DANIEL G. PETERSON, SUSAN R. WESSLER, & ANDREW H. PATERSON (2002)

CBCS
Cot-Based Cloning & Sequencing
Fast ... Powerful ... Efficient ...

TABLE 1. CBCS *vs*. shotgun sequencing for various plants, animals, fungi, and protists. The CBCS/shotgun ratio (column VII) is an estimate of the relative number of clones that would need to be sequenced to attain a given level of sequence complexity coverage using CBCS divided by the number of shotgun clones that would need to be sequenced to attain the same coverage level - the lower the CBCS/Shotgun ratio, the greater the advantage of CBCS.

KEY

I. DIVISION, Species	**V. Sum of kinetic complexities of all components in Cot curve**
II. Common name	**VI. Estimated kinetic complexity of genome (IV + V) in bp**
III. 1C DNA content	**VII. CBCS/Shotgun ration (VI ÷ III)***
IV. Base pair content of foldback DNA	**VIII. Genome size reference, Cot/complexity reference, endnotes**

* Because the kinetic complexity of foldback DNA is unknown, the foldback fraction of each genome was assigned a 'kinetic complexity' equivalent to the number of base pairs it contains, i.e., foldback DNA was treated as if it were 'single-copy' in nature.

K I N G D O M P L A N T A E

I	II	III	IV	V	VI	VII	VIII
PTERIDOPHYTA							
Osmunda claytoniana	interrupted fern	9.60E+10	0.00E+00	1.92E+10	1.92E+10	0.2	1,1,AK
Osmunda cinnamomea	cinnamon fern	9.60E+10	0.00E+00	1.92E+10	1.92E+10	0.2	1,1,AK
Osmunda regalis	royal fern	9.60E+10	0.00E+00	1.92E+10	1.92E+10	0.2	1,1,AK
MAGNOLIOPHYTA							
Arabidopsis thaliana	Arabidopsis	1.25E+08	1.25E+07	7.01E+07	8.26E+07	0.66	2,3,BL
Arachis hypogaea	peanut	1.71E+09	0.00E+00	6.18E+08	6.18E+08	0.36	4,5,CK
Solanum lycopersicum	tomato	9.54E+08	1.14E+08	6.21E+08	7.35E+08	0.77	6,7,CL
Gossypium raimondii	D-genome cotton	1.25E+09	8.78E+07	3.92E+08	4.79E+08	0.38	8,9,BL
Glycine max	soybean	1.81E+09	1.27E+08	7.28E+08	8.55E+08	0.47	6,10,BL
Glycine max	soybean	1.81E+09	7.24E+07	5.57E+08	6.30E+08	0.35	6,11,BL
Petroselinum crispum	parsley	1.91E+09	1.03E+08	2.28E+08	3.31E+08	0.17	6,12,BL
Pisum sativum	pea	4.17E+09	1.67E+08	6.72E+08	8.39E+08	0.2	6,13,CL
Gossypium herbaceum	A-genome cotton	1.93E+09	1.35E+08	3.82E+08	5.17E+08	0.27	8,9,BL
Gossypium hirsutum	cotton	2.25E+09	1.35E+08	4.12E+08	5.46E+08	0.24	6,9,BL
Nicotiana tabacum	tobacco	4.43E+09	9.31E+08	2.83E+08	1.21E+09	0.27	6,14,BL
Luffa cylindrica	sponge gourd	2.37E+08	4.74E+06	8.46E+07	8.93E+07	0.38	16,16,BIL
Trichosanthes anguina	snake gourd	3.09E+08	1.86E+07	7.38E+07	9.24E+07	0.3	16,16,BIL
Benincasa hispida	ash gourd	2.68E+08	3.22E+07	9.27E+07	1.25E+08	0.47	16,16,BIL
Coccinia indica	ivy gourd	2.76E+08	3.86E+07	1.59E+08	1.98E+08	0.72	16,16,BIL
Cucumis sativus	cucumber	3.67E+08	5.87E+07	7.42E+07	1.33E+08	0.36	6,16,BL
Luffa acutangula	ridge gourd	6.38E+08	5.10E+07	1.70E+08	2.21E+08	0.35	16,16,BIL
Daucus carota	carrot	5.84E+08	0.00E+00	1.93E+08	1.93E+08	0.33	17,18,CM
Helianthus tuberosus	Jerusalem artichoke	1.21E+10	0.00E+00	6.66E+09	6.66E+09	0.55	4,19,DM
Anemone virginiana	tall thimbleweed	8.61E+09	6.46E+08	2.20E+09	2.85E+09	0.33	4,20,EN
Anemone cylindrica	candle anemone	8.97E+09	6.73E+08	2.11E+09	2.79E+09	0.31	4,20,EN
Anemone coronaria	crown anemone	8.15E+09	6.12E+08	3.22E+09	3.83E+09	0.47	4,20,EN
Anemone pavonina	peacock anemone	1.20E+10	8.99E+08	5.16E+09	6.06E+09	0.51	4,20,EN
Anemone blanda	Greek thimbleweed	1.45E+10	1.09E+09	5.17E+09	6.26E+09	0.43	4,20,EN
Vigna mungo	black gram	1.02E+09	6.12E+07	5.30E+08	5.92E+08	0.58	29,29,BIL
Vigna aconitifolia	moth bean	3.06E+09	1.53E+08	1.44E+09	1.59E+09	0.52	29,29,BIL
Vigna radiata	mung bean	1.33E+09	1.06E+08	5.61E+08	6.68E+08	0.5	29,29,BIL
Vigna radiata	mung bean	5.79E+08	1.16E+07	3.14E+08	3.26E+08	0.56	6,15,CL
Sorghum bicolor	sorghum	7.60E+08	1.22E+08	1.68E+08	2.90E+08	0.38	6,21,BL
Zea mays	maize	2.50E+09	7.51E+07	8.80E+08	9.55E+08	0.38	6,22,CL
Secale cereale	rye	9.17E+09	3.67E+08	2.52E+09	2.89E+09	0.32	8,23,CL
Allium cepa	table onion	1.55E+10	1.12E+09	9.50E+08	2.07E+09	0.13	6,24,BL
Triticum aestivum	wheat	1.60E+10	6.39E+08	3.59E+09	4.23E+09	0.27	6,25,DL
Linum usitatissimum	flax	6.76E+08	1.35E+07	2.91E+08	3.05E+08	0.45	4,26,CL
Pennisetum americanum	pearl millet	2.32E+09	5.23E+08	3.36E+07	5.57E+08	0.24	27,28,BL
Tulipa gesneriana	Didier's tulip	2.37E+10	3.56E+09	2.22E+09	5.77E+09	0.24	30,30,CO

Picea glauca	white spruce	8.10E+09	0.00E+00	5.74E+09	5.74E+09	0.71	31,31,CK
Pinus banksiana	jack pine	1.25E+10	0.00E+00	2.89E+09	2.89E+09	0.23	31,31,CK
Pinus lambertiana	sugar pine	3.66E+10	0.00E+00	7.82E+09	7.82E+09	0.21	31,31,CK
Pinus resinosa	red pine	1.80E+10	0.00E+00	5.16E+09	5.16E+09	0.29	31,31,CK

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* Because the kinetic complexity of foldback DNA is unknown, the foldback fraction of each genome was assigned a 'kinetic complexity' equivalent to the number of base pairs it contains, i.e., foldback DNA was treated as if it were 'single-copy' in nature.

K I N G D O M A N I M A L I A

I	II	III	IV	V	VI	VII	VIII
CNIDARIA							
Aurelia aurita	jellyfish	7.04E+08	2.82E+07	4.70E+08	4.98E+08	0.71	32,32,BL
ECHINODERMATA							
Arbacia punctulata	purple sea urchin	8.59E+08	2.58E+07	6.10E+08	6.36E+08	0.74	33,34,CL
NEMATA							
Panagrellus silusiae	beer nematode	8.69E+07	8.08E+06	5.62E+07	6.43E+07	0.74	35,35,BL
Caenorhabditis elegans	*C. elegans*	9.70E+07	4.85E+06	7.76E+07	8.25E+07	0.85	36,37,CO
NEMERTEA							
Cerebratulus lacteus	nemertean worm	1.35E+09	6.76E+07	7.70E+08	8.38E+08	0.62	32,32,BL
ANNELIDA							
Siboglinum fiordicum	pogonophoran worm	5.61E+09	6.17E+08	1.67E+09	2.29E+09	0.41	38,38,DL
MOLLUSCA							
Crassostrea virginica	Eastern oyster	6.66E+08	5.99E+07	3.80E+08	4.40E+08	0.66	32,32,BL
Crassostrea gigas	Pacific oyster	1.15E+09	5.76E+07	8.06E+08	8.64E+08	0.75	39,39,DHO
Spisula solidissima	surf clam	1.16E+09	4.63E+07	8.20E+08	8.66E+08	0.75	32,32,BL
Aplysia californica	sea hare (slug)	1.74E+09	1.22E+08	8.43E+08	9.65E+08	0.56	40,41,BL
Ilyanassa obsoleta	mud dog whelk	2.84E+09	5.11E+08	1.12E+09	1.63E+09	0.57	42,42,BL
ARTHROPODA							
Limulus polyphemus	horseshoe crab	2.70E+09	1.89E+08	1.80E+09	1.99E+09	0.74	32,32,BL
Cancer borealis	Jonah crab	2.17E+09	0.00E+00	6.51E+08	6.51E+08	0.3	44,44,DP
Libinia emarginata	spider crab	2.13E+09	0.00E+00	6.40E+08	6.40E+08	0.3	44,44,DP
Drosophila melanogaster	fruit fly	1.80E+08	2.52E+07	7.01E+07	9.53E+07	0.53	45,46,BL
Chironomus tentans	non-biting midge	1.93E+08	7.72E+06	1.74E+08	1.82E+08	0.94	47,48,CO
Apis mellifera	honeybee	3.38E+08	1.35E+07	3.10E+08	3.23E+08	0.96	49,49,CL
Musca domestica	house fly	8.59E+08	5.15E+07	2.93E+08	3.44E+08	0.4	50,49,CO
Antheraea pernyi	oak silkmoth	9.65E+08	4.83E+07	3.57E+08	4.05E+08	0.42	51,51,CL
Galleria mellonella	honeycomb moth	4.83E+08	8.20E+07	2.95E+08	3.77E+08	0.78	52,53,BL
Bombyx mori	silkworm moth	5.02E+08	0.00E+00	2.80E+08	2.80E+08	0.56	52,54,BK
Sarcophaga bullata	flesh fly	5.89E+08	2.35E+07	5.39E+08	5.63E+08	0.96	55,56,GL
Prosimulium multidentatum	black fly	1.87E+08	9.35E+06	1.05E+08	1.14E+08	0.61	57,57,DO
Calliphora vicina	blowfly	2.58E+08	1.55E+07	2.27E+08	2.43E+09	0.94	89,89,BHL
CHORDATA							
Branchiostoma lanceolatum	lancelet (amphioxus)	5.65E+08	5.53E+07	3.87E+08	4.43E+08	0.78	58,59,CL
Acipenser ruthenus	sterlet (sturgeon)	1.80E+09	4.33E+08	1.01E+09	1.44E+09	0.8	60,61,BL
Carassius auratus	crucian carp	1.64E+09	9.84E+07	1.18E+09	1.28E+09	0.78	62,62,CL
Barbus barbus	barbel fish	1.77E+09	8.83E+07	1.27E+09	1.36E+09	0.77	62,62,CL
Barbus barbus	barbel fish	1.73E+09	2.00E+08	9.25E+08	1.13E+09	0.65	63,63,CL
Cyprinus carpio	common carp	1.83E+09	1.28E+08	1.32E+09	1.45E+09	0.79	62,62,CL
Cyprinus carpio	common carp	1.06E+09	1.61E+08	5.17E+08	6.77E+08	0.64	64,64,CIL
Barbus tetrazona	tiger barb	7.04E+08	8.52E+07	3.99E+08	4.84E+08	0.69	63,63,CL
Abramis brama	bream	1.27E+09	1.03E+08	6.22E+08	7.25E+08	0.57	63,63,CL

Leuciscus cephalus	dace	1.34E+09	1.47E+08	5.64E+08	7.11E+08	0.53	63,63,CL
Rutilus rutilus	roach	5.73E+08	5.79E+07	2.69E+08	3.27E+08	0.57	64,64,CIL
Clupea harengus	Atlantic herring	5.80E+08	1.44E+08	2.28E+08	3.72E+08	0.64	64,64,CIL
Sprattus sprattus	European sprat	6.38E+08	7.53E+07	3.44E+08	4.19E+08	0.66	64,64,CIL
Thymallus thymallus	European grayling	1.23E+09	1.71E+08	2.81E+08	4.52E+08	0.37	64,64,CIL
Oncorhynchus mykiss	rainbow trout	1.65E+09	4.61E+08	1.33E+08	5.94E+08	0.36	64,64,CGIL
Coregonus lavaretus	Baltic whitefish	1.86E+09	3.34E+08	2.23E+08	5.57E+08	0.3	64,64,CGIL
Salvelinus fontinalis	brook trout	2.06E+09	3.92E+08	2.16E+08	6.08E+08	0.29	64,64,CGIL
Salmo trutta	brown trout	2.85E+09	1.71E+08	1.14E+09	1.31E+09	0.46	65,66,CL
Scaphiopus couchi	Couch's spadefoot	9.00E+08	1.80E+07	5.46E+08	5.64E+08	0.63	67,67,CO
Xenopus laevis	African clawed frog	2.61E+09	9.38E+07	1.42E+09	1.51E+09	0.58	33,68,CL
Bufo marinus	marine toad	3.80E+09	3.04E+08	1.00E+09	1.31E+09	0.34	67,67,CO
Bufo bufo	common toad	6.76E+09	1.35E+09	1.41E+09	2.76E+09	0.41	69,69,CL
Rana clamitans	green frog	6.00E+09	1.20E+08	1.35E+09	1.47E+09	0.24	67,67,CO
Ambystoma tigrinum	tiger salamander	2.96E+10	1.78E+09	6.07E+09	7.85E+09	0.26	43,67,FL
Necturus maculosus	mudpuppy	7.77E+10	4.66E+09	1.68E+09	6.34E+09	0.08	43,67,FL
Triturus cristatus	great-crested newt	2.22E+10	2.22E+09	1.04E+10	1.27E+10	0.57	69,69,CL
Python reticularis	reticulated python	1.69E+09	2.04E+08	1.20E+09	1.40E+09	0.83	70,70,CL
Caiman crocodilus	spectacled caiman	2.59E+09	3.31E+08	1.71E+09	2.04E+09	0.79	70,70,CL
Terrapene carolina triungius	Eastern box turtle	4.03E+09	1.09E+09	2.19E+09	3.28E+09	0.81	70,70,CL
Gallus domesticus	chicken	1.20E+09	1.79E+08	4.02E+08	5.81E+08	0.49	71,72,CO
Gallus domesticus	chicken	1.20E+09	2.56E+08	8.15E+08	1.07E+09	0.9	71,73,CL
Cairina moschata	Muscovy duck	1.28E+09	1.78E+08	9.33E+08	1.11E+09	0.87	88,73,CL
Columba livia domestica	rock pigeon	1.41E+09	2.44E+08	9.91E+08	1.23E+09	0.88	71,73,CL
Junco hyemalis hyemalis	slate-colored junco	1.44E+09	5.76E+07	9.16E+08	9.73E+08	0.68	74,74,CO
Bos taurus	cow	3.20E+09	9.60E+07	1.50E+09	1.60E+09	0.5	75,76,BL
Rattus norvegicus	Norway rat	3.24E+09	2.92E+08	1.67E+09	1.96E+09	0.6	77,78,CHL
Homo sapiens	human	3.20E+09	2.88E+08	1.64E+09	1.93E+09	0.6	79,80,CL
Ellobius talpinus	common mole lemming	2.86E+09	3.15E+08	1.90E+09	2.22E+09	0.78	81,81,BL
Ellobius lutescens	transcauc. mole lemming	3.03E+09	3.33E+08	2.00E+09	2.34E+09	0.77	81,81,BL
Mesocricetus auratus	Syrian hamster	3.42E+09	3.96E+08	2.17E+09	2.57E+09	0.75	82,83,CL
Cricetulus griseus	Chinese hamster	3.09E+09	3.92E+08	2.41E+09	2.81E+09	0.91	82,83,CL
Phodopus sungorus sungorus	Djungarian hamster	1.75E+09	2.75E+08	1.10E+09	1.38E+09	0.79	83,83,CIL
Spermophilus undulatus	long-tailed souslik	1.84E+09	1.47E+08	1.21E+09	1.36E+09	0.74	84,84,CIL
Spermophilus parryi	Arctic souslik	2.55E+09	3.32E+08	1.58E+09	1.91E+09	0.75	84,84,CIL
Spermophilus relictus	Tien Shan souslik	1.84E+09	1.65E+08	1.23E+09	1.40E+09	0.76	84,84,CIL
Spermophilus spermophilus	European souslik	1.63E+09	9.80E+07	9.81E+08	1.08E+09	0.66	84,84,CIL
Spermophilus dauricus	Daurian souslik	1.74E+09	3.99E+08	8.17E+08	1.22E+09	0.7	84,84,CIL
Spermophilus pygmaeus	little souslik	2.55E+09	3.32E+08	1.56E+09	1.89E+09	0.74	84,84,CIL
Spermophilus major	russet souslik	2.55E+09	5.10E+08	1.38E+09	1.89E+09	0.74	84,84,CIL
Spermophilus fulvus	large-toothed souslik	2.55E+09	4.34E+08	1.51E+09	1.94E+09	0.76	84,84,CIL
Mus domesticus	house mouse	3.19E+09	0.00E+00	2.47E+09	2.47E+09	0.77	82,85,CK
Rattus rattus	black rat	2.92E+09	0.00E+00	2.04E+09	2.04E+09	0.7	86,85,CK
Sciurus carolinensis	gray squirrel	1.50E+09	0.00E+00	8.77E+08	8.77E+08	0.58	85,85,CIK
Tamias striatus	Eastern chipmunk	1.30E+09	0.00E+00	9.77E+08	9.77E+08	0.75	85,85,CIK
Gerbilis gerbillus	lesser Egyptian gerbil	1.30E+09	0.00E+00	9.59E+08	9.59E+08	0.74	85,85,CIK
Cricetus cricetus	common hamster	3.32E+09	0.00E+00	2.18E+09	2.18E+09	0.66	82,85,CK
Peromyscus pennsylvanicus	deer mouse	2.20E+09	0.00E+00	1.68E+09	1.68E+09	0.76	85,85,CIK
Microtus pennsylvanicus	meadow vole	2.54E+09	0.00E+00	1.84E+09	1.84E+09	0.72	87,85,CK

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K I N G D O M F U N G I

I	II	III	IV	V	VI	VII	VIII
ZYGOMYCOTA							
Phycomyces blakesleeanus	algal fungus	6.60E+07	5.61E+06	3.49E+07	4.05E+07	0.61	94,94,CL
ASCOMYCOTA							
Neurospora crassa	neurospora	4.00E+07	1.20E+06	2.25E+07	2.37E+07	0.59	95,90,BL

K I N G D O M P R O T I S T A

I	II	III	IV	V	VI	VII	VIII
MYXOMYCOTA							
Achlya bisexualis	Achlya fungus	4.19E+07	8.38E+05	3.41E+07	3.49E+07	0.83	91,91,BL
EUGLENOPHYTA							
Euglena gracilis	Euglena	1.45E+09	2.61E+08	6.02E+08	8.63E+08	0.6	92,92,BL
DINOFLAGELLATA							
Crypthecodinium cohnii	heterotroph. dinoflag.	3.67E+09	1.47E+08	1.36E+09	1.51E+09	0.41	93,93,JL

Endnotes

A. Fraction of single-copy DNA estimated from the curve using the "two Cot-decade" principle (see ref. 96).

B. Kinetic complexities (in bp) for the components of the Cot curve were stated in the corresponding paper.

C. Complexity for each component calculated using formula (1C x F)/R where 1C = genome size in bp, F = fraction of genome occupied by component, and R = mean repeat number of component.

D. Complexity calculated as described in endnote C above except only value for single-copy DNA could be used (i.e., no repeat frequency data or extremely poor data for repetitive fractions)

E. Cullis and Schweizer (1974) suggest that all anemones studied have two major kinetic components with Cot½ values of 1 (repetitive) and 2000 (single copy), respectively. Consequently, these values were used in calculating sequence complexity as described in endnote C.

F. Fraction of DNA in single-copy DNA not given in paper. However, assuming 10% foldback, the single-copy component fraction was estimated as 1 - (0.1 foldback + sum of fractions for repetitive components). For each component, complexity was calculated

G. These species are recent tetraploids. Consequently, their low-copy Cot components have repeat values of approximately 2 rather than 1 (see ref. 63).

H. Genome size and/or complexity values were given in daltons and converted into nt by dividing by 660.

I. Calculated using the formula G = (4,639,221 bp x 0.22)/ksc where 4,639,221 is the genome size of *E. coli*, 0.22 is the rate constant for *E. coli*, and ksc is the rate constant for the single-copy component of the test organism's genome

J. Fraction of single-copy component and genome size were given. The k for the single-copy fraction was determined from the genome size by adapting the formula in endnote I. The Cot½ for the repetitive fraction was estimated from the curve, and the mean repeat iteration was determined by dividing the k for the repeat component by the k for the single-copy component. The value in column IV then was calculated using the formula given in endnote C.

K. No information on foldback DNA was available in the Cot paper.

L. The fraction of the genome in the foldback component was stated in the Cot paper.

M. S1 nuclease digestion of DNA prevented estimation of the fraction of the genome in the foldback component.

N. The foldback component was assigned a value of 7.5% based on curves of *A. blanda* and *A. virginiana* shown in the paper (see ref. 20).

O. While not explicitly stated by the authors, the fraction of the genome in the foldback component could be estimated based on the Cot curve figure(s).

P. The fraction of foldback DNA is > 25% indicating possible error in the Cot analysis.

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