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(12) **United States Plant Patent**  
**Mehlenbacher et al.**(10) **Patent No.:** US PP25,022 P3  
(45) **Date of Patent:** Nov. 4, 2014

- (54) **CORYLUS PLANT NAMED ‘DORRIS’**
- (50) Latin Name: *Corylus avellana*  
Varietal Denomination: Dorris
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- (\*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 50 days.

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(65) **Prior Publication Data**

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Botanical denomination: *Corylus avellana*.

Variety designation: ‘Dorris’.

**BACKGROUND**

The present invention relates to a new and distinct cultivar of *Corylus* plant, (hazelnut, filbert) botanically known as *Corylus avellana*, and hereinafter referred to by the name ‘Dorris’. *Corylus avellana* is in the family Betulaceae.

The new *Corylus* resulted from a controlled cross of female parent OSU 309.074 (unpatented) and male parent ‘Delta’ (unpatented) made in 1997 by Shawn A. Mehlenbacher and David C. Smith. Hybrid seeds from the cross were harvested in August 1997, stratified, and seedlings grown in the greenhouse during the summer of 1998. From this cross, a total of 307 seedling trees were planted in the field in Corvallis, Oreg., USA in October, 1998. ‘Dorris’ was discovered and selected by the Inventors as a single plant within the progeny of the stated cross-pollination in a controlled environment in Corvallis, Oreg.

‘Dorris’ was originally assigned the designation OSU 876.041, which indicates the row and tree location of the original seedling. OSU 309.074 is from a cross of ‘Tonda Gentile delle Langhe’ (unpatented)×OSU 23.017 (unpat-

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- (58) **Field of Classification Search**  
USPC ..... Plt./152  
See application file for complete search history.

*Primary Examiner* — Anne Grunberg*Attorney, Agent, or Firm* — Klarquist Sparkman, LLP**(57) ABSTRACT**

A new and distinct cultivar of *Corylus* plant named ‘Dorris’ characterized by a spreading plant habit and low vigor, yellowish-green developing and fully expanded leaves during the spring and summer, resistance to eastern filbert blight caused by the fungus *Anisogramma anomala* (Peck) E. Müller, presence of random amplified polymorphic DNA markers 152-800 and 268-580, expression of incompatibility alleles S<sub>1</sub> and S<sub>12</sub> in the styles, and DNA fingerprints at 14 of 24 microsatellite marker loci differ from both parents OSU 309.074 and ‘Delta’, and from one parent at an additional 9 marker loci.

**5 Drawing Sheets****2**

ented). ‘Tonda Gentile delle Langhe’ is an important cultivar in Piemonte, northern Italy. OSU 23.017 is from a cross of ‘Barcelona’ (unpatented)×‘Extra Ghiaghli’ (unpatented). ‘Extra Ghiaghli’, obtained from Greece, is a clone of the important Turkish cultivar ‘Tombul’ (unpatented). ‘Delta’ was released by the Oregon Agricultural Experiment Station in 2002.

The new cultivar was asexually reproduced by rooted suckers annually for eight years (2003-2010) in Corvallis, Oreg. The new cultivar was also asexually propagated by whip grafting in 2004 in Corvallis, Oreg. The unique features of this new *Corylus* are stable and reproduced true-to-type in successive generations of asexual reproduction.

**SUMMARY OF THE INVENTION**

The following traits have been repeatedly observed and are determined to be the unique characteristics of ‘Dorris’. These characteristics in combination distinguish ‘Dorris’ as a new and distinct cultivar:

1. Spreading plant habit and low vigor.
2. Yellowish-green developing and fully expanded leaves during the spring and summer.
3. Resistance to eastern filbert blight caused by the fungus *Anisogramma anomala* (Peck) E. Müller.
4. Presence of random amplified polymorphic DNA markers 152-800 and 268-580 in DNA of ‘Dorris’ amplified by the polymerase chain reaction. These two markers are linked to a dominant allele for resistance to eastern filbert blight from the cultivar Gasaway (unpatented).

5. Expression of incompatibility alleles  $S_1$  and  $S_{12}$  in the styles,  
 6. DNA fingerprints at 14 of 24 microsatellite marker loci differ from both parents OSU 309.074 and 'Delta', and from one parent at an additional 9 marker loci. The microsatellite primers are shown in Table 1, and allele sizes are shown in Table 2. DNA fingerprints of grandparent 'Tonda Gentile delle Langhe' and great-grandparents 'Barcelona' and 'Extra Ghiaghli' are also shown in attached Table 2.

In comparisons in two replicated trials conducted in Corvallis, Oreg., plants of the new *Corylus* differed from plants of the *Corylus avellana* cultivar Barcelona (unpatented), and other cultivars and selections of *Corylus avellana* known to the Inventors primarily in nut size, nut shape, kernel percentage (ratio of kernel weight to nut weight), frequency of blank nuts (nuts lacking kernels), time of pollen shed, time of nut maturity, length of the husk or involucre, and plant size.

#### BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying colored photographs illustrate the overall appearance of the new cultivar, showing the colors as true as it is reasonably possible to obtain in colored reproductions of this type. Foliage colors in the photographs may differ slightly from the color values cited in the detailed botanical description which accurately describe the colors of the new *Corylus*.

FIG. 1 shows a tree of the new cultivar 'Dorris' growing in a field in the summer, in Corvallis, Oreg.

FIG. 2 shows the tree of the new cultivar 'Dorris' growing in a field in January, in Corvallis, Oreg.

FIG. 3 shows typical nuts, raw kernels, and blanched kernels of 'Dorris' hazelnut compared to those of 'Jefferson' hazelnut.

FIG. 4 shows husks of 'Dorris' hazelnut tree.

FIG. 5 shows the typical nuts, raw kernels, and blanched kernels of 'Dorris' hazelnut compared to those of 'Barcelona' hazelnut and other hazelnut cultivars.

#### DETAILED PLANT DESCRIPTION

The cultivar Dorris has not been observed under all possible environmental conditions. The phenotype may vary somewhat with variations in environment such as temperature and light intensity, without, however, any variance in genotype. The aforementioned photographs and following observations and measurements describe plants grown in Corvallis, Oreg. under commercial practice outdoors in the field during the fall, winter and spring. Plants used for the photographs and description were propagated by tie-off layering and growing on their own roots, and about seven years old. In the following description, color references are made to The Royal Horticultural Society Colour Chart, 1966 Edition, except where general terms of ordinary dictionary significance are used.

Botanical classification: *Corylus avellana* cultivar Dorris.

Parentage:

*Female, or seed, parent.*—*Corylus avellana* selection 309.074 (unpatented).

*Male, or pollen, parent.*—*Corylus avellana* cultivar Delta (unpatented).

Propagation (type rooted suckers):

*Time to initiate roots.*—About 30 days at 20° C.

*Time to produce a rooted young plant.*—About six months at 22° C.

*Root description.*—Fine to thick; freely branching; creamy white in color.

Propagation (type whip grafting):

*Time to budbreak on the scions.*—Bout 14 days at 25° C.

*Time to produce a grafted plant.*—About six months at 25° C.

Plant description:

*General appearance.*—Perennial shrub. Spreading plant habit.

*Growth and branching habit.*—Freely branching; about 15 lateral branches develop per plant. Pinching, i.e., removal of the terminal apices, enhances branching with lateral branches potentially forming at every node.

*Size.*—Plant height is about 4 meters; plant diameter or spread is about 5 meters.

*Vigor.*—low vigor growth habit.

*Lenticels.*—8 circular within 1 square centimeter (counted on dormant scions).

Lateral branch description:

*Length.*—About 32 cm.

*Diameter.*—About 6 mm.

*Internode length.*—About 3.0 cm.

*Texture.*—Smooth, glabrous.

*Strength.*—Strong.

*Color.*—Immature — 152B; mature — 152B.

Foliage description:

*Arrangement.*—Alternate, simple.

*Length.*—About 10.2 cm.

*Width.*—About 9.1 cm.

*Shape.*—Oblong to ovate.

*Apex.*—Obtuse to acute.

*Base.*—Cordate.

*Margin.*—Serrate.

*Texture.*—Upper and lower surfaces — slightly pubescent.

*Venation pattern.*—Pinnate.

*Leaf bud shape.*—Globular.

*Time of leaf bud burst.*—Midseason, 11 days after 'Barcelona'.

*Color.*—Developing foliage, upper surface 144A, lower surfaces: 187A. Fully expanded foliage, upper surface: Spring and summer, 143A; late summer and fall, 143A. Fully expanded foliage, lower surface: Spring and summer, 139C; late summer and fall, 139C. Venation, upper surface: Spring and summer, 139C; late summer and fall, 139C. Venation, lower surface: Spring and summer, 139D; late summer and fall, 139D. Leaf bud, 179C.

Petiole description:

*Length.*—About 2.7 cm.

*Diameter.*—About 1.8 mm.

*Texture.*—Upper and lower surfaces — pubescent.

*Color.*—Upper surface: Spring and summer, 139D; late summer and fall, 139D. lower surface: Spring and summer, 139D; late summer and fall, 139D.

Flower description:

*Male inflorescences.*—Catkins, color prior to elongation 194C.

*Female inflorescence.*—Style color 048B.

*Stigma coloration.*—048B.

*Time of female flowering.*—Midseason, 2 weeks after 'Barcelona'.

*Time of pollen shed.*—Midseason, around the same time as 'Daviana' (unpatented).

## Involure description:

*Involucre constriction.*—Absent.*Involucre length.*—25% longer than nuts.*Strength of serration of indentation.*—Moderate.*Pubescence.*—Little.*Thickness of callus at base.*—Moderate callus at base similar to 'Barcelona'.*Description of jointing of bracts.*—Involucre slit to the base on one side. Involucre does not adhere to nut after drop. 90% of nuts fall free of the husk. A few nuts are in tubular husks.

## Nut description:

*Length.*—About 19.1 mm.*Width.*—About 20.7 mm.*Depth.*—About 18.2 mm.*Nut shape.*—Round.*Nut shape index [(width+depth)/2\*length].*—1.02.*Nut compression index (width/depth).*—1.14.*Nut shell color.*—164B.*Nut weight.*—About 3.35 grams to 3.39 grams.*Predominant number of fruits per cluster.*—2-3 nuts per cluster.*Stripes on shell.*—None.*Fruit apex.*—Slight (not prominent).*Size of the fruit pistil scar.*—Small (~1 mm×2 mm).*Nut curvature of the basal scar.*—Flat (plane).*Frequency of blank nuts.*—7%.*Time of nut maturity.*—About same time as 'Barcelona' (unpatented).*Husk length.*—About 25% longer than the nuts.*Kernel weight.*—About 1.40 grams.*Kernel percentage (kernel weight/nut weight).*—About 43%.*Kernel shape.*—Round-oblate.*Kernel cross section shape.*—Circular.*Kernel base shape.*—Flat.*Lateral grooves.*—Rare and not prominent in the kernel.

Disease/pest resistance: Plants of the new *Corylus* are highly resistant to eastern filbert blight caused by the fungus *Anisogramma anomala* (Peck) E. Müller. Plants of the new *Corylus* are highly resistant to bud mites (*Phytoptus avellanae* Nal.), while plants of 'Tonda Gentile delle Langhe' are highly susceptible, and plants of 'Barcelona' are highly resistant.

Temperature tolerance: Tolerates temperatures from -10 to 38° C. in the field in Corvallis, Oreg.

TABLE 1-continued

Primers and annealing temperatures for the 24 microsatellite marker loci used to fingerprint 'Dorris' and other hazelnut cultivars.								
Locus	Repeat motif	Size	T <sub>a</sub>	n	He	Ho		
A613	(TC) <sub>13</sub> (CA) <sub>12</sub>	149-177	60	14	0.85	0.85		
A614	(TC) <sub>17</sub> (CA) <sub>10</sub>	125-156	60	14	0.85	0.85		
	NNN(CA) <sub>6</sub>							
A616	(AC) <sub>11</sub>	136-162	60	13	0.85	0.85		
A640	(CT) <sub>15</sub>	354-378	67	11	0.80	0.73		
	(CA) <sub>13</sub>							
B107	(CT) <sub>14</sub>	112-151	55	14	0.85	0.80		
B617	(GA) <sub>15</sub>	280-298	60	9	0.80	0.78		
B619	(TC) <sub>21</sub>	146-180	60	14	0.88	0.88		
B634	(AG) <sub>15</sub>	218-238	60	9	0.76	0.76		
B657	(AG) <sub>15</sub>	210-228	60	8	0.84	0.98		
B671	(AG) <sub>6</sub> NN	221-249	60	13	0.86	0.88		
	(GA) <sub>17</sub>							
5								
B709	(GA) <sub>21</sub>	219-233	60	8	0.74	0.76		
B733	(TC) <sub>15</sub>	161-183	60	8	0.68	0.68		
B741	(GT) <sub>5</sub> (GA) <sub>12</sub>	176-194	60	10	0.77	0.78		
B749	(TC) <sub>12</sub>	200-210	60	6	0.60	0.64		
B751	(GA) <sub>15</sub>	141-153	60	7	0.80	0.80		
B774	(AG) <sub>15</sub>	195-213	60	8	0.80	0.80		
B776	(GA) <sub>17</sub>	134-148	60	7	0.71	0.60		
B795	(TC) <sub>8</sub> Ns(CT) <sub>7</sub>	296-332	60	12	0.76	0.74		
	Ns(CT) <sub>10</sub>							
	Ns(TC) <sub>5</sub>							
	(TAA) <sub>5</sub>	167-226	60	14	0.80	0.80		
	(GAA) <sub>12</sub>							
15	C115							
KG809	(AGG) <sub>6</sub>	333-345	55	5	0.66	0.64		
KG811	(GA) <sub>17</sub>	240-278	58	12	0.83	0.82		
KG827	(CT) <sub>13</sub> AA	264-282	67	9	0.78	0.84		
	(CA) <sub>7</sub>							
20	KG830	(CT) <sub>14</sub>	279-311	67	9	0.79	0.78	
	GTATT							
	(CA) <sub>8</sub>							
	(AAT) <sub>5</sub>							
	Soman-G							
25	Locus	PIC	r	LG	Primers	5'-3'		
A613		0.85	0.00	11	Ned-CACACGCCTTGTCACTCT			
					TT (SEQ ID NO: 1)			
A614		0.84	0.00	6	Hex-TGGCAGAGCTTGTCAGC			
					TT (SEQ ID NO: 3)			
30	A616	0.83	0.00	8	Fam-CACTCATACCGCAAACTC			
					CA (SEQ ID NO: 5)			
A640		0.7	0.04	10	F-TGCCTCTGCAGTTAGTCATC			
					AAATGTAGG			
					(SEQ ID NO: 7)			
35	B107	0.83	0.02	10	Ned-GTAGGTGCACTTGATGTG			
					CTTTAC (SEQ ID NO: 9)			
B617		0.78	0.01	8	Fam-TCCGTGTTGAGTATGGAC			
					GA (SEQ ID NO: 11)			
B619		0.7	0.00	3	Fam-AGTCGGCTCCCCTTTCT			
					C (SEQ ID NO: 13)			
40	B634	0.73	0.00	4	Hex-CCTGCATCCAGGACTCAT			
					TA 60 (SEQ ID NO: 15)			
B657		0.82	-0.08	11	Ned-GAGAGTGCCTCTCCTCT			
					GG (SEQ ID NO: 17)			
B671		0.84	-0.01	9	Hex-TGCCAGTGCATACTCTG			
					AT G (SEQ ID NO: 19)			
45	B709	0.70	-0.01	5	Ned-CCAAGCACGAATGAACTC			
					AA (SEQ ID NO: 21)			
B733		0.63	0.00	7.2	Ned-CACCTCTTCACCACCTC			
					AT (SEQ ID NO: 23)			
B741		0.74	0.00	5	Fam-GTTCACAGGCTTTGGGT			
					TT (SEQ ID NO: 25)			
50	B749	0.51	-0.03	1	Hex-GGCTGACAACACAGCAGA			
					AA (SEQ ID NO: 27)			
B751		0.77	0.01	7.2	Fam-AGCTGGTTCTCGACATT			
					CC (SEQ ID NO: 29)			
B774		0.77	0.01	5	Ned-GTTTGCGAGCTATTGT			
					CA (SEQ ID NO: 31)			
55	B776	0.67	0.07	6	Fam-TGTATGTACACACGGAGA			
					GAGAGA (SEQ ID NO: 33)			
B795		0.74	0.01	NA	Fam-GACCCACAAACATAACC			
					TATCTC (SEQ ID NO: 35)			
C115		0.77	0.00	4	Fam-ATTTCAGCAGATAATAC			
					AGG (SEQ ID NO: 37)			
60	KG809	0.60	0.01	4	Hex-AGGCATCAGTTCATCAA			
					(SEQ ID NO: 39)			
KG811		0.81	0.01	2	Ned-AAGGCAGCACTCGCTCAC			
					(SEQ ID NO: 41)			
KG827		0.75	-0.04	9	Fam-AGAACTCCGACTAATAAT			
					CCTAACCCCTTGC			
					(SEQ ID NO: 43)			
65								

TABLE 1-continued

Primers and annealing temperatures for the 24 microsatellite marker loci used to fingerprint 'Dorris' and other hazelnut cultivars.

KG830	0.76	0.00	9	Ned-TGGAGGAAGTTTGAAATG GTAGTAGAGGA (SEQ ID NO: 45)
Soman-G	0.51	-0.27	NA	Hex-TGGCGTTGCAACATATTCTC (SEQ ID NO: 47)

Locus	Primers 5'-3'	Reference
A613	R-CCCTTCACATGTTGCTT (SEQ ID NO: 2)	Gurcan et al. 2010
A614	R-GCAGTGGAGGATTGCTGACT (SEQ ID NO: 4)	Gurcan et al. 2010
A616	R-ATGGCTTTGCTTCGTTTG (SEQ ID NO: 6)	Gurcan et al. 2010
A640	Fam-CGCCATATAATTGGGATG CTTGTG (SEQ ID NO: 8)	Gurcan et al. 2010
B107	R-AACACCATTGAGTCTTCA AAAGC (SEQ ID NO: 10)	Boccacci et al. 2005; Gokirmak et al. 2009
B617	R-TGTTTTGGTGGAGCGATG (SEQ ID NO: 12)	Gurcan et al. 2010
B619	R-GCGATCTGACCTCATTGTTG (SEQ ID NO: 14)	Gurcan et al. 2010
B634	R-GTGCAGAGGTTGCACTC (SEQ ID NO: 16)	Gurcan et al. 2010
B657	R-AGCCTCACCTCCAACGAAC (SEQ ID NO: 18)	Gurcan et al. 2010
B671	R-ACCAGCTCTGGGCTAACAC (SEQ ID NO: 20)	Gurcan et al. 2010
B709	R-GCGGTTCTCGTTGTACACT (SEQ ID NO: 22)	Gurcan et al. 2010
B733	R-CATCCCCTGTTGGAGTTTC (SEQ ID NO: 24)	Gurcan et al. 2010
B741	R-CGTGTTGCTCATGTGTTGTG (SEQ ID NO: 26)	Gurcan et al. 2010
B749	R-TCGGCTAGGGTTAGGGTTT (SEQ ID NO: 28)	Gurcan et al. 2010
B751	R-AAACTCAAATAAAACCCCTG CTC (SEQ ID NO: 30)	Gurcan et al. 2010
B774	R-TGTGTGTGGTCTGTAGGC ACT (SEQ ID NO: 32)	Gurcan et al. 2010
B776	R-TGAGGGGAAGAGGTTTGATG (SEQ ID NO: 34)	Gurcan et al. 2010
B795	R-TGGGCATCATCCAGGTCTA (SEQ ID NO: 36)	Gurcan et al. 2010
C115	GTTCCAGATCTGCCTCCATATAA T (SEQ ID NO: 38)	Bassil et al. 2005b, Gokirmak et al. 2009
KG809	F-GGAAGGTGAGAGAAATCAAGT (SEQ ID NO: 40)	Gurcan and Mehlenbacher 2010
KG811	F-GAACAACTGAAGACAGCAAAG (SEQ ID NO: 42)	Gurcan and Mehlenbacher 2010
KG827	GAGGGAGCAAQTCAAAGTTGAGA AGAAA (SEQ ID NO: 44)	Gurcan and Mehlenbacher 2010
KG830	AAAGCAACTCATAGCTGAAGTCCA ATCA (SEQ ID NO: 46)	Gurcan and Mehlenbacher 2010
Soman-G	R-GCCATCTTAGAAAGTTCGATA CAG (SEQ ID NO: 48)	unpublished

Primer fluorescent tags are FAM, HEX, and NED.

Ta: annealing temperature ( $^{\circ}$  C.)

N: number of alleles

He: expected heterozygosity

$H_0$ : observed heterozygosity

PIC: polymorphism information content

Fig. polymorphism information con-

LG: linkage group

TABLE 2

Allele sizes in 'Dorris' and  
other hazelnut cultivars at 24 microsatellite loci.

	Tag	Locus	'Dorris'	'309.074'	'Delta'	'Tonda Gentile delle Langhe'
5	NED	A613	149/167	157/167	149/177	151/157
	HEX	A614	132/158	125/132	143/158	125/135
	FAM	A616	148/150	148/158	150/150	148/150
10	FAM	A640	372/374	368/374	362/372	354/368
	NED	B107	112/122	112/152	122/130	134/152
	FAM	B617	286/296	294/296	286/286	286/296
	FAM	B619	156/164	164/174	156/164	148/164
	HEX	B634	226/226	226/226	226/234	226/226
	NED	B657	210/226	210/226	222/226	218/226
15	HEX	B671	227/247	227/237	235/247	237/241
	NED	B709	227/227	227/227	227/227	227/227
	NED	B733	171/179	171/173	173/179	171/173
	FAM	B741	177/186	177/177	177/186	177/184
	HEX	B749	206/206	206/208	206/208	206/208
	FAM	B751	143/151	143/153	143/151	149/153
20	NED	B774	203/207	203/203	207/213	203/211
	FAM	B776	137/137	137/137	137/150	137/137
	FAM	B795	330/330	330/330	314/330	312/330
	FAM	C115	194/215	173/194	197/215	173/173
	HEX	KG809	336/345	336/339	345/345	336/339
	NED	KG811	254/264	242/254	254/264	254/264
	FAM	KG827	270/282	268/282	270/270	266/268
25	NED	KG830	295/297	291/295	291/297	291/295
	HEX	SM NG	196/200	196/200	196/196	196/200

	Tag	Locus	'Barcelona'	'Extra Ghiaghli'	'Gasaway'
30	NED	A613	151/159	167/169	159/161
	HEX	A614	125/131	125/150	143/158
	FAM	A616	142/150	150/158	148/148
	FAM	A640	354/374	374/374	362/368
	NED	B107	112/134	116/116	122/128
	FAM	B617	286/290	294/296	292/296
	FAM	B619	156/170	164/174	170/174
35	HEX	B634	226/226	226/226	220/232
	NED	B657	218/222	210/222	224/228
	HEX	B671	223/227	227/247	235/247
	NED	B709	225/233	225/227	227/227
	NED	B733	171/173	171/171	173/173
	FAM	B741	177/186	177/184	186/188
	HEX	B749	208/208	208/208	206/208
40	FAM	B751	143/153	143/147	143/143
	NED	B774	203/207	195/203	203/209
	FAM	B776	135/137	135/137	146/150
	FAM	B795	330/330	296/310	314/316
	FAM	C115	173/194	182/194	215/218
	HEX	KG809	336/336	336/339	336/345
45	NED	KG811	258/264	240/242	254/258
	FAM	KG827	280/282	276/282	270/280
	NED	KG830	291/295	291/295	291/305
	HEX	SM NG	196/200	196/200	196/196

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## SEQUENCE LISTING

&lt;160&gt; NUMBER OF SEQ ID NOS: 48

<210> SEQ ID NO 1  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 1

cacacgcctt gtcactcttt

20

<210> SEQ ID NO 2  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 2

ccctttcac atgttgctt

20

<210> SEQ ID NO 3  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 3

tggcagagct ttgtcagctt

20

<210> SEQ ID NO 4  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 4

gcagtggagg attgctgact

20

<210> SEQ ID NO 5  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 5

cactcataacc gcaaactcca

20

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<210> SEQ ID NO 6
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 6
atggcttttg cttcggtttg                                         20

<210> SEQ ID NO 7
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 7
tgcctctgca gtttagtcac aaatgtagg                                         29

<210> SEQ ID NO 8
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 8
cgccatataa ttgggatgct tggtg                                         25

<210> SEQ ID NO 9
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 9
gtaggtgcac ttgatgtgct ttac                                         24

<210> SEQ ID NO 10
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 10
aacaccatat tgagtcttcc aaagc                                         25

<210> SEQ ID NO 11
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 11
tccgtgttga gtatggacga                                         20

<210> SEQ ID NO 12
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

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<400> SEQUENCE: 12

tgttttggc ggagcgatg

19

<210> SEQ ID NO 13

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 13

agtccggctcc ccttttctc

19

<210> SEQ ID NO 14

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 14

gcgatctgac ctcatttttg

20

<210> SEQ ID NO 15

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 15

cctgcatacca ggactcattha

20

<210> SEQ ID NO 16

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 16

gtgcagaggt tgcactcaaa

20

<210> SEQ ID NO 17

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 17

gagagtgcgt ctccctctgg

20

<210> SEQ ID NO 18

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 18

agcctcacct ccaacgaac

19

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<210> SEQ ID NO 19  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 19

ttgccagtgc atactctgat g

21

<210> SEQ ID NO 20  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 20

accagctctg ggcttaacac

20

<210> SEQ ID NO 21  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 21

ccaaggcacga atgaactcaa

20

<210> SEQ ID NO 22  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 22

gcgggttctc gttgtacact

20

<210> SEQ ID NO 23  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 23

cacccttttc accacccat

20

<210> SEQ ID NO 24  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 24

catcccctgt tggagtttc

20

<210> SEQ ID NO 25  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide

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<400> SEQUENCE: 25

gttcacaggc tgttgggttt

20

<210> SEQ ID NO 26

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 26

cgttgtgctc atgtgttgta

20

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<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 27

ggctgacaac acagcagaaa

20

<210> SEQ ID NO 28

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 28

tccggctaggg tttagggtttt

20

<210> SEQ ID NO 29

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 29

agctggttct tcgacattcc

20

<210> SEQ ID NO 30

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 30

aaactcaaat aaaacccctg ctc

23

<210> SEQ ID NO 31

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 31

gttttgcgag ctcattgtca

20

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<210> SEQ ID NO 32
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 32

tgtgtgtggc tctgtttttt

```

21

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<210> SEQ ID NO 33
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 33

tgtatgtaca cacggagaga gaga

```

24

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<210> SEQ ID NO 34
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 34

tgaggggaa aggtttgatg

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20

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<210> SEQ ID NO 35
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 35

gacccacaaa caataaccta tctc

```

24

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<210> SEQ ID NO 36
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 36

tgggcatcat ccaggtcta

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19

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<210> SEQ ID NO 37
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 37

attttccgca gataatacag g

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21

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<210> SEQ ID NO 38
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

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&lt;400&gt; SEQUENCE: 38

gtttccagat ctgcctccat ataat

25

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 18

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 39

aggcatcagt tcatccaa

18

&lt;210&gt; SEQ ID NO 40

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 40

ggaaggtgag agaaaatcaag t

21

&lt;210&gt; SEQ ID NO 41

&lt;211&gt; LENGTH: 18

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 41

aaggcggcac tcgctcac

18

&lt;210&gt; SEQ ID NO 42

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 42

gaacaactga agacagcaaa g

21

&lt;210&gt; SEQ ID NO 43

&lt;211&gt; LENGTH: 30

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 43

agaactccga ctaataatcc taacccttgc

30

&lt;210&gt; SEQ ID NO 44

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 44

gagggagcaa gtcaaagttg agaagaaa

28

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- continued

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<210> SEQ ID NO 45  
<211> LENGTH: 29  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide  
<400> SEQUENCE: 45

tggaggaagt tttgaatggc agtagagga

29

<210> SEQ ID NO 46  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide  
<400> SEQUENCE: 46

aaagcaactc atagctgaag tc当地atca

28

<210> SEQ ID NO 47  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide  
<400> SEQUENCE: 47

tggcggttgca acatatttc

20

<210> SEQ ID NO 48  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic polynucleotide  
<400> SEQUENCE: 48

gccatcttta gaaagttcga tacag

25

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We claim:

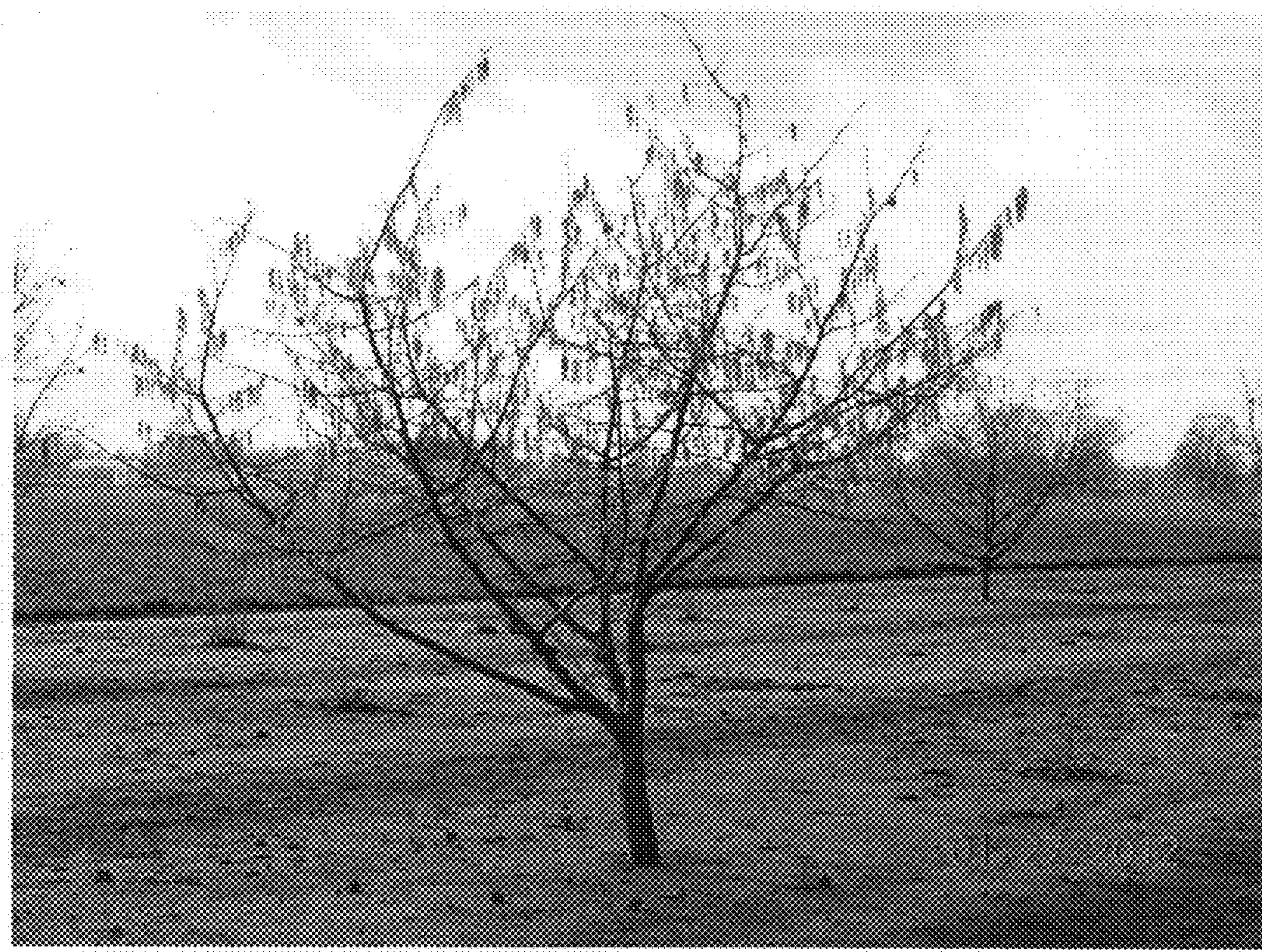
1. A new and distinct cultivar of *Corylus* plant named 'Dorris', as illustrated and described.

\* \* \* \* \*

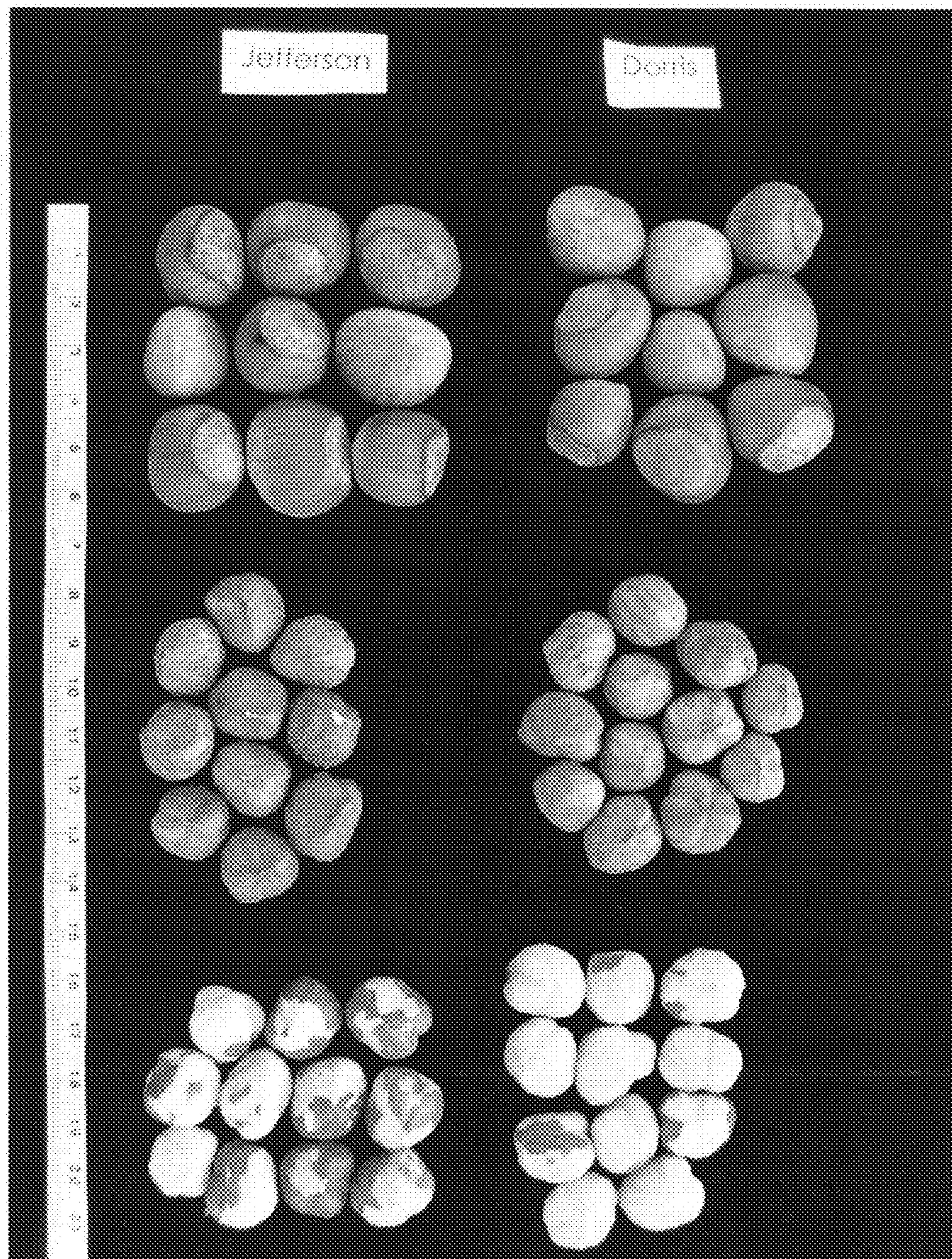
45



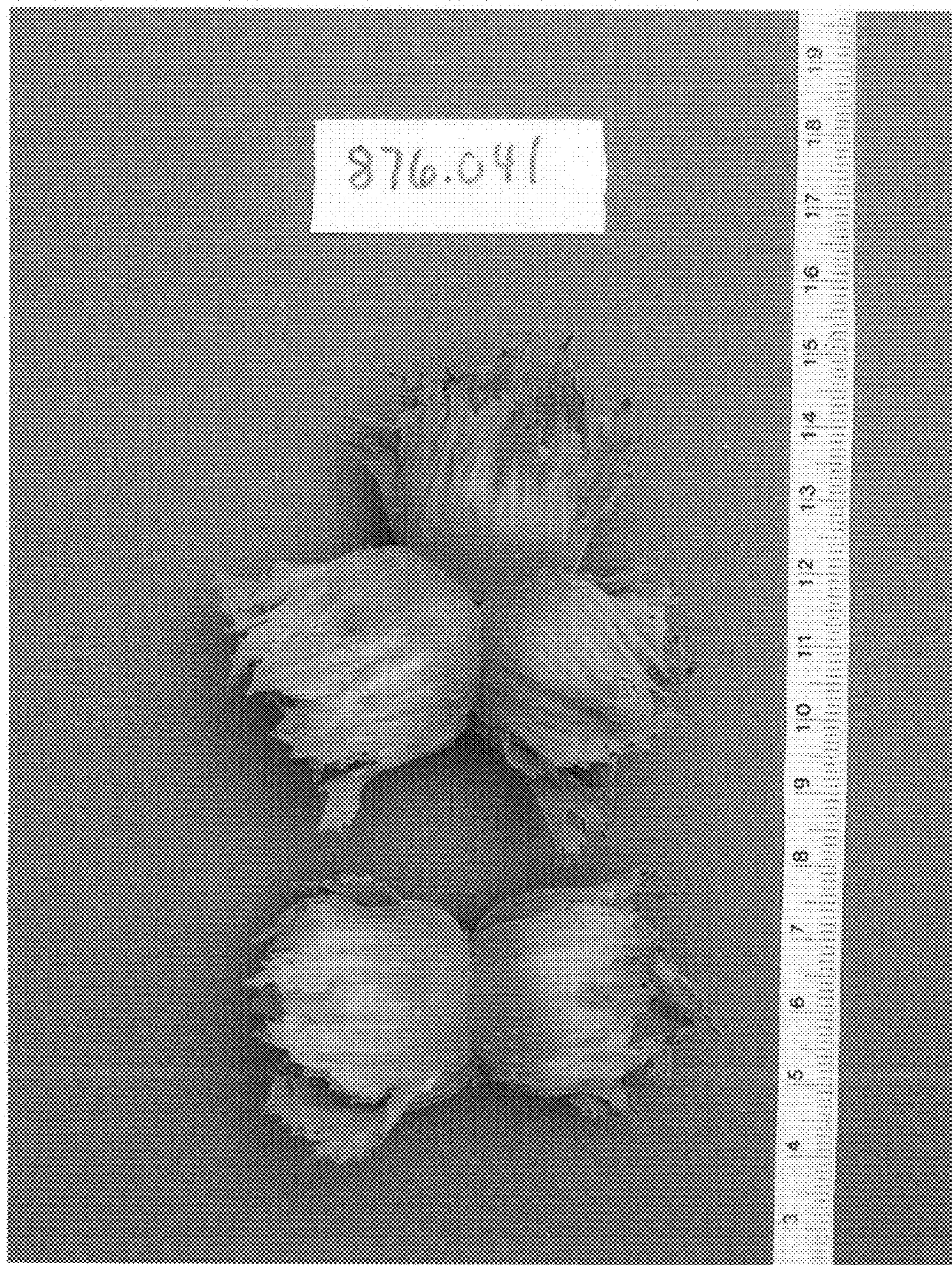
**FIG. 1**



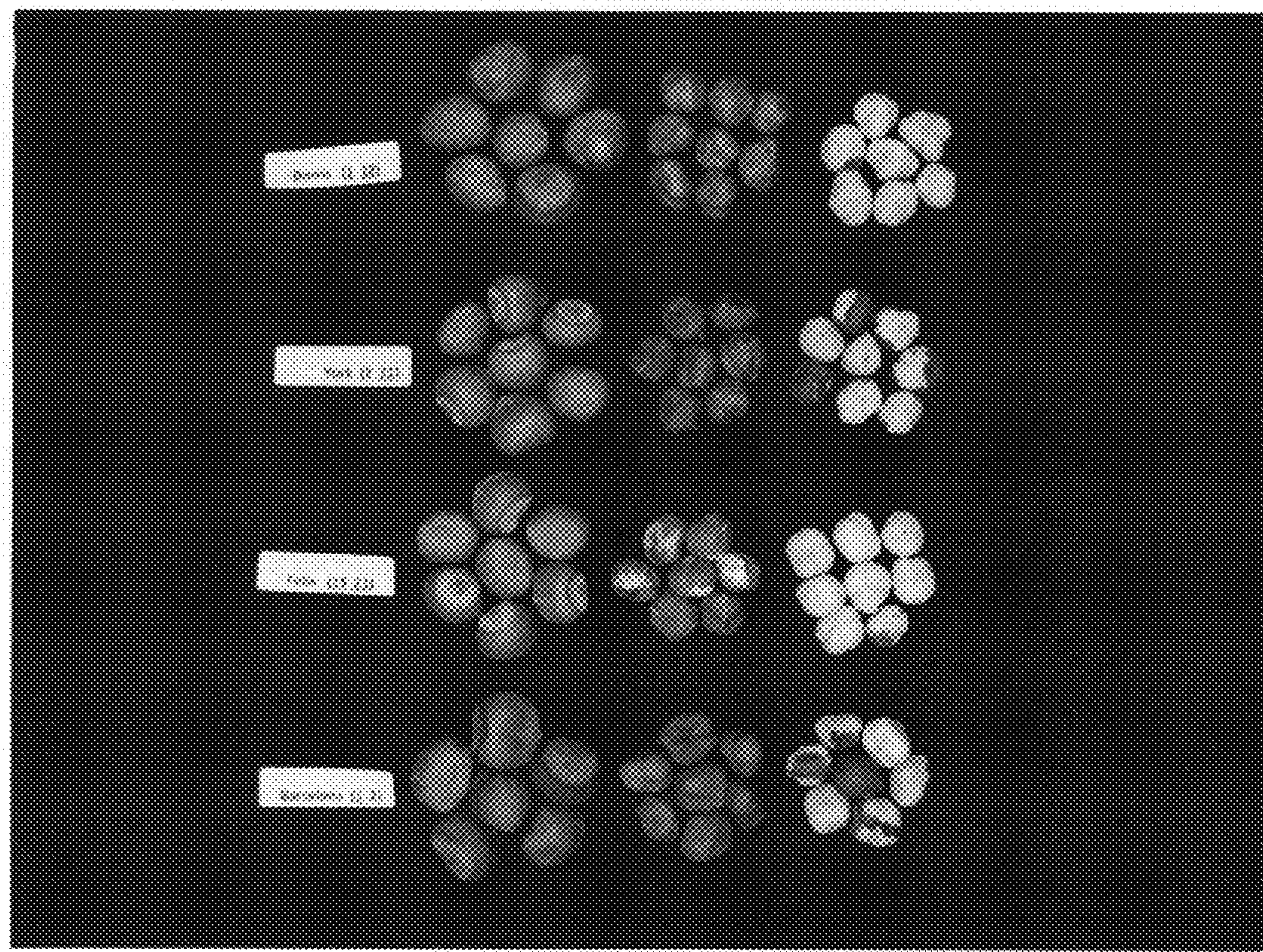
**FIG. 2**



**FIG. 3**



**FIG. 4**



**FIG. 5**