

Molecular Phylogeny and Evolution of Avena L.

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Background

Status

The genus Avena L. (Poaceae) belongs to the tribe Aveneae. Avena sativa is an economically important crop.

Usage

Avena strigosa, Avena barbata, or Avena sterilis, are important sources of resistance to crown rust, stem rust, and powdery mildew.

Necessary

As an important gene pool for improving cultivated oats and related species, this genus occupies a most important status in cereal plants.

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It is important to clarify the phylogenetic relationships of *Avena* species



Baum BR, 1977. Oats: Wild and cultivated. A monograph of the genus Avena L.

Taxonomic treatment

燕麦属物种分类和染色体组的确定

种组	种	染色体数	基因组
section	species	Chromosome no	genome
Avenotrichon (Holub)) Baum A. macrostachya Bal. ex Coss. et Dur	2n = 4x = 28	$C_m C_m C_m C_m$
Ventricosa Baum	A. clauda Dur	2n = 2x = 14	ՇբՇբ
		2n = 2x = 14	ՇթՇթ
		2n = 2x = 14	$C_{\sigma}C_{\sigma}$
Agraria Baum	A. macrostacnya:	2n = 2x = 14	A _s A _s
		2n = 2x = 14	As As
	as an outbreeding,	2n = 2x = 14	A _s A _s
Tanaia Dana		2n = 2n = 14	A. A.
Tenuicarpa Baum	perenniai / j	2n = 4x = 20 2n = 4x = 28	
		2n = 4n = 20 2n = 12	
		2n = 2x = 14 2n = 2r = 14	A.A.
	A. damascena Raj. Et Baum	2n = 2x = 14	Aa Aa
	A. hirtula Lag.	2n = 2x = 14	A _c A _c
	A. longiglumis Dur.	2n = 2x = 14	A ₁ A ₁
	A. lusitanica (Tab. Mor.) Baum	2n = 2x = 14	As As
	A. matritensis Baum	2n = 2x = 14	As As
	A. wiestii Steud.	2n = 2r = 14	Δ. Δ.
Ethiopica Baum	A. abyssinica Hochst.	2n = 4x = 28	AABB
	A. vaviloviana (Malz.) Mordv.	2n = 4x = 28	AABB
Pachycarpa Baum	A. maroccana Gdgr.	2 n = 4x = 28	AACC
	A. murphyi Ladiz.	2n = 4x = 28	AACC
	A. insularis Ladız.	$2n = 4\pi = 28$	AACO
Avena	A. jatua L. A. hubrida Deterro	2n = 0, = 42	
	A. nyonaa Peterin. A. occidantalis Dur	2n = 01 = 42 2n = 6n = 42	
	A. sativa L.	2n = 6x = 42	AACCDD
	A. STEPTITS L.	2 n = ox = 42	AACCOL
	<i>A. trichophylla</i> C. Koch	2 n = 61 = 42	AACODD



Background

Evolution

- Remains a matter of debate

chromosome pairing

(Rajhathy 1966; Rajhathy and Thomas 1974; Baum 1977; Thomas 1992; Leggett and Thomas 1995)

Genomic In Situ Hybridization

(GISH; Chen and Armstrong 1994; Jellen et al. 1994a)

in situ hybridization using molecular probes

(Murai and Tsunewaki 1987; Fominaya et al. 1995; Katsiotis et al. 1996; Linares et al. 1998; Irigoyen et al. 2001)

the use of molecular markers

(Sanchez de la Hoz and Fominaya 1989; O'Donoughue et al. 1995; Alicchio et al. 1995; Ronald et al. 1997; Kianian et al. 1999; Jin et al. 1999; Nocelli et al. 1999; Li et al. 2000*a*, 2000*b*; Loskutov and Perchuk 2000; Drossou et al. 2004; Fu and Williams 2008; Li et al. 2009; Morikawa and Nishihara 2009)

the comparison of nucleotide sequences

(Cheng et al. 2003; Irigoyen et al. 2006; Nikoloudakis et al. 2008; Nikoloudakis and Katsiotis 2008; Peng et al. 2008, 2010).





A genome origin

The A-genome diploids were originally subdivided into the As genome (A. strigosa) and modified A-genome species (Ac, Ad, Al, and Ap) according to their karyotypes.

Evidences about the A genome progenitor of Avena polyploidy

Species	For or Against	Morphology	Chromosome pairing behaviour	Karyotyping	GISH	Molecular evidence
As genome						
A strigosa	For		Kihara and Nishiyama 1932;	Rajhathy and Thomas 1974;	Chen and Armstrong 1994;	Linares 1996;
			Rajhathy and Morrison 1960;	Fominaya et al. 1988;	Jellen et al. 1994;	Linares 1998;
			Marshall and Myers1961;	Linares 1992;	Leggett and Markhand	Irigoyen et al. 2001;
				Leggett and Thomas 1995	1995	Irigoyen et al. 2006
	Against		Ladizinsky and Zohary 1968;	Jellen et al. 1993;		Linares et al. 1998
			Ladizinsky 1998; Leggett 1998	Jellen and Gill 1996		
A wiestii	For			Rajhathy and Thomas 1974		Li et al. 2000b;
						Irigoyen et al. 2006;
						Fu and Williams 2008
A hirtula	For			Rajhathy and Thomas 1974		Irigoyen et al. 2006
Ac genome						
A canariensis	For	Ladizinsky and	Thomas 1992			Liet al. 2000b ;
		Zohary 1971;				Nikoloudakis et al. 2008
		Baum et al. 1973;				
		Craiget al. 1974				
Ad genome	-					
A damascena	For					Li et al. 2009
Al genome						
A longiglumis	For					Rodionov et al. 2005;
						Nikoloudakis et al. 2008

Background

Genome origin





D genome origin

No such A-genome diploid was found in the present study.

Should share higher genetic similarity with the hexaploid species but lower with the AC-genome tetraploid species.

It has been suggested that a D-genome species never existed and that the D genome is in fact a derived A genome.

Many studies have suggested that the A and D genomes are very closely related.



The origin of the allopolyploid members in the genus has long been a controversial matter •numerous translocations and unknown levels of homology •high affinity between the chromosomes of the A, B, and D genomes •genetically controlled regulatory mechanism



Research objectives

- The development and application of molecular methods in oat has been relatively slow compared to other crops.
- Presently, there is little evidence at the nucleotide level to suggest how Avena species evolved.
 - Especially for the plastid DNA sequence information that had been widely used in other plants to investigate the relationship among diploid species and the maternal genome donors of polyploids.





AVENA	Results	
psba-trnH spacer		aby1AB bar14AB bar16AB
	his47As	his47As
	hie/18Ae	his48As his49As
		bar17AB1
	nis49As	bar17AB2
	bre20As	bar19AB
	bre21As	bre20As bre21As
	hir44As	hir44As
	hir42As	hir42As his51As bis50As
	his51As	str113As
	his50As	vav116AB
	str113As	vav115AB
	str111As	wie120As
	wie121As	snud65ACD
	wie120As	aby3AB aby2AB



Results

psba-trnH spacer









Results

[psba-trnH spacer]

	hir43As hir46As		hir43As hir46As
dam33	Ad	dam33Ad	
lus57A	s	lus57As	
LucEGA	-	lus56As	
IUSDOM	15	fat41ACD	
dam35	Ad	dam35Ad	
dam34	Ad	dam34Ad	



Methods

*The analyses of chloroplast sequence data left many questions concerning infrageneric relationships in *Avena* unanswered, particularly concerning the origins of the B and D genomes.





Results

Six unit classes

		*	20		40		, e	so.
•l ong B1	cons{b	TOTTTTATG	GTCACCCGAC	GACGGGGTI	AAATAT	GCGTTTTAT	TTNTNANTGT	FT T 62
•Long Δ1	cons(a	TTTTTTTTATTG	GTCACGCGAC	GACGGGGTA	TGGGCGAA	AATATTT	ATOTOATTGT	TTT 62
•Short M1	short m1	TCCTTTT	GTCACCCAC	GICGGIGTI	a la	IGGACGTTT	TTTTT. TTG.	49
I ong M1	long m1	TCTTTTT TC	GTCNCGGCTC	GICG	GN	TGGCGCGT	TOTOTOTOT	TTG 48
•Short C1	iong_mi	TCTTTTT TC	GTCACCCC		· · · · · · · · · · · · · · · · · · ·	COTCOTTA		
•Short D1		TTTTTT TC	GTAAAGTC			COLCOTING	TADADAD TT	TTG 40
Short Di	cons(u	111111	Jon Add 10.			JOGGCGTIA.		110 40
				*	100	* rmmaaaamm/		
	CONS(D	a) coordoordoordo	TAGIIIIAI.	Gecencera			GGTGAACICO	CGA 125
	cons(a	.GACGGICGGIGG	FICGITITAT.	GCCGIGGIA	AAC GGGG.		GGIGA.CICC	UGA 120
	short_m1	CGGAGCACCGTGC	FICGIGITITIC	GGCATGGTA	AAGTGTGG.	TTTTGCATGC	GGGAGCTC	106
	long_m1	CGGTACCTCGTGC	ICCCTTTTT	GCTGGGGTA	AAAAGTGG	GGATTCGCAI	AGG TAAGCAA	GAC 110
	cons{c	CGGTACCTCGAGC	эт. Сттттттт	IGCTGGGATA	AAAAATGG(G. ATTCGCAI	A <mark>GG</mark> TAAGCAA(GAC 100
	cons{d	CGTTCGCTGTTGC	JICGICTITIG	GCGGCGGTA	AAATGG	GTAAAG <mark>G</mark> CAI	A <mark>GG</mark> TATGTAA.	AAC 100
		*	140	*	160	*	180	
	cons{b	GGGGTTGAATCAG	CA <mark>gag</mark> aatg <mark>g</mark> a	lgctggag <mark>g</mark> g	G <mark>aag</mark> gcat <i>i</i>	AAG <mark>GAGAAA</mark>	CGGGGTACAG	AAC 185
	cons{a	GGGGTTGAATCAC	C.GA <mark>G</mark> AATG <mark>G</mark> A	lgctggag <mark>gg</mark>	G <mark>aag</mark> gcat <i>i</i>	AAG <mark>GAGAAA</mark>	CGGAGT.CAG	AAC 180
	short_m1	.GGGTGTAGG.CJ	AC <mark>GAT</mark> AATG.A	lgctggag <mark>g</mark> t	G <mark>GTG</mark> GCATI	AAG <mark>GG</mark> GAAA(CGGCGTGCAG	AAC 165
	long_m1	CATCGTGTAGGC	AT <mark>ga<mark>g</mark>aatg.a</mark>	lGCTGGAG <mark>GG</mark>	G <mark>CAA</mark> GCATI	AAGTACCCC	C <mark>GGCGT</mark> TCAG	AAC 171
	cons(c	CATCGTGTAGGC	AT <mark>GA<mark>G</mark>AATG.A</mark>	lGCTGGAG <mark>GG</mark>	G <mark>CAA</mark> GCATI	AAG. ATCTC	CGGCGTGCAC	AAC 160
	cons{d	CATAGTGTAGGC	AT <mark>ga<mark>g</mark>aatg.</mark> A	IGCTGGAG <mark>C</mark> G	G <mark>CAA</mark> GCATI	AAG <mark>GGAGAA</mark>	A <mark>gtggtgcac</mark> ,	AAC 161
								
		*	200	*	220	*	240	
	cons{b	ATGTC GGATGCG	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAAC	FCCGAAGTTA	AGC 247
	cons{a	ATGTC GGATGCG	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAAC	FCCGAAGTTAL	AGC 242
	short m1	ATG <mark>A</mark> C GGATGCGI	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAACT	FCCGAAGTTAL	AGC 227
	long m1	ATGTC GGATGCG	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAAC	FCCGAAGTTA	AGC 233
	cons{c	ATGTC GGATGCG	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAAC	FCCGAAGTTA	AGC 222
	cons{d	ATGTC GGATGCG	ATCATACCAGO	ACTAAAGCA	CCGGATCCO	CATCAGAAC	FCCGAAGTTA	AGC 223
	-							
		* 260	*	28	n	*	300	*
	cons(b	GTGCTTGGGCGA	GAGTAGTACTA	GGATGGGTG	ACCTCCTG	GAAGTCCT	CGTGTTGCAT	308
	cons(a	GTGCTTGGGCGAG	GAGTAGTACTA	GGATGGGTG	ACCTCCTG	GAAGTCCT	GTGTTGCAT	CCC 303
	short m1	GTGCTTGGGCGAG	GAGTAGTACTA	GGATGGGTG	ACCTCCTG	GAAGTCCT	CGTGTTGCAT	CCC 288
	long m1	GTGCTTGGGCGA	FAGTAGTACTA	GGATGGGTG	ACCTCCTG	GAAGTCCT	CGTGTTGCAT	294
	cons(c	GTGCTTGGGCGM	CORTOGRACIA	GGITGGGTG	ACCTCCTG	GANGTOCT	GTGTTGC AT	283
	cons(d	GTGCTTGGGCGA	CAGTAGTACIA	GGITGGGTG	ACCTCCTC	CANGTOCIC CANGTOCT	CTGTGTTGCAT	CC 294
	constu	010C11000CGX	JAGTAGTACTA	100×100010	ACCICCIG	JOAAOTCCI (COROLIGOATO	204







Summary of the 5S unit class)

		1 1 77 IN IN IN I						
种名	染色体数	基因组	Long	Long	Long	Short	Short	Short
Species	2n	Genome	A1	B1	M1	C1	D1	M1
A. abyssinica	4X	AABB	+	+				
A. agadiriana	4X	AABB	+	\frown				
A. atlantica	2X	Á, Á,	+	(+)				
A. barbata	4X	AABB	+					
A. brevis	2X	A _s A _s	+					
A. canariensis	2X	AcAc	+				\frown	
A. clauda	2X	ՇբՇբ				+	(+)	
A. damascena	2X	AdAd	+					
A. eriantha	2X	ՇբՇբ				+		
A. fatua	бX	AACCDD	+			+	+	
A. hirtula	2X	A _s A _s	+					
A. hispanica	2X	A _s A _s	+					
A. insularis	4X	AACC	+	\frown		+		
A. longiglumis	2X	A ₁ A ₁	+	+		+		
A. lusitanica	2X	A _s A _s	+	\bigcirc				
A. macrostachya	4X	$C_m C_m C_m C_m$			+			+
A. maroccana	4X	AACC	+			+	\frown	
A. murphyi	4X	AACC	+				+	
A. occidentalis	6X	AACCDD	+			+		
A. sativa	бX	AACCDD	+			+	+	
A.sativa(hulless)	6X	AACCDD	+	+		+	+	
A. sterilis	бX	AACCDD	+			+	+	
A. strigosa	2X	A _s A _s	+					
A. vaviloviana	4X	AABB	+	+				
A. ventricosa	2X	$C_{\sigma}C_{\sigma}$				+		
A. wiestii	2X	A _s A _s	+					



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