A challenge: who/what/when/where/why are our telomeres?

--Coe, EH

Telomeres are significant structures -- the maize telomeres doubly so in light of the evolutionary history of the maize genome, and of the many discoveries in maize about cytogenetic behavior, including broken ends, rings, fragments, and the processes of synapsis (*N.B.* the role of base motifs in other species: Phillips, C. et al., Identification of chromosome sequence motifs that mediate meiotic pairing and synapsis in C. elegans, Nature Cell Biol. 11:934-942, 2009). We do not yet know enough about maize telomeres. Mapping genetically and physically would be supportive.

The updated Genetic 2008 maps in MaizeGDB provide best estimates for coordinates of the telomeres, which I reviewed and revised in September 2010 (Table 1). The v.2 genome-build erected by Fusheng Wei, presented in WebFPC, was the foundation for placements. The URL for his expert synthesis of the maize genome is: http://www.genome.arizona.edu/fpc/WebAGCoL/maize/WebFPC/. Version 1 was used in previous estimates (MNL 83:17) as of October 2008.

Current placement was inferred in silico from BLAST matches or hybridizations of telomere-specific sequences (e.g., pMTY9ER, pBF266) at one end of a contig, consonant with positions of genetically mapped markers. When these criteria were insufficient, best positions were inferred relative to markers on IBM2. Improved v.2 placements were defined for the 2S, 3L, 6L, 7L, 7S, and 9S telomeres. The evidence is strong, though indirect, for map locations of 2L, 3L, 5S, 5L, 6S, 6L, and 9S. Mapped markers that fall beyond the telomeres are mostly, if not entirely, artifacts of mapping analysis in particular studies.

The challenge posed here is much more significant than map coordinates – and more significant than just their physical location and structure and fluidity – it is toward the tools necessary to unveil their functional involvement in central themes of cytogenetics. Among these themes are *evolution of distinct synaptic partners; mechanics of synaptic "finding"; roles of motifs and sequences; and repair of broken ends*.

Table 1. Estimated Genetic 2008 map locations of telomeres as of Sep 2010.

Name	Ctg	cM	Evidence
telomere1S	1	0	Reviewed Sep 2010 (EHC): Mapped by inference from BLAST of pMTY9ER and pMTY7SC1, associated at the left end of ctg1, and BLAST of subtelomeric clones S46925 S46926 U39641 and U39642 to BAC c0014I07 at left end of ctg1 distal to IBM2 marker umc1354
telomere1L	67	286+/-2	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated from BACs that hybridize with pMTY9ER, located at the end of ctg67 beyond the distal-most markers, anchoring and orienting this contig
telomere2S	485	0	Reviewed Sep 2010 (EHC): Mapped by inference from BLAST of subtelomeric clones S46925 S46926 U39641 and U39642 to BAC b0500C18 in ctg485 at the end of 2S in v.2, and by RFLP placement of bnl(tas1a)
telomere2L	110	183+/-2	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated from the right end of ctg110, distal to IBM2 marker AY111236
telomere3S	111	0	Reviewed Sep 2010 (EHC): Mapped by inference from BAC filter hybridizations of subtelomeric clone U39641(pMTY7SC1) to BACs at the left end of ctg111, distal to umc2118
telomere3L	153	209+/-1	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate revised, estimated from ctg153, placed by IBM2 marker umc1594; ctg152, the next-nearest, has BAC filter hybridizations of pMTY7SC1 and pMTY9ER that are ambiguously distributed
telomere4S	154	0	Reviewed Sep 2010 (EHC): Mapped by inference from BAC filter hybridizations of subtelomeric clones S46925 S46926 U39641 and U39642 to BACs at left end of ctg154, distal to IBM2 marker umc2278
telomere4L	203	189+/-2	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated in silico by inference from BLAST of subtelomeric clones S46925 S46926 U39641 and U39642 to BAC b0528L21 in ctg203 at its right end, distal to IBM2 markers bnlg1890 and umc1707, orienting this contig
telomere5S	204	0	Reviewed Sep 2010 (EHC): Mapped by inference from left end of ctg204, distal to IBM2 marker AI676903
telomere5L	254	173+/-3	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated by inference from the right end of ctg254, distal to IBM2 marker umc1153
telomere6S	256	0	Reviewed Sep 2010 (EHC): Mapped by inference from left end of ctg256, distal to IBM2 markers fdx1, fdx2, and umc2310
telomere6L	291	138+/-2	Reviewed Sep 2010 (EHC): Revised Genetic 2008 coordinate estimated by inference from the right end of ctg291, distal to IBM2 markers hir3 and umc2324
telomere7S	714	0	Reviewed Sep 2010 (EHC): Mapped in silico by inference from BLAST of subtelomeric clones S46926 and U39642 to BAC c0203N21 in ctg714 at the end of 7S in v.2; markers bnl(tas1j), p-pMTY9ER, p-pMTY7SC1 are at the "right" end of ctg714, and IBM2 marker umc2177 is in the adjacent contig, ctg293.
telomere7L	325	158+/-3	Reviewed Sep 2010 (EHC): Revised Genetic 2008 coordinate estimated by inference from the right end of ctg325, distal to IBM2 marker AY109703
telomere8S	326	0	Reviewed Sep 2010 (EHC): Mapped by inference from left end of ctg326, distal to IBM2 marker csu319
telomere8L	366	160+/-1	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate inferred from BLAST of subtelomeric clones S46925 S46926 U39641 and U39642 to BAC c0447I13 at right end of ctg366, distal to IBM2 marker AY109853
telomere9S	441	0	Reviewed Sep 2010 (EHC): Mapped by inference beyond left end of ctg368, IBM2 markers umc109 and umc1957; ctg441 is placed in v.2 to the left of ctg368 and contains BACs hybridizing with knob probes (i.e., K9S) but has no markers on IBM2
telomere9L	391	164+/-4	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated by inference from the right end of ctg391, distal to IBM2 markers AW216329, umc1505, and AI901738
telomere10S	392	0	Reviewed Sep 2010 (EHC): Mapped by inference from BAC filter hybridizations of pMTY9ER and pMTY7SC1, associated in parts of ctg392 with the distal-most IBM2 markers, umc48a and others, on 10S
telomere10L	420	136+/-2	Reviewed Sep 2010 (EHC): Genetic 2008 coordinate estimated in silico from BLAST of subtelomeric clones S46925 S46926 U39641 to BAC b0310F06 at the "right" end of ctg420, with BACs that hybridize with pMTY9ER and pMTY7SC1 probes