



p53 binding sites in transposons

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A commentary on

Definition of a consensus binding site for p53

by el-Deiry, W. S., Kern, S. E., Pietenpol, J. A., Kinzler, K. W., and Vogelstein, B. (1992). *Nat. Genet.* 1, 45–49.

Repeated regions of the genome harbor more functional information than commonly assumed. Two decades ago, a highly influential paper describing the consensus binding site for the key transcription factor p53 was published in *Nature Genetics* by el-Deiry et al. (1992). Recently, it has been observed that many p53 binding sites are species-specific (Jegga et al., 2008), suggesting a remarkable flexibility in the p53 gene regulatory network. Consistent with this idea, several recent studies have reported the existence of p53 binding sites in sequences of primate-specific interspersed repeats, including retroviral long terminal repeats (LTRs; Wang et al.,

2007), short (Alus; Zemojtel et al., 2009; Cui et al., 2011), and long interspersed nuclear elements (LINEs; Harris et al., 2009), highlighting the role of transposition in the emergence of cis-regulatory elements (Feschotte, 2008; Schmidt et al., 2012).

We reanalyzed the 20 genomic sequences originally used by el-Deiry et al. (1992) to construct the p53 consensus binding motif. All of these binding sites could be uniquely mapped to the reference human genome sequence (hg19). Strikingly, as many as seven of these binding sites (~35%) reside in one of three repeat classes: LTR, LINE, and DNA transposons (Table 1). Interestingly, this small set includes members of the primate-specific LTR10 and MER61 families, which were previously identified as enriched in copies with a functional p53 site (Wang et al., 2007). Additionally, we found that one of the early reported p53 binding sites is composed of a low-complexity repeat.

In summary, the original work of el-Deiry et al. (1992) published 20 years ago already contained evidence for the involvement of transposable elements in spreading species-specific p53 binding sites. This raised the question: how many more gems are hidden in previously generated data sets?

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Table 1 | Characterization of 20 sequences reported by el-Deiry et al. (1992).

Clone ^a	Genomic location (hg19)	Name	Family	Class
s57	chr13: 114536915–114536965	–	–	–
N22	chr11: 44182113–44182162	–	–	–
11A2	chr14: 100093893–100093943	–	–	–
W211	chr6: 116275323–116275368	L2a	L2	LINE
W7B2	chr13: 52641535–52641585	MER61E	ERV1	LTR
3H	chr2: 191494065–191494114	HSMAR2	TcMar/Mariner	DNA
8A	chr4: 15767109–15767147	L2a	L2	LINE
532	chr6: 170765704–170765758	–	–	–
64A2	chr6: 88193436–88193496	HERVIP10FH	ERV1	LTR
W7A1	chr7: 22821881–22821930	–	–	–
S61	chr2: 32539190–32539238	L1ME3B	L1	LINE
1183	chr10: 121965614–121965661	–	–	–
N42	chr7: 47737939–47737989	–	–	–
S201	chr12: 113554293–113554341	–	–	–
S1503	chr17: 9443256–9443316	–	–	–
S92I	chr19: 44049878–44049927	–	–	–
S592II	chr19: 44049787–44049836	–	–	–
2Nb	chr6: 40151946–40151995	LTR10B1	ERV1	LTR
9H	chr4: 49630288–49630337	–	–	–
CBE10d	Un_gl000220: 101981–102031	(CCTTG) _n repeat	–	–

^aClone names, as originally reported by el-Deiry et al. (1992).