | | | | | | | | | | | | | | | | | | |
 | | | | |
 | and a | | | | |
 | | |
 | | | | | | | | | | | | | | | | | | | | | | | | |
| D | 7. Jargahaw app. dissociation [34] Tri10008 &
7. Intercident care, dissociation (30) Tri10223 &
 | 99,78 | 89,78 | 10,41 1 | 6,28
8.78 97.64
 | | 200 | 360 | 240 | 218
 | 258 | 175 | 103 177 | 121 | 100 Z | 12,36 91
1736 91
 | 19,52
19.52 | 100 | 100
 | 2 N | 26 | 26 | 52 | 12
12 | 44 | 45 | | 1 | 17 | 1 | 1 | | • | 0 | 0 | | 0 | 0 | | 0 | 0 | | |
| В | Jarguhan app. disseconder [H] Tri10008. It. Targuhan app. disseconder [H] Tri10523. F T. Investment (H) Tri10526. G
 | 98,78
98,08
99,91 | 89,78
89,16 | 58 5 | 6,78
6,08 97,97
9.91 99.71
 | | 255 | 260 | 240 | 218 223
 | 218 222 25 | 175
187
171 | 168 1
172 1
224 1 | 188
171
179 7 | 100 7.
100 7. | 0,36 9/
0,36 9/
100
 | 19,52
19,52
33 3 | 100
100 | 100 × 11 k
 | 2 2 | 76 | 26 | 52
52
34 | 53
53
24 | 44
44
22 | 45
45
79 | 6
6
3 | 0 | 15 | 0 | 1
0
16 | 1 | 0
14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | |
| В | 7. Jarguhan app. disocondar (34) 1011008 h.
7. Jarguhan app. disocondar (34) 1011523 F
T. timphewii (34) 1013159 G
T. Limothewii (38) 101433 at
 | 98,78
98,08
88,91
88,91 | 89,78
89,16
100 | 99,41 5
58 5
89,82 5
99,92 5 | 0,78
8,08 97,9
9,91 89,7
9,91 99,7
 | 47
1 89,16
1 99.16 | 255 | 260
255
0 | 240
255
0 | 218
223
25
 | 258
283
25
35 | 175
187
171
171 | 168 1
172 1
228 1
279 1 | 148
171
228 7.
179 7 | 500 X
500 X
2,86 | 12,36 98
12,36 98
100
100
 | 6,52
6,52
72 3 | 100
100
72,36 7
73,86 7 | 100
2,86 72,8
 | 2 24 | 76 | 76
76
0 | 53
53
24 | 53
53
24
34 | 44
44
77
77 | 45
45
71 | 61
65
29 | 1
0
16 | 15 | 1
0
16 | 1
0
16 | 12 | 0
26
56 | 0 | 0 | 000 | 0000 | 000 | 000 | 0 | 0 0 0 | | |
| В | 7. Inryahaw app. disoconider [40] 11.112008 ii.
7. Inryahaw app. disoconider [30] Tx11523 F
T. Jimopherwit [30] Tx113159 G
T. Jimopherwit [31] Tx13159 G
T. Jimopherwit [31] Tx1258 J
 | 98,78
98,08
88,91
88,91
88,91 | 89,78
89,16
500
500
500 | 99,43 5
58 5
89,82 5
89,82 5
89,82 5 | 9,78
8,08 97,97
9,91 89,71
9,91 89,71
9,91 89,71
 | 47
k 89,16
k 89,16
k 89,16 | 200
255
200
200 | 260
255
0
200 | 240
255
0 | 218
223
25
25
25
 | 218
222
25
25
25
25 | 175
187
171
171
171 | 168
172
228
228
228
228 | 148
171
228 7
228 7
228 7 | 500 7.
500 7.
2,36
2,36
2,36 | 12,36 91
12,36 91
100
100
100
 | 0,57
0,57
72 3
72 3
72 3 | 100
100
72,36 7
72,36 7
72,36 7 | 500
2,36 72,3
2,36 72,3
2,36 72,3
 | 5 N
N
300 | 76
76
0 | 35
35
0 | 53
53
24
25
26
24 | 53
53
24
24
24 | 64
64
77
77
77 | 45
45
71
71
71 | 45
45
29
29
29 | 1
0
16
16 | 1)
16
0
0 | 1
0
16
16 | 1
0
16
16
16 | 1
12
12
12 | 0
26
26 | 0 0 0 | 000 | 0
0
0 | 0 0 0 0 | 00000 | 0 0 0 0 | 0 0 0 | 0 0 0 0 | | |
| В | 7. Jacquines upp. disconsider [8] Tal3008 &
T. Jacquines upp. disconside [8] Tal3023 &
T. Jimophereii [8] Tal3159 G
T. Jimophereii [8] Tal3043 g
T. Jimophereii [9] Tal3258 1
T. Jimophereii upp. armeniacum [8] Tal3156 J
 | 98,78
98,08
88,91
88,91
88,91
92,84 | 89,78
89,16
500
500
98,92 | 99,43 5
58 5
89,82 5
89,82 5
89,82 5
90,76 5 | 9,78
8,08 97,97
9,91 89,77
9,91 89,77
9,91 89,77
9,91 89,77
9,84 90,72
 | 47
k 89,16
k 89,16
k 89,16
t 90,1 | 200
255
200
200
98,82 | 260
255
0
200
96,92 | 240
255
0
98,92 | 218
283
25
25
25
 | 218
223
25
25
25
0 | 175
187
171
171
171
171
149 | 168
172
228
228
228
228
228
228
207 | 148
171
228 7
228 7
228 7
228 7
228 8 | 500 7.
500 7.
2,36
2,36
2,36
3,78 9 | 12,36 91
12,36 91
100
100
100
11,34 81
 | 6,57
6,57
72 3
72 3
72 3
6,36 \$ | 100
100
72,86 7
72,86 7
72,86 7
80,72 8 | 100
2,36 72,3
2,36 72,3
2,36 72,3
3,78 80,7
 | 100 N | 76
76
0
500
91,24 | 26
26
0
91,24 | 53
53
24
24
24 | 53
53
24
24
24
0 | 64
64
77
77
77
54 | 45
45
71
71
71
56 | 45
45
29
29
29
56 | 1
0
16
16
16 | 17
16
0
0
0 | 1
0
16
16
16 | 1
0
16
16
16
16 | 1)
1)
1)
1)
1) | 0
26
26
26 | 0 0 0 | 00000 | 0
0
0 | 0 0 0 0 | 0 0 0 0 | 0 0 0 0 0 | 0 0 0 0 | 0 0 0 0 0 | | |
| В | Jorgishen opp. disconsistic [0] Tel18208 F. T. Izegishen opp. disconsistic [0] Tel1825 F. T. Isinghevei (opp. arwanisana [0] Tel1815 F.
 | 99,79
98,08
88,91
88,91
88,91
90,84
90,84 | 89,78
89,16
500
500
98,90
88,90
88,90 | 90,41 5
58 5
89,82 5
89,82 5
89,82 5
90,75 5
90,75 5 | 9,78
8,08 97,97
9,81 89,77
9,81 89,77
9,81 89,77
0,84 90,72
0,84 90,72
 | 47
k 89,16
k 89,16
k 89,16
k 89,16
t 90,1
k 90,1 | 200
255
200
200
98,82
98,82 | 260
255
0
900
98,92
98,92 | 240
255
0
9
98,90
98,90 | 218
233
25
25
25
100
 | 218
233
25
25
25
0 | 175
187
171
171
171
171
149
149 | 168
172
228
228
229
229
200
200 | 14X
171
228 7.
228 7.
228 7.
228 7.
206 8
206 8 | 500 7.
500 7.
2,36
2,36
2,36
2,36
3,73 8
3,73 8 | 12,35 97
12,35 97
100
100
11,34 88
11,34 88
 | 0,57
0,57
72 3
72 3
72 3
0,36 8
0,36 8 | 100
100
72,36
72,36
72,36
72,36
80,73
80,73
80,73
80,73 | 200
2,36 72,3
2,36 72,3
2,36 72,3
3,78 80,7
3,78 80,7
 | 5 N
300
300
91,34
91,34 | 76
76
0
91,24
91,24 | 25
25
0
91,24
91,24 | 53
53
24
24
24
24 | 53
53
24
24
24
0 | 44
44
77
77
77
54
54 | 45
45
71
71
71
71
56
56 | 45
29
29
29
56
56 | 1
0
16
16
16 | 17
16
0
0
0
0 | 1
0
16
16
16 | 1
0
16
16
16
16 | 1
17
17
17
17
17
17
17
17 | 0
26
26
16
16 | 0 0 0 0 | 000 000 | 0
0
0
0 | 0 0 0 0 | 00000 | 0000000 | 0 0 0 0 0 | 0 0 0 0 0 0 0 | | |
| в | Jorgahm pp, discontatis [40] 1410008 ii
<i>T. Inregulam pp, discontatis [40]</i> 1418129 f
<i>T. Interpherent</i> [40] 1418149 f
<i>T. Interpherent</i> [40] 141013 jj
<i>T. Interpherent</i> [40] 141013 f
<i>T. Interpherent</i> [40] 141015 f
<i>T. Interpherent</i> [40] 1411516 f
<i>T. Interpherent</i> (40] 1411518 K
<i>Ac.</i> speciation KEPT [40]
 | 99,79
98,08
88,91
88,91
88,91
90,84
90,84
92,61 | 89,78
89,16
500
500
88,90
88,90
88,90
88,90
82,68 | 99,41 0
58 5
89,82 5
89,82 5
89,82 5
90,76 5
90,76 5
90,76 5 | 9,78
8,08 97,61
9,81 89,71
9,81 89,71
9,81 89,71
9,84 90,72
9,84 90,72
9,84 90,72
 | 47
k 89,16
k 89,16
k 89,16
k 90,1
k 90,1
k 91,98 | 200
255
100
98,82
98,82
92,69 | 240
255
0
98,92
98,92
92,69 | 240
255
0
98,90
98,90
92,68 | 218
283
25
25
25
100
93,63
 | 218
233
25
25
0
93,63 | 175
187
171
171
171
171
169
169 | 168
172
228
228
229
207
207
158 | 14.8
171
228 7,
228 7,
228 7,
228 7,
206 8
206 8
157 8 | 5050 7,
5050 7,
2,366
2,366
3,728 9,
3,728 9,
3,728 9,
3,728 9, | 12,36 91
12,36 91
100
100
11,34 81
11,34 81
11,34 81
11,34 81
 | 9,57
9,57
72 3
72 3
72 3
10,36 8
10,36 8
10,36 8 | 100
100
72,86
72,86
72,86
80,73
80,73
80,73
83,27
8 | 500
2,36 72,3
2,36 72,3
2,36 72,3
3,78 80,7
3,78 80,7
3,78 80,7
8,27 88,2
 | 100 N
100 N
100 N
100 N
100 N
100 N
100 N
100 N
100 N
100 N | 76
76
0
91,24
91,24
91,24
73,45 | 25
25
0
91,24
91,24
22,45 | 53
53
24
24
24
24
100
81,38 | 53
53
24
24
24
0
81,88 | 44
44
77
77
75
54
54 | 45 H H H H H H H H H H H H H H H H H H H | 45
45
29
29
29
56
56
56
26 | 1
0
16
16
16
16
16
12 | 17
16
0
0
0
0
14 | 1
0
15
15
15
15
15
15
15 | 1
0
16
16
16
16
12 | 1
17
17
17
17
17
17
17
18 | 0
26
26
26
16
15
12 | 0
0
0
0
0
14 | 0 0 0 0 14 | 0
0
0
0
14 | 0
0
0
0
14 | 0000 | 0000000 | 0 | 0 0 0 0 0 0 0 | | |
| В | Jorgahon pp. discociadis [40] Tat1800 it. T. torgahon pp. discociadis [40] Tat1812 fi
T. throughout [40] Tat1812 fo
T. throughout [41] Tat1315 fi
T. throughout [41] Tat1325 it T. throughout [42] Tat1325 it T. throughout [42] Tat135 it T. throughout [42] Tat135 it T. throughout [43] Tat135 it T. throughout [44] Tat135 it T. throughout [45] Tat135 it T. throughout
 | 99,79
98,08
88,91
88,91
88,91
90,84
90,84
90,84
92,61
92,93 | 89,78
89,16
200
200
98,90
98,90
92,68
90,15 | 99,41 0
58 5
89,82 5
89,82 5
90,76 5
90,76 5
92,53 5
92,84 5 | 9,78
8,08 97,61
9,81 89,71
9,81 89,71
9,81 89,71
9,84 90,7
9,84 90,7
9,84 90,7
9,84 90,7
9,84 90,7
 | 47
k 89,16
k 89,16
k 89,16
k 90,15
c 90,1
k 91,98
k 92,67 | 200
255
300
98,82
98,82
92,69
90,35 | 360
255
0
98,92
98,92
92,69
90,15 | 240
255
0
98,92
98,92
92,68
90,15 | 218
283
25
25
25
25
90,63
91,83 | 218
283
25
25
0
98,62
91,28
 | 175
187
171
171
171
171
549
549
549 | 168
172
228
228
228
228
200
200
158 | 148
171
228 7
228 7
228 7
228 7
228 7
206 8
206 8
157 8
157 8
2 8 | 200 7.
200 7.
2,36
2,36
2,36
2,78 9.
2,78 9.
2,78 9.
1,27 7.
8,27 7. | 2,16 97
2,16 97
100
100
11,16 81
11,14 81
11,14 81
11,14 81
11,14 81
11,14 81
11,14 81
11,14 81
 | 9,52
9,52
72 3
72 3
72 3
1,36 8
1,36 8
1,36 8
1,89 8
1,89 8 | 100
100
72,36
72,36
80,78
80,78
80,78
83,27
83,21
8 | 500
2,36 72,3
2,36 72,3
2,36 72,3
3,78 80,7
3,78 80,7
3,78 80,7
8,27 88,2
8,21 88,2 | 5 N
300
300
1 91,24
1 91,24
1 91,24
1 73,81
1 73,81
 | 76
76
0
91,24
91,24
91,24
73,45
73,22 | 35
35
0
81,34
81,34
73,45
78,22 | 58
58
26
26
24
20
81,88
81,02 | 53
53
24
24
24
0
81,88
81,02 | 64
64
77
77
54
54
54 | 45
45
29
29
29
29
29
56
56
56
25 | 45
45
29
29
56
56
56
26
0 | 1
0
16
16
16
16
12
17 | 17
16
0 0 0 0
14
16 | 1
0
15
15
15
15
17 | 1
0
16
16
16
16
12
12 | 1
17
17
17
17
17
17
18 | 0
35
35
35
35
35
35
32
32
37 | 0
0
0
0
14
16 | 0000014 | 0
0
0
0
14
16 | 0
0
0
0
14
16 | 0
0
0
0
14
16 | 000000000000000000000000000000000000000 | 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 | | |
| В | Lengthen app. discontation [10] (181003) K. Lengthen app. discontation [10] (181023) F. T. Interpletives [10] (181023) K. T. Interpletives [10] (181024) JI Linterpletives [10] (181024) JI Linterple
 | 98,78
98,08
98,91
98,91
90,84
90,84
92,61
92,61
92,93 | 89,78
89,55
500
500
98,92
88,92
82,68
90,35
90,4 | 90,41 5
58 58,52 5
80,52 5
80,35 5
90,35 5
90,35 5
90,35 5
90,35 5
90,36 5
90,46 5 | 9,78
8,08 97,97
9,81 89,77
9,81 89,77
9,81 89,77
0,84 90,77
0,84 90,77
0,84 90,77
0,84 90,77
0,84 90,77
0,84 90,77
0,84 90,77
0,84 90,77 | 47
k 89,16
k 89,16
k 89,16
k 90,16
c 90,1
k 91,68
k 92,67
1 92,75
 | 240
255
200
98,82
98,82
92,49
90,25
90,4 | 255
0
255
9
90,92
92,69
90,15
90,4 | 240
255
0
88,00
88,00
82,68
90,15
90,4 | 218
223
25
25
25
90,61
91,82
91,82 | 218
283
25
25
25
0
93,63
91,28
91,28
91,22 | 175
187
171
171
171
189
169
169
181,27
181,11 4 | 148 172 1
228
2
228 2
229 2
229 2
200 2
158 1
168 1 | 148
171
228 7
228 7
228 7
228 7
228 7
206 8
206 8
157 8
2 8
2 8
2 8 | 200 7,
200 7,
2,36
2,36
2,36
2,36
3,72 8
3,72 8
3,72 8
3,72 8
3,27 7,
3,27 7,
3,21 7, | 2,16 9
2,16 9
100
100
11,24 8
1,24 8
9,45 8
9,45 8
9,22 8 | 0,52
0,52
72 3
72 3
12,36 8
0,36 8
0,36 8
0,89 8
0,89 8
0,86 8
0,86 8
 | 100
100
72,36
72,36
72,36
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,72
80,7 | 1000
2,36 72,3
2,36 72,3
2,36 72,3
3,78 80,7
3,78 80,7
3,78 80,7
3,78 80,7
3,78 80,7
3,78 80,7
3,78 80,7
3,78 80,7
4,21 81,2
4,21 81,2 | 5 N
300
91,30
91,30
91,30
91,30
91,30
91,20
73,40
 | 76
76
900
91,24
91,24
91,24
72,45
73,22
73,22 | 75
75
0
0
91,34
91,34
72,45
72,22
72,22 | 58
58
24
26
26
81,88
81,82
81,62
81,62 | 53
53
24
24
24
24
0
81,88
81,02
81,02 | 64
64
77
77
54
54
90,48
90,48 | 45
45
78
78
56
56
56
26
100 | 45
45
29
29
29
56
56
26
0 | 1
0
16
16
16
16
12
17
17 | 17
16
0
0
0
0
0
14
15 | 1
0
16
16
16
16
12
17
16 | 1
0
16
16
16
16
12
17
26 | 1
17
17
17
17
17
18
18
18 | 0
26
26
26
26
26
27
27
26 | 0
0
0
0
14
16
15 | 0 0 0 0 14 16 15 | 0
0
0
0
14
15 | 0
0
0
0
14
15 | 0
0
0
0
14
16
15 | 0
0
0
0
0
0
0
13
12 | 0
0
0
0
0
0
2 | 0 0 0 0 0 0 0 0 | | |
| В | Longchen app. dissociaties [20] 1141003 F. Longchen app. dissociaties [20] 1141004 F. Longchen app. [20] 112104 G. Longchen 20 [20] 112104 G. <li< th=""><th>99,792
98,092
88,912
88,912
88,912
90,845
90,845
90,845
92,612
92,932
92,932
92,932</th><th>89,78
89,56
500
500
98,92
92,68
90,55
90,4</th><th>99,41 5
98 5
89,42 5
90,75 5
90,75 5
92,51 5
92,84 5
92,88 5</th><th>9,28
8,08 97,99
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 92,49
0,93 92,49
0,97 92,49</th><th>47
k 89,16
k 89,16
k 89,16
k 90,16
k 91,08
k 92,67
h 92,71</th><th>240
255
200
98,82
98,82
92,69
90,25
90,4</th><th>360
255
0
90,92
91,92
92,69
90,15
90,4</th><th>240
255
0
98,92
98,92
92,43
90,45
90,4</th><th>218
223
25
25
25
93,63
91,28
91,12</th><th>218
223
25
25
0
93,62
95,22</th><th>175
187
171
171
171
173
169
169
169
169</th><th>148
172
228
228
228
228
228
228
228
228
228
2</th><th>148
171
228 7,
228 7,
228 7,
228 7,
206 8
206 8
157 8
2 8
2 8
2 8
2 8
2 8
2 8
2 8
2 8
2 8
2</th><th>200 7,
200 7,
2,36
2,36
2,36
3,73 8
1,27 8
1,27 7,
1,21 7,
1,21 7,</th><th>2,16 97
2,16 97
1000
1000
11,34 88
11,34 88
11,3</th><th>9,52
9,57
72 3
72 3
72 3
72 3
72 3
72 3
72 3
72</th><th>100
100
12,36
72,36
72,36
80,78
80,78
81,78
83,27
83,21
84,21
84,21
84,21
84,21
85,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21</th><th>100
2,86 72,3
2,86 72,3
2,86 72,3
2,86 72,3
0,78 80,7
0,78 80,7
0,78 80,7
0,78 80,7
1,27 83,2
1,21 83,2
1,21 83,2</th><th>5 N
300
5 100
5 10</th><th>76
76
0
91,24
91,24
91,24
73,45
73,22
73,22</th><th>76
76
0
91,34
91,34
73,45
73,22
73,22</th><th>58
58
24
24
24
100
81,88
81,02
81,02</th><th>53
53
24
24
24
0
81,88
81,02
81,02</th><th>64
64
77
77
54
54
54
90,68</th><th>45
45
78
78
78
56
56
56
26
25</th><th>45
45
29
29
29
56
56
56
20
0</th><th>1
0
16
16
16
16
16
12
17
15</th><th>17
16 0 0 0 0 0 14
16 15</th><th>1
0
56
56
56
56
56
52
12
12
56</th><th>1
0
16
16
16
16
12
17
26</th><th>1
12
12
12
12
12
12
13
18
18
12</th><th>0
26
26
26
26
26
27
27
26</th><th>0
0
0
0
14
15</th><th>0
0
0
14
15</th><th>0
0
0
0
14
15</th><th>0
0
0
0
14
15</th><th>0
0
0
0
0
14
16
15</th><th>0
0
0
0
0
0
1
1
1
2</th><th>0
0
0
0
0
0
2</th><th>0 0 0 0 0 0 0 0</th><th></th><th></th></li<> | 99,792
98,092
88,912
88,912
88,912
90,845
90,845
90,845
92,612
92,932
92,932
92,932 | 89,78
89,56
500
500
98,92
92,68
90,55
90,4 | 99,41 5
98 5
89,42 5
90,75 5
90,75 5
92,51 5
92,84 5
92,88 5 | 9,28
8,08 97,99
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
9,91 89,79
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 92,49
0,93 92,49
0,97 92,49 | 47
k 89,16
k 89,16
k 89,16
k 90,16
k 91,08
k 92,67
h 92,71 | 240
255
200
98,82
98,82
92,69
90,25
90,4 | 360
255
0
90,92
91,92
92,69
90,15
90,4 | 240
255
0
98,92
98,92
92,43
90,45
90,4 | 218
223
25
25
25
93,63
91,28
91,12 | 218
223
25
25
0
93,62
95,22 | 175
187
171
171
171
173
169
169
169
169 | 148
172
228
228
228
228
228
228
228
228
228
2 | 148
171
228 7,
228 7,
228 7,
228 7,
206 8
206 8
157 8
2 | 200 7,
200 7,
2,36
2,36
2,36
3,73 8
1,27 8
1,27 7,
1,21 7,
1,21 7, | 2,16 97
2,16 97
1000
1000
11,34 88
11,34 88
11,3 | 9,52
9,57
72 3
72 3
72 3
72 3
72 3
72 3
72 3
72 | 100
100
12,36
72,36
72,36
80,78
80,78
81,78
83,27
83,21
84,21
84,21
84,21
84,21
85,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21
86,21 | 100
2,86 72,3
2,86 72,3
2,86 72,3
2,86 72,3
0,78 80,7
0,78 80,7
0,78 80,7
0,78 80,7
1,27 83,2
1,21 83,2
1,21 83,2 | 5 N
300
5 100
5 10 | 76
76
0
91,24
91,24
91,24
73,45
73,22
73,22 | 76
76
0
91,34
91,34
73,45
73,22
73,22 | 58
58
24
24
24
100
81,88
81,02
81,02 | 53
53
24
24
24
0
81,88
81,02
81,02 | 64
64
77
77
54
54
54
90,68 | 45
45
78
78
78
56
56
56
26
25 | 45
45
29
29
29
56
56
56
20
0 | 1
0
16
16
16
16
16
12
17
15 | 17
16 0 0 0 0 0 14
16 15 | 1
0
56
56
56
56
56
52
12
12
56 | 1
0
16
16
16
16
12
17
26 | 1
12
12
12
12
12
12
13
18
18
12 | 0
26
26
26
26
26
27
27
26 | 0
0
0
0
14
15 | 0
0
0
14
15 | 0
0
0
0
14
15 | 0
0
0
0
14
15 | 0
0
0
0
0
14
16
15 | 0
0
0
0
0
0
1
1
1
2 | 0
0
0
0
0
0
2 | 0 0 0 0 0 0 0 0 | | |
| В | Legalson app. discontation [10] (18103) F. Legalson app. discontation [10] (18103) F. Linsopheres [10] (18103) F. Linsopheres [10] (18104) app. (18104) app. (18104) app. (18104) app. (18104) app. (18104) app. (18104) F. Linsopheres (190) enversionanon [10] (18105) K. Linsopheres (190) enversionanon [10] (18105) K. Ac quadratical A4213 M. As quadratical A42143 M.
 | 99,792
98,002
88,91
88,91
90,84
90,84
90,84
90,84
90,84
90,84
90,92 | 89,78
89,16
200
200
98,92
98,92
92,68
90,4
Full so | 99,40 9
98,42 8
89,42 8
89,42 8
90,76 9
90,76 9
92,81 9
92,81 9
92,81 9 | 9,28
9,28 97,91
9,91 89,79
9,91 89,79
9,91 89,79
9,81 89,79
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,84 90,72
0,95 92,90
10,95 92,90
10,95 92,95
10,95 92,95
1 | 47
k 89,16
k 89,16
k 89,16
k 90,16
k 91,08
k 92,67
1 92,71
mont)
 | 240
255
200
98,82
98,82
90,45
90,4 | 360
255
0
900
98,92
99,49
90,45
90,4 | 240
215
0
98,90
92,60
90,15
90,4 | 2218
2233
25
25
25
93,63
91,83
91,83
91,83 | 218
223
25
25
0
93,63
95,28
95,22
54,32
 | 175
187
171
171
171
169
169
83,27
83,11
4
differences | 148 172 1
273 2
228 2
228 2
229 2
200 2
158 1
158 1
158 1 | 148
171
228 7.
228 7.
228 7.
228 7.
228 7.
228 7.
228 8.
206 8
206 8
157 8
2 8
2 8 | 200 7,
200 7,
2,36 2,36 2,36 3,78 9,28 4,27 7,
3,72 9,21 7,
3,21 7,
2,21 7, | 2,35 97
2,35 97
1000
1000
11,34 88
11,34 88
11,3 | 9,52
9,52
72 3
72 3
72 3
72 3
72 3
72 3
72 3
72
 | 100
120
72,36
72,36
72,36
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,78
80,79
80,79
80,79
80,79
80,79
80,79
80,79
80,79
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,70
80,7 | 200
2,36 72,3
2,36 72,3
2,36 72,3
2,36 72,3
3,73 80,7
3,73 80,7
8,27 83,2
8,21 83,2
8,21 83,2 | 5 N
300
1 91,34
1 91,34
1 91,34
1 91,34
1 91,34
1 91,21
1 73,21 | 76
76
0
91,24
91,24
91,24
73,45
73,22
74,22 | 76
76
0
91,34
91,34
72,45
78,32
78,32 | 58
58
24
24
24
24
24
81,38
81,38
81,02
81,02 | 53
53
24
24
24
0
81,88
81,02
81,02 | 64
64
77
77
54
54
90,68
90,68 | 45
45
78
78
78
54
56
25
100 | 45 45 72 72 72 75 55 55 70 0 | 1
0
16
16
16
16
12
17
16 | 17
16 0 0 0 0 0 14
16 15 | 1
0
16
16
16
16
12
17
16
1 0 16 16 16 16 16 12 17 26	1 17 17 17 17 17 18 18 17	0 35 35 35 35 35 35 32 37 35	0 0 0 14 15 55	0 0 0 0 14 15	0 0 0 0 14 15	0 0 0 0 14 15 25	0 0 0 0 0 14 16 15	0 0 0 0 0 0 0 0 0 1 1 1 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0																																	
в	 Lengtham oper Ansocial [4] (1103) is Tangtham operations [4] (1103) is Tangtham operations [2] (1103) is Tangtham [2] (1103) is As quadrations [2] (1103) is As quadrations (2) (1103) is As quadrati	99,79 98,09 88,91 88,91 90,84 90,84 92,61 92,97 A	89,78 89,16 200 200 90,00 92,68 90,45 90,45 90,4 Full so 0	99,40 9 98,42 8 89,42 8 99,52 8 90,76 9 92,58 9 92,88 9 92,88 9 02,88 9 02,88 9 02,88 9 02,88 9 02,88 9 02,88 9	9,28 9,08 97,60 9,91 89,71 9,91 89,71 9,91 89,71 9,91 89,71 0,94 90,72 0,94 90,72	47 k 89,16 k 89,16 k 89,16 k 90,16 c 90,1 k 91,08 k 92,67 t 92,71 mont) c <u>F</u> 0 259	2403 2555 200 98,82 98,82 90,45 90,45 90,4 50,25	260 255 0 200 98,92 99,49 90,4 90,4	240 215 0 98,40 92,48 90,45 90,4 5: Flankt 0	2218 2233 25 25 25 93,63 91,83 91,83 91,82 91,82 0	218 223 25 25 0 91,63 91,28 91,22 91,420,42 91,4	175 187 171 171 171 171 169 169 93,27 93,11 1 0	148 172 1228 1228 1228 1228 1228 1228 1228	148 171 228 7. 228 7. 228 7. 228 7. 228 7. 228 8. 206 8 206 8 157 8 2 8 2 6 4 6 8	200 7, 200 7, 2,36 2,36 2,36 2,36 3,72 9,23 4,27 7, 3,72 9,27 7, 3,27 7, 3,27 7, 3,27 7, 3,27 7, 3,21 7, 3,21 7,	2,35 97 2,35 97 100 100 11,34 88 11,34 88	P0,52 P0,52 P2 3 P2 3 P2 3 P2 3 P2 3 P2 3 P2 4 P2 4	100 120 72,36 72,36 72,36 72,36 88,73 88,73 88,73 88,27 88,27 88,21 88,21 88,21 88,21 80,2	200 2,36 72,38 2,36 72,3 2,36 72,3 2,36 72,3 3,73 80,7 3,73 80,7 8,27 83,2 8,21 83,2 3 0 5	5 N 300 300 1 95,34 1 95,24 1 95,25 1	76 76 91,24 91,24 91,24 73,45 73,22 73,22	76 76 0 91,34 91,34 73,45 78,22 72,22	53 53 24 26 26 26 26 26 26 26 26 26 26 26 26 26	53 53 24 24 24 81,02 81,02 81,02	64 64 77 77 54 54 54 90,68	45 45 78 78 78 56 56 25 100	45 45 72 72 75 56 56 24 0	1 0 16 16 16 12 17 16	17 16 0 0 0 0 14 16 15	1 0 16 16 16 16 17 16	1 0 16 16 16 16 16 12 17 26	1 17 17 17 17 17 18 18 17	0 26 26 26 26 27 27 26	0 0 0 14 15	0 0 0 0 14 15	0 0 0 0 14 15	0 0 0 0 14 15 55	0 0 0 0 0 14 15	0 0 0 0 0 0 0 0 0 13 12	000000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0		
В	I. Inciplion opt. Amountal [16] [11033] in Therefore on the product of	99,78 98,08 88,91 88,91 88,91 92,84 92,61 92,61 92,93 92,97 A	89,78 89,16 500 500 900 88,90 92,68 90,15 90,4 Full es <u>88</u> 0	99,44 5 58 52 5 89,42 5 89,42 5 90,75 5 92,51 5 92,51 5 92,81 5 92,81 5 0,261 (% d 0 0	9,28 9,08 97,96 9,01 89,71 9,81 89,71 9,81 89,71 9,81 89,71 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,93 92,90 0,93 92,90 0,94 92,90	47 k 89,16 k 89,16 k 90,16 c 90,1 c 90,1 k 91,08 k 91,08 k 92,71 model <u>c 50</u> 1 92,71 model <u>c 50</u> 2 90,1 k 91,08 k 92,71 model <u>c 50</u> 2 90,1 k 91,06 k 91,07 k 9	2403 2555 200 98,82 92,69 90,45 90,45 90,4 50 50	200 255 0 200 98,92 92,69 90,15 90,4 <u>A</u> 200	240 215 0 98,00 92,48 90,4 57 Flash 0 0	2218 233 25 25 25 93,63 91,82 91,82 91,82 0 0 0	218 223 25 25 0 91,63 95,655,655,755,755,755,755,755,755,755,75	175 187 171 171 171 171 188 149 98,41 98,41 1 4 6 6 0 0	148 172 1228 1228 1228 1228 1228 1228 1228	148 171 171 228 7 228 7 228 7 228 7 206 8 206 8 206 8 157 8 2 8 2 6 3 3 3	200 7, 200 7, 2,36 2,36 2,36 2,36 2,36 2,36 2,36 2,3	2,35 97 2,35 97 1000 1000 10,45 87 9,45 87 9,252 87 9,252 87 9,252 87 9,252 87 9,252 87 9,252 87 9,253 87 9,253 87 9,253 87 9,255 87 9,555	H9,57 H9,57 72 3 72 3 72 3 12,36 5 L2,86 5 L2,	100 100 12,36 72,36 72,36 72,36 72,36 80,78 80,78 81,78 82,78 83,27 83,27 83,27 84,27 84,27 80,78 80,79	000 2,16 72,8 2,86 72,8 2,86 72,8 0,78 80,7 8,27 83,2 8,21 83,2 8,21 83,2 0 0 0	0 N 1 300 1 300 1 95,24 1 95,24 1 95,24 1 95,24 1 77,22 1	76 76 90 91,24 91,24 91,24 73,45 73,22 73,22	76 76 0 11,34 11,24 71,22 71,22 71,22	52 53 34 34 24 100 81,82 81,62 81,62	53 53 24 24 24 0 81,02 81,02	64 64 77 77 54 54 54 90,68	45 45 78 78 78 54 54 25 100	45 45 72 72 75 55 55 70 0	1 0 16 16 16 12 17 17	17 16 0 0 0 0 14 16 15	1 0 16 16 16 16 16 16 16 12 17 16	1 0 16 16 16 16 12 17 26	1 17 17 17 17 17 17 18 18 17	0 35 35 35 35 35 35 32 32 32 35	0 0 0 0 14 16 15	0 0 0 0 14 15	0 0 0 0 14 15	0 0 0 14 16 15	0 0 0 0 14 16 15	0 0 0 0 0 0 0 0 1 1 2	000000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0		
B	I. aregulation appel attences and the [14 [14103] is a Tampilation appellation [10] [1411315 is G T. tampilation [10] [1411315 is G T. tampilation [10] [1411315 is G T. tampilation [10] [141131 is G T. tampilation (10] are attencing [10] [141131 is G T. anogenetic appearation (10] [141131 is G A. optimizer Attilder N317 I. A. optimizer Attilder N317 I. A. optimizer Attilder N317 I. T. anotherms co. Channe apping [10] NM220209 A. T. anotherm co. NMA have [10] c. T. anotherm co. NMA have [10] c. T. anotherm co. State apping [10] NM220209 A. T. anotherm co. State apping [10] NM22	99,78 98,08 98,91 92,81 92,83 92,61 92,93 92,97 A	89,78 89,16 200 200 88,80 82,60 82,60 82,60 82,60 90,15 90,4 7 ml m 200	99,48 5 89,42 5 89,42 5 89,42 5 89,42 8 90,76 5 92,51 5 92,48 5 0 0 0 0 0 0 0 0 0 0 0 0 0	9,28 8,08 97,95 9,81 89,75 9,81 89,75 9,81 89,75 9,81 89,75 9,84 90,75 0,84 90,75 0,94 90,75 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,95 90,95 0,05 90,95	47 k 29,14 k 29,14 k 29,14 k 29,14 k 90,14 k 90,14 k 91,98 k 92,47 k 92,71 month <u>F</u> 0 12 0 22 0 25 0 25 0 0 0 0 0 0 0 0 0 0 0 0 0	200 255 200 98,82 92,69 90,25 90,4 G 50 50 50	260 255 0 90,92 90,49 90,45 90,45 90,4 200	240 215 0 88,40 82,48 90,15 90,4 5 Flank5 0 200	218 213 25 25 25 91,61 91,82 91,83 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,82 91,93 9	218 223 25 25 25 25 0 93,63 95,63 95,63 95,63 95,63 95,22 9 2 2 2 2 2 2 2	175 187 171 171 171 171 169 169 169 169 169 169 169 16	168 1 172 2 228 2 228 2 228 2 200 2 158 2 9,60 5 8	143 171 171 228 7 228 7 228 7 228 7 228 7 228 7 228 8 206 8 206 8 206 8 206 8 206 8 206 8 206 8 206 8 207 8 208 7 208 8 208 7 208 7	2000 7. 2000 7. 2,266 2,272 2,272 2,275	2,36 97 2,36 97 2,36 97 100 100 100 10,30 10,34 88 11,34 88 11,34 88 11,34 88 11,34 88 11,34 88 12,45 82 9,22 82 9,23 82 9,24 83 9,25 84 9,25 84 10,25 84 1	H9,57 H9,57 72 3 72 3 72 3 72 3 72 3 72 3 72 3 72	100 100 120,36 72,36 72,36 72,36 88,73 89,73 89,73 89,73 80,75 80,75	000 2,86 72,8 2,86 72,8 2,86 72,8 0,78 80,7 8,07 80,7 8,27 83,2 8,21 83,2 8,21 83,2 0 0	0 N N 1 300 1 95,24 1 95,25 1 95,2	76 76 0 91,24 91,24 78,25 78,22 78,22	36 36 0 11,24 11,24 11,24 11,24 11,22 11,22 11,22	52 53 34 24 20 81,02 81,02 81,02	53 53 24 24 24 0 81,02 81,02 81,02	64 64 77 77 54 54 90,68	45 45 77 77 78 56 56 56 25 100	43. 43.9 9.9 9.9 53.5 34 0 0	1 0 16 16 16 16 12 17 17	17 16 0 0 0 0 14 14 15	1 0 16 16 16 16 16 16 17 17 16	1 0 16 16 16 16 12 17 16	1 17 17 17 17 17 17 18 18 17	0 35 35 35 35 35 35 32 37 35	0 0 0 0 0 24 25	0 0 0 0 0 14 15	0 0 0 0 14 15	0 0 0 0 14 26 25	0 0 0 0 14 15	0 0 0 0 0 0 1 1 1 2	000000000000000000000000000000000000000	0 0 0 0 0 0 0 0		
B D	1. Englaber opp-dancescheil (pf 11003) eff 1. Englaber opp-dancescheil (pf 11013) eff 1. Englaber of (pf 11013) eff 1. Englaber of (pf 11013) eff 1. Englaber of (pp - answire) (pf 11013) eff 1. Englaber of (pf - answire) (pf 11013) eff 1. Englaber of (pf - answire)	99,78 98,08 98,91 98,91 90,84 90,84 92,61 92,93 92,97 A 200 99,14	29,78 29,78 200 500 500 88,60 82,61 90,45 90,4 Full m 90,55 90,4	99,88 5 58 52 5 29,52 5 29,52 5 90,75 5 90,75 5 92,53 5 92,54 5 92,54 5 0,75 6 92,54 5 92,54 5 92,54 5 0 0 0 99,14	9,28 9,08 97,66 9,01 99,70 9,91 99,71 9,91 99,71 9,91 99,71 9,91 99,71 9,91 99,71 9,91 99,71 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 90,72 0,84 92,40 0,97 92,20 10 10 10 10 10 10 10 10 10 1	47 k 29,14 k 29,14 k 29,16 k 90,15 c 90,1 c 90,1 k 91,98 k 92,67 1 92,71 month c 90 c 90	2403 2555 200 98,82 92,69 90,45 90,4 50 50 50 50 222	280 255 0 920 98,92 90,45 90,4 <u>A</u> 200 90,24	240 215 0 88,00 82,01 90,4 90,4 90,4 90,4 90,4 90,4 90,4 90,4	218 213 25 25 25 25 91,61 91,28 91,20 91,20 0 0 99,24	218 223 25 25 25 25 0 93,63 95,28 95,28 95,22 2 2 2 2 2 2 2	175 187 171 171 171 171 171 169 149 83,27 83,81 0 0 0 0 2	1488 1 172 2 228 2 228 2 229 2 229 2 200 2 200 2 158 2 8,40 8 3 3 3 3 3 3	148 171 171 228 7 2 2 2 2	2000 7. 5000 7. 2,36 2,36 2,36 2,36 2,36 2,36 2,36 2,36	2,36 99 10,36 99 1000 1000 1000 1000 1000 1000 1000 1	0,57 12,37 32,	100 100 72,36 7 72,36 7 72,36 7 80,73 8 80,73 8 81,21 8 81,21 8 81,21 8 81,21 8 70 0 0 0 0	2,36 72,3 2,36 72,3 2,36 72,3 2,36 72,3 3,78 80,7 3,78 80,7 4,78 80,7 4,78 80,7 4,79 80,7 4,79 80,7 4,79 80,7 4,70 80,7 5,70 80,7 7,70 80,7 7,70 80,7 7,70 80,7 7,70 80,7 7,70 80,7 7,70 80,7 7,70 80,	0 N N i 300 i 90,34 i 90,34 i 90,34 i 90,34 i 91,22 i 71,22 i	7% 7% 0 91,24 91,24 91,24 73,25 73,22 73,22	76 76 0 11,24 11,24 11,24 71,22 71,22	52 53 34 34 34 34 34 34 81,02 81,02 81,02	53 53 24 24 0 81,88 81,02 81,02	64 64 77 77 54 54 90,68	45 45 71 71 71 56 55 55 55 55 55	43. 47.9 79.95 55.6 24.0 0	1 0 16 16 16 16 12 17 16	17 16 0 0 0 0 14 16 15	1 0 16 16 16 16 16 16 17 17	1 0 16 16 16 16 16 17 26	1 17 17 17 17 17 18 18 18	0 26 26 26 27 27 26	0 0 0 0 0 0 24 25	0 0 0 0 14 15	0 0 0 0 14 15	0 0 0 0 14 14 25	0 0 0 0 0 0 14 15	0 0 0 0 0 0 1 1 1 2 2	0 0 0 0 0 2	0 0 0 0 0 0 0		
B D	2. Surgiolam opt. discussion [10] (11100) E 7. Surgiolam opt. discussion [10] (11100) E 7. Surgiolam opt. [10] (11100) E 7. Surgiolam opt. and anti- rity and anti- transphere opt. and anti- stantism opt. (Random J. K. 1997) <i>A. explaining ADD Conf. (Random J. Rev.)</i> <i>J. antismo opt. (Random J</i>	99,78 98,08 98,91 88,91 96,84 96,84 92,61 92,93 92,97 A 500 100 99,14 500	89,78 89,78 200 200 200 200 200 20,0 93,00 92,40 90,45 90,4 0 99,14 200	99,14 5 98 50 89,82 5 89,82 5 89,82 5 90,76	9,28 8,08 97,95 9,81 89,75 9,81 89,77 9,81 89,77 9,81 89,77 9,84 90,77 0,84 90,77 0,84 90,77 0,84 90,77 0,84 90,77 0,84 90,77 0,84 90,77 0,84 90,77 0,81 92,80 0,81 92,80 0,81 92,80 0,81 92,80 0,81 92,80 0,81 92,80 0,81 92,80 0,81 90,71 0,81 90,71 0,81 92,70 0,81 92,70 0,91 92,80 0,91 92,90 0,91 92,90	47 4 89,14 4 89,14 4 89,14 4 99,14 4 99,14 4 99,14 4 99,14 4 92,67 5 92,75 5 92,75	280 255 100 98,82 90,85 90,85 90,85 90,85 90,85 90,85 90,85 90,85 90,95	280 255 0 98,92 98,92 90,45 90,45 200 200 99,24 200	240 215 0 88,00 82,40 82,40 80,15 90,4 5 Flash 0 90,4 0 91,24 200	2188 2183 215 215 215 215 215 215 215 215 215 215	218 223 25 25 25 25 9 45,28 95,22 95,22 10 10 10 10 2 2 2 2 99,24	175 187 171 171 171 171 171 171 171	1488 1 172 2 228 2 228 2 200 2 158 2 8 3 3 3 3 3 3 3 3 3 3 3	148 171 171 228 7 228 7 228 7 228 7 228 7 228 8 206 8 207 8 208 8 208 208 8 208 8 200 8 20	2000 7. 2000 7. 2,36 2,37 2,37 2,37 2,37 2,37 2,37 2,37 2,37 2,37 2,57	2,36 97 (2,36 97 100 100 100 100 100 100 100 100 100 10	9,57 99,57 72 3 72 3 72 3 72 3 72 3 72 3 72 3 72	200 200 200 20,86 72,36 72,36 72,36 84,73 84,73 84,27 8	500 2,36 72,3 2,36 72,3 2,36 72,3 2,36 72,3 3,73 80,7 3,73 80,7 3,73 80,7 3,73 80,7 8,27 83,2 8,21 88,2 0 0 0 0	0 N N i 200 i 90,24 1 90,24 1 91,22 i 71,22 i	0 76 76 9 500 9 5124 9 5124 9 5124 9 5124 9 522 7 3,22 7 3,22	76 76 0 11,24 11,24 72,22 72,22	53 53 34 34 34 35 36 36 36 36 36 36 36 36 36 36 36 36 36	53 53 24 24 24 81,02 81,02	64 64 77 77 78 54 54 90,68	45 47 71 71 73 54 54 54 100	63. 63. 79. 79. 56. 56. 56. 56. 56. 56. 56. 56. 56. 56	1 0 16 16 16 16 16 16 12 17 16	17 16 0 0 0 0 14 15 15	1 0 16 16 16 16 16 16 12 17 16	1 0 16 16 16 16 12 17 26	1 17 17 17 17 17 18 18 18 17	0 36 36 36 36 36 36 36 36 37 36	0 0 0 0 0 54 25	0 0 0 0 14 16 15	0 0 0 0 14 16 15	0 0 0 0 14 16 25	0 0 0 0 0 14 16 15	0 0 0 0 0 0 1 1 1 2 2	000000000000000000000000000000000000000	0 0 0 0 0 0 0 0		
B D	2. Surghade opp. discosting. [10] (1010) E. J. Franceski, Franceski and [10,1010) E. J. Franceski K. Franceski and Franceski K. J. F. Stangherevi (JP, 1010) H. J. Stangherevi (JP, and JP, 1010) H. J. Stangherevi (Sp. and Sp. And Sp. And Sp. And A. And Sp. And Sp. And Sp. And Sp. And Sp. And A. And Sp. And Sp. And Sp. And Sp. And Sp. And J. Lanstone on Sub-Mark (JP) H. J. Antonion S. Shak Marka (JP) H. Antonion S. Shak Marka (JP) H. Antonion Statistical H. Shaka (JP) H. Antonion Statistical	99,78 99,08 99,08 99,91 90,84 90,84 90,84 90,84 90,84 90,84 90,97 100 90,97 100 91,14 100 99,57	89,78 89,78 200 200 200 88,90 82,60 82,61 90,55 90,55 90,55 90,55 90,55 200 90,53	99,34 5 98 50 89,52 5 89,52 5 90,56 5 90,56 5 92,58 5 92,88 5 02,88 5 00,16 5 92,88 5 00,16 5 92,88 5 00,16 5 0 0 0 0 0 0 0 0 0 0 0 0 0	9,28 8,28 97,96 9,31 89,77 9,31 89,77 9,34 89,77 0,34 90,77 0,34 90,77 0,35 90,77	47 4 89,16 4 89,16 4 89,16 4 99,15 1 99,15 1 99,15 4 91,18 4 92,10 5 92,15 5 92,15 1 99,15 1 99,15	200 255 100 96,82 92,85 90,45 90,4 50 50 50 50 50 50 50 50 50 50 50 50 50	280 255 0 98,92 98,92 92,69 90,45 90,4 200 99,24 200 99,24 200 99,24	240 215 0 188,00 192,68 190,45 0 191,34 200 191,34 200 191,34 200 191,35	2118 213 215 215 215 215 215 215 215 215 215 215	218 228 25 25 25 25 9 45,28 95,28 95,22 2 2 2 94,24 96,24 96,25	175 247 171 171 171 249 249 249 249 249 249 249 249 249 2 2 2 2	1488 1 172 228 228 228 228 228 228 228 228 228 2	248 273 275 272 228 7 228 7 228 7 228 226 8 256 8 257 8 2 2 8 2 3 3 3 3 3 3 3 0 0	000 7 000 7 0,36 1,86 1,86 1,86 1,27 8 1,27 8 1,27 7 1,21 7	0,36 99 (7,36 99 100 100 100 100 100 100 100 100 100 1	9,57 99,57 72 3 72 3 72 3 12,26 5 12,86 5 12,8	100 100 120 120 120 120 120 120	000 0,16 72,8 2,86 72,8 2,86 72,8 0,72 80,7 3,73 80,7 3,74 80,7 4,74 80,7 7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,7 7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,7 7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,7 7 8,74 80,77 8,77 80,77 9,77 80,77 9,77 80,77 9,77 80,77 9,77 80,77 80,77 80,77 9,77 80,	0 NO N 1 200 1 95,24 1 95,24 1 95,24 1 97,22 2 77,21 2 77,22 2 70,00 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7% 7% 0 91,24 91,24 91,24 78,22 78,22	76 0 0 11,24 72,25 72,22 72,22	52 53 24 24 24 24 24 24 24 24 24 24 24 24 24	53 53 24 24 24 24 81,02 81,02	64 64 77 77 54 54 90,68	45 47 71 71 54 54 54 25 26	43 43 79 79 79 79 55 55 56 56 56	1 0 16 16 16 16 16 16 12 17 16	17 16 0 0 0 0 0 14 16 15	1 0 16 16 16 16 16 16 16 16 16 16 16 16 16	1 0 16 16 16 16 16 17 16	1 17 17 17 17 17 18 18 18 17	0 36 36 36 36 36 36 36 37 37 36	0 0 0 0 0 14 26 25	0 0 0 0 14 16 15	0 0 0 0 14 16 15	0 0 0 0 54 55 55	0 0 0 0 0 0 14 16 15	0 0 0 0 0 0 0 11 12	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0		

Fig. 4 Pairwise comparisons of sequences from the taxa included in the A genome group (top), the B genome group (middle) and the D group (bottom). The comparisons include the full nucleotide sequences (left), the 5' flanking regions (middle) and the encoded proteins (right). The nucleotide sequences are

The full length *T. aestivum* nucleotide sequences and one *Ae. tauschii* sequence (Ae231) are identical and all sequences are >99% similar (Fig. 4, bottom left panel). Also the 5'flanking region and proteins are highly conserved with maximum three nucleotide differences or amino acid substitutions respectively (Fig. 4, bottom panel centre and right).

The **B**/**G**/Ae. speltoides group include six sequences from the 'emmer' group (A-F), five sequences from the 'timopheevii' group (G-K) and three from Ae. speltoides (L–N) (Fig. 4 middle panel). The full length nucleotide sequences from the polyploid taxa are 89-100% similar, but none of the sequences from polyploid taxa are more than 94% similar to any of the Ae. speltoides sequences. One sequence of the 'emmer' group (T. aestivum cv. Bob White) is identical to sequences of the domesticated representatives of the 'timopheevii' group but only up to 90% similar to other members of the 'emmer' group. With this exception, sequences within the respective groups 'emmer' and 'timopheevii' are >98% similar. Excluding the Bob White allele, emmer group 5'flanking regions are >99% similar having just one nucleotide difference. The 'timopheevii' group display two distinct 5'flanking regions with 24 nucleotide differences. The proteins have 0-18 amino acid substitutions and no gaps (Fig. 4 middle panel right). The Bob White protein is identical to the proteins in the 'timopheevii' group and has 16 or 17 amino acid substitutions compared to other proteins in the 'emmer' group. Only one amino acid substitution is found among the remaining 'emmer' group proteins and there are no substitutions in the 'timopheevii' group.

compared according to % similarity below the diagonals and number of differences above the diagonals. The protein sequences were compared according to differences below and gaps above diagonals. Differences minus gaps equal amino acid substitutions

Discussion

The present study includes samples of most, if not all, potential donors of all wheat genomes. For a more thorough representation of Triticeae diversity it also includes a number of wild, diploid species belonging to other genera. Further, it includes representatives of the frequently neglected 'timopheevii' group. Phylogenetic analysis and pairwise comparisons were based on a complete nuclear gene spanning more than 2.2 kb in all samples.

The three T. aestivum gene copies from cv. Chinese Spring have previously been mapped to chromosome 5A, 5B and 5D using an uploid lines (Madsen et al. 2013). Their positions in the tree confirm that they have been inherited from the diploid genome donors and that these donors are T. urartu (A), Ae. speltoides (B) and Ae. tauschii (D) in line with the increasingly accepted view (Haider 2013; Peng et al. 2011). Including less or other taxa and accessions of both Triticum and Aegilops, largely the same patterns were found by Petersen et al. (2006). One interesting finding is that, Amblyopyrum which van Slageren (1994) excludes from the Aegilops based on morphology, here falls within Triticum and Aegilops though with no support. Petersen et al. (2006) found high support for a position within Triticum and Aegilops.

The A genome group

The sequences representing *T. urartu* and *T. monococcum* together with one sequence from each of the polyploid wheat samples form a monophyletic group with high support (BS = 100%). This A genome group has two distinct subgroups containing among others T. urartu and T. monococcum, respectively. These subgroups represent the A^u and A^m genome. The only polyploid taxon in the A^m group is T. zhukovskvi. This is in agreement with Dvorak et al. (1993) who found evidence of A^m as well as A^u genomes in T. zhukovskyi and suggested it to originate from hybridization between T. timopheevii and T. *monococcum*. Accordingly an A^{u} gene copy was also expected in T. zhukovskyi but we were unable to isolate it. It could be mutated in a way that prevents amplification with the current primes, but it is also possible that the A^{u} gene copy has been replaced by the A^m copy through heterogenous chromosome pairing. The apparent loss of A^u DNA in T. zhukovskyi has also been observed by Baum and Bailey (2004) and Dvorak et al. (1993). Within the A^{u} group, the sequences from the 'timopheevii' wheats form a wellsupported clade (BS = 91%). A prominent characteristic of the 'timopheevii' group A^{u} allele is a 69 bp deletion in the 5'flanking region, but also SNP's contribute to differentiate this allele form other A^{u} sequences. The deletion in the 5'flanking region includes cis acting regulatory elements previously identified (Madsen et al. 2013). It is therefore very likely that the gene regulation is affected. The A genome allele of the T. turgidum subsp. dicoccoides accession Tri18485 is identical to the allele of T. aestivum cv. Chinese Spring whereas those of Tri18508 and Tri18523 both have 8 differences resulting in 1 and 3 amino acid substitutions in the encoded proteins (Fig. 4). These results show that exotic breeding materials for the A genome may provide novel PAPhy_a alleles but they are not guaranteed to do so. It is therefore advisable to use molecular screening methods to support the breeding effort.

The **D** genome group

All sampled sequences from *Ae. tauschii* form a strongly supported group together with three identical sequences from *T. aestivum*, thus supporting that *Ae. tauschii* is the **D** genome donor of wheat. One sequence from *Ae. tauschii* (Ae 231) is identical to those of *T. aestivum* whereas the other *Ae. tauschii* sequences have 10 or 20 nucleotide differences, respectively (Fig. 4). One accession (AE229) has

nucleotide differences in the 5'flanking region and the encoded protein (Fig. 4). Whereas the **D** genome $PAPhy_a$ gene copy thus seems to be very conserved within *T. aestivum*, the variation among sequences in *Ae. tauschii* may potentially be useful for crop improvement. As for *T. turgidum*, it should be useful to apply molecular screening methods to ensure that *Ae. tauschii* specimens harbour novel alleles before crossing.

The B genome group

Aegilops speltoides has hitherto also been postulated to carry the S genome (Friebe et al. 1995). In the current tree it groups within a highly supported clade (BS = 100%) which also contains sequences from the **B** and **G** genome. This finding is in agreement with Kilian et al. (2007) and Golovnina et al. (2007) both of which found that the B and G genomes can be understood as two examples of Ae. speltoides haplotype diversity sequestered by independent hybridization events. Since the B and G genomes are both derived from Ae. speltoides, a more appropriate nomenclature for the group would be \mathbf{B}^{b} (emmer group), **B**^g (timopheevii group) and **B**^s (Ae. spel*toides*). Within the highly supported (BS = 100%) **B** genome group, sequences from the hexaploid wheats are placed in either of two strongly supported groups: one includes sequences from two T. aestivum cultivars and tetraploid T. turgidum, and the other includes sequences from one T. aestivum cultivar (Bob White), T. zhukovskyi and the four T. timopheevii accessions. A sequence from one of the accessions of Ae. speltoides is strongly supported (BS = 86%) as the sister group to the latter Bob White plus T. timopheevii and T. zhukovskyi clade and sequences from the remaining two accessions of Ae. speltoides are weakly supported (BS = 64%) as their sister group, thus rendering Ae. speltoides paraphyletic. It is reasonable to assume that the 'timopheevii' group sequences in this clade are representatives of the \mathbf{B}^{g} genome since the \mathbf{B}^{b} and \mathbf{B}^{g} genomes are known to be very similar (Kilian et al. 2007) and the other 'timopheevii' group sequences clearly belongs to the A genome group. The deepest bifurcation in the group splits a weakly supported (BS = 64%) clade with Ae. speltoides and the \mathbf{B}^{g} genome Triticum's from the strongly supported (BS = 100%) \mathbf{B}^{b} genome Triticum's. The position of the Bob White sequence appears to be an abnormality, which can be explained by the use of the T. timopheevii hybrid Timstein in breeding Bob White (GRIS database: http:// wheatpedigree.net/sort/show/8192). Thus, it is an example of genetic variation of the PAPhy_a gene which has already been introduced in bread wheat from the 'timopheevii' group by chance. The five accessions belonging to the 'timopheevii' group produced only two different PAPhy_a sequences from the \mathbf{B}^{g} genome locus. The sequences distinguish domesticated and wild accessions and differ in 25 aligned positions due to one SNP and a 24 bp indel. Sequences assigned to the \mathbf{B}^{b} genome are more diverse than those of the \mathbf{B}^{g} genome. The least similar \mathbf{B}^{b} genome alleles are those of Tri18508 and Tri18523 which differ in 47 aligned positions because of 18 SNPs and 7 indels. On the other hand, identity was found between the sequences from Chinese Spring (a hexaploid) and Tri18485 (a tetraploid). The three T. turgidum sequences have identical 5'flanking sequences to Chinese Spring, whereas Villa Jurez has one SNP. Only the sequence Tri18508 encodes a different protein than the other $\mathbf{B}^{\mathbf{b}}$ alleles (one amino acid substitution).

Perspectives for the improvement of MGPA in bread wheat

It was demonstrated that direct progenitors of bread wheat, Ae. tauschii and T. turgidum, may carry PAPhy_a gene copies which are identical to those of bread wheat or copies with up to 44 nucleotide differences. Some of these differences were found in the 5'flanking region and others resulted in amino acid substitutions in the encoded proteins. Thus, it is very likely that alleles with different activity profiles are available. Further, it should be possible to evaluate them before introgression in bread wheat by direct comparison of the MGPA in candidate specimens with specimens of the same species carrying PAPhy_a gene(s) identical to those of bread wheat. The effect of amino acid substitutions on the enzyme properties can be evaluated after recombinant expression of the proteins as demonstrated by Dionisio et al. (2011).

Additional gene variation is found in *T. timopheevii* and *T. zhukovskyi*. As discussed above, the *T. timopheevii* \mathbf{B}^{g} genome allele has already been transferred to *T. aestivum* cv. Bob White (and presumably

many other cultivars breed from Timstein). Bob White does not have a high MGPA (Madsen et al. 2013) so the \mathbf{B}^{g} genome allele does not appear to confer very expression levels or a much more active enzyme. It should be considered though, that Bob White also has an allele on the A genome which is most likely nonfunctional because of a frameshift insertion. It is therefore not possible to precisely evaluate the potential of the T. timopheevii allele based on Bob White MGPA. The T. timopheevii A^u allele with its notable deletion of regulatory elements in the promotor is very likely to provide a different expression level but it cannot be predicted if it will be higher or lower. Also the A^m allele of T. zhukovskyi and T. monococcum holds promise, since T. monococcum is known to have a high MGPA (Madsen et al. 2013).

However, the search for better expressed *PAPhy_a* alleles does not need to be restricted to very close relatives of wheat. Rye translocation lines have long been used in wheat breeding (Graybosch 2001) and it is clear from Fig. 3 that considerable genetic variation is available in the *Secale*. Rye has consistently shown higher MGPA compared to wheat and barley (Eeckhout and De Paepe 1994; Madsen et al. 2013; Steiner et al. 2007; Viveros et al. 2000), but it remains to be examined if the *Secale* genes will prove as active when transferred to wheat.

Acknowledgements This work was supported by the Danish Ministry of Food, Agriculture and Fisheries (Grant No. 3304-FVFP-08-M-07-01).

Compliance with ethical standards

Conflict of interest The authors declare they have no conflict of interest.

References

- Baum BR, Bailey LG (2004) The origin of the A genome donor of wheats (*Triticum*: Poaceae)—a perspective based on the sequence variation of the 5S DNA gene units. Genet Resour Crop Evol 51:183–196
- Brinch-Pedersen H, Sorensen LD, Holm PB (2002) Engineering crop plants: getting a handle on phosphate. Trends Plant Sci 7:118–125
- Brinch-Pedersen H, Madsen CK, Holme IB, Dionisio G (2013) Increased understanding of the cereal phytase complement for better mineral bio-availability and resource management. J Cereal Sci 59:373–381

- CLCbio (2007) White paper on alignment speed and quality. http://www.clcbio.com/files/whitepapers/wp_alignment speed_A4.pdf. Accessed 7 March 2016
- Dionisio G et al (2011) Cloning and characterization of purple acid phosphatase phytases from wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), maize (*Zea maize* L.) and rice (*Oryza sativa* L.). Plant Physiol 156:1087–1100
- Dreisigacker S, Kishii M, Lage J, Warburton M (2008) Use of synthetic hexaploid wheat to increase diversity for CIM-MYT bread wheat improvement. Aust J Agric Res 59:413-420
- Dvorak J, Terlizzi P, Zhang HB, Resta P (1993) The evolution of polyploid wheats: identification of the A genome donor species. Genome 36:21–31
- Eeckhout W, De Paepe M (1994) Total phosphorus, phytatephosphorus and phytase activity in plant feedstuffs. Anim Feed Sci Technol 47:19–29
- El Baidouri M et al (2017) Reconciling the evolutionary origin of bread wheat (*Triticum aestivum*). New Phytol 213:1477–1486
- Feng D-F, Doolittle RF (1987) Progressive sequence alignment as a prerequisite to correct phylogenetic trees. J Mol Evol 25(4):351–360
- Fernández-Calvín B, Orellana J (1994) Metaphase I-bound arms frequency and genome analysis in wheat-*Aegilops* hybrids.
 3. Similar relationships between the B genome of wheat and S or S l genomes of *Ae. speltoides*, *Ae. longissima* and *Ae. sharonensis*. Theor Appl Genet 88:1043–1049
- Friebe B, Tuleen NA, Gill BS (1995) Standard karyotype of *Triticum searsii* and its relationship with other S-genome species and common wheat. Theor Appl Genet 91:248–254
- Golovnina K, Glushkov S, Blinov A, Mayorov V, Adkison L, Goncharov N (2007) Molecular phylogeny of the genus *Triticum* L. Plant Syst Evol 264:195–216
- Graybosch RA (2001) Mini review: uneasy unions: quality effects of rye chromatin transfers to wheat. J Cereal Sci 33:3–16
- Haider N (2013) The origin of the B-genome of bread wheat (*Triticum aestivum* L.). Russ J Genet 49:263–274
- Holme IB, Dionisio G, Brinch-Pedersen H, Wendt T, Madsen CK, Vincze E, Holm PB (2012) Cisgenic barley with improved phytase activity. Plant Biotechnol J 10:237–247
- Huang S, Sirikhachornkit A, Su X, Faris J, Gill B, Haselkorn R, Gornicki P (2002) Genes encoding plastid acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the *Triticum/Aegilops* complex and the evolutionary history of polyploid wheat. Proc Natl Acad Sci USA 99:8133–8138
- Kearse M et al (2012) Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28: 1647–1649
- Kihara H (1944) Discovery of the DD-analyser, one of the ancestors of *Triticum vulgare*. Agric Hortic 19:13–14
- Kilian B et al (2007) Independent wheat B and G genome origins in outcrossing *Aegilops* progenitor haplotypes. Mol Biol Evol 24:217–227
- Li L-F, Liu B, Olsen KM, Wendel JF (2015a) Multiple rounds of ancient and recent hybridizations have occurred within the *Aegilops–Triticum* complex. New Phytol 208:11–12
- Li L-F, Liu B, Olsen KM, Wendel JF (2015b) A re-evaluation of the homoploid hybrid origin of *Aegilops tauschii*, the donor of the wheat D-subgenome. New Phytol 208:4–8

- Madsen CK, Dionisio G, Holme IB, Holm PB, Brinch-Pedersen H (2013) High mature grain phytase activity in the Triticeae has evolved by duplication followed by neofunctionalization of the purple acid phosphatase phytase (PAPhy) gene. J Exp Bot 64:3111–3123
- Marcussen T et al (2014) Ancient hybridizations among the ancestral genomes of bread wheat. Science 345(6194): 1250092. doi:10.1126/science.1250092
- McFadden ES, Sears ER (1944) The artificial synthesis of *Triticum spelta*. Rec Genet Soc Am 13:26–27
- McFadden ES, Sears ER (1946) The origin of *Triticum spelta* and its free-threshing hexaploid relatives. J Hered 37:81–107
- Møller MG, Taylor C, Rasmussen SK, Holm PB (2003) Molecular cloning and characterisation of two genes encoding asparagine synthetase in barley (*Hordeum vulgare* L.). Biochim Biophys Acta 1628:123–132
- Oettler G (2005) The fortune of a botanical curiosity—triticale: past, present and future. J Agric Sci 143:329–346
- Peng J, Sun D, Nevo E (2011) Domestication evolution, genetics and genomics in wheat. Mol Breed 28:281–301
- Perugini LD, Murphy JP, Marshall D, Brown-Guedira G (2008) Pm37, a new broadly effective powdery mildew resistance gene from *Triticum timopheevii*. Theor Appl Genet 116:417–425
- Petersen G, Seberg O, Yde M, Berthelsen K (2006) Phylogenetic relationships of *Triticum* and *Aegilops* and evidence for the origin of the A, B, and D genomes of common wheat (*Triticum aestivum*). Mol Phylogenet Evol 39:70–82
- Rabinovich SV (1998) Importance of wheat-rye translocations for breeding modern cultivar of *Triticum aestivum* L. Euphytica 100:323–340
- Salamini F, Ozkan H, Brandolini A, Schäfer-Pregl R, Martin W (2002) Genetics and geography of wild cereal domestication in the near east. Nat Rev Genet 3:429–441
- Salse J et al (2008) New insights into the origin of the B genome of hexaploid wheat: evolutionary relationships at the SPA genomic region with the S genome of the diploid relative *Aegilops speltoides*. BMC Genom 9:1–12
- Sarkar P, Stebbins GL (1956) Morphological evidence concerning the origin of the B genome in wheat. Am J Bot 43:297–304
- Stamatakis A (2006) RAxML-VI-HPC: maximum likelihoodbased phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22:2688–2690
- Steiner T, Mosenthin R, Zimmermann B, Greiner R, Roth S (2007) Distribution of phytase activity, total phosphorus and phytate phosphorus in legume seeds, cereals and cereal by-products as influenced by harvest year and cultivar. Anim Feed Sci Technol 133:320–334
- van Slageren MW (1994) Wild wheats: a monograph of Aegilops L. and Amblyopyrum (Jaub. & Spach) Eig (Poaceae): a revision of all taxa closely related to wheat, excluding wild Triticum species, with notes on other genera in the tribe Triticeae, especially Triticum. Wageningen Agricultural University papers; 94-7. ISBN-9067543772
- Viveros A, Centeno C, Brenes A, Canales R, Lozano A (2000) Phytase and acid phosphatase activities in plant feedstuffs. J Agric Food Chem 48:4009–4013
- Wagenaar EB (1966) Studies on the genome constitution of *Triticum timopheevi* Zhuk. II. The *T. timopheevi* complex and its origin. Evolution 20:150–164