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# Mobile element-based forensic genomics

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**Abstract**

Mobile elements are commonly referred to as selfish repetitive DNA sequences. However, mobile elements represent a unique and underutilized group of molecular markers. Several of their characteristics make them ideally suited for use as tools in forensic genomic applications. These include their nature as essentially homoplasy-free characters, they are identical by descent, the ancestral state of any insertion is known to be the absence of the element, and many mobile element insertions are lineage specific. In this review, we provide an overview of mobile element biology and describe the application of certain mobile elements, especially the SINEs and other retrotransposons, to forensic genomics. These tools include quantitative species-specific DNA detection, analysis of complex biomaterials, and the inference of geographic origin of human DNA samples.


*Keywords:* Mobile element; Forensic genomics; SINEs

## 1. Introduction to mobile elements

Mobile elements are repetitive DNA sequences with the unique ability to move and/or make copies of themselves. They can comprise between 40 and 90% of genomes [1–3]. While individual insertions tend to be either neutral or deleterious, their prevalence in eukaryotic genomes indicates that their presence is, on the whole, selectively advantageous. Several studies suggest that they play important roles in genome structure, genome instability and gene expression [1,4–11]. For instance, the movement of these elements can change genomes by insertion mutagenesis [9,12–16], insertion-mediated genomic deletions [15,17-20], and transposition-mediated transduction [15,21–24]. Further, the widespread presence of very similar DNA sequences throughout a genome promotes recombination, including both equal and unequal crossover events [9,15,25,26], segmental duplication [27], gene conversion [28–30], exon shuffling [23,31] and chromosomal rearrangements [32].

Mobile elements are divided into two classes based on their method of mobilization (Fig. 1) [33]. Class I mobile elements utilize a "copy and paste" method referred to as retrotransposition. In this process, the original DNA copy in the genome is first transcribed to RNA. The transcript is used as a template to form a DNA molecule that is then inserted into a new location in the genome via a process known as target primed reverse transcription [34]. Autonomous class I elements encode some or all of the enzymes needed to accomplish their mobilization. These retrotransposons are subdivided into several subgroups based on autonomy and sequence characteristics. The autonomous class I elements include LTR (long terminal repeat) retrotransposons that share many characteristics with retroviruses [35]. Also autonomous are the non-LTR retrotransposons, which are usually 4–6 kb

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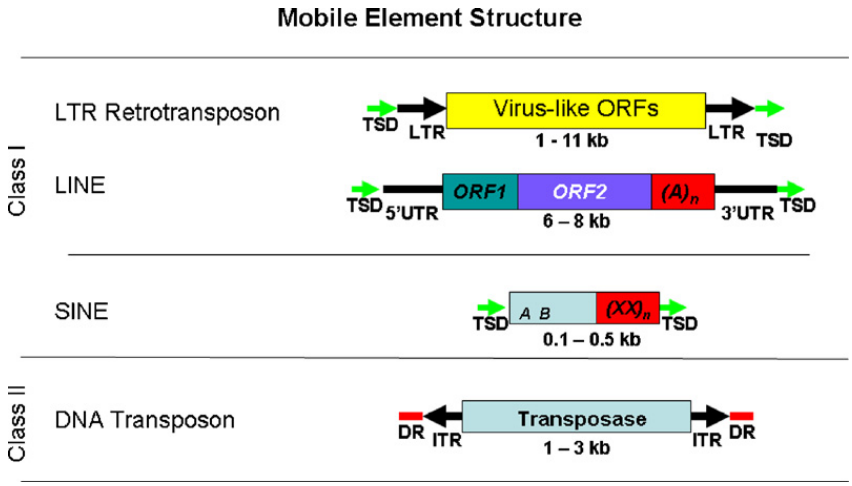


Fig. 1. General structure for the two classes of mobile elements. Class I elements of the LTR variety are flanked by both long terminal repeats (LTRs) and target site duplications (TSDs), which are produced during integration into the genome. These autonomous retrotransposons encode several polypeptides related to viruses. LINEs typically contain two open reading frames. Finally, SINEs do not contain any open reading frames. Instead, they use the enzymatic machinery of LINEs to mobilize in a genome. They are transcribed by RNA polymerase III which recognizes the A and B promoter sequences that make up part of the SINE sequence itself. SINEs also often have a repetitive motif at the 3′ end $((XX)_n)$. Autonomous class II elements, the DNA transposons contain an open reading frame for transposase and are typically flanked by inverted terminal repeats (ITRs) and direct repeats (DRs).

long. A typical example is the LINE-1 (long interspersed element-1) repeat of mammals. LINE-1 elements contain two open reading frames (ORFs). The first, short ORF encodes a protein thought to have a nucleic acid binding function [36–39]. The second ORF encodes a protein with both endonuclease and reverse-transcriptase properties [40,41]. It is via this enzymatic machinery that a LINE is able to mobilize after transcription by RNA polymerase II [42]. The endonuclease of LINE-1 and other non-LTR retrotransposons recognize specific target sequences in order to initiate the insertion process [43,44].

Class II elements, the DNA transposons and their derivatives, are common in many organisms from bacteria to humans. First discovered by Barbara McClintock in maize [45], DNA transposons differ from class I elements in that they utilize a DNA intermediate when mobilizing. They may utilize a "cut and paste" (conservative) or "copy and paste" method (replicative). In the former case, an entire DNA segment that includes the coding sequences and associated non-coding regions is excised from where it resides and reinserted into the genome at a different location. This process is mediated by the action of transposase, which is encoded by the autonomous element. Usually, transposase binds to both the inverted repeats of the transposon and a target site in the genome where the transposon will reinsert. The target site is cut and the transposon is then inserted.

Non-autonomous versions exist for both classes I and II elements. These elements lack the coding sequences typical of autonomous elements. Instead, they are believed to "hijack" the machinery of autonomous elements to accomplish their mobilization [46,47]. Several examples include TRIMs (terminal-repeat retrotransposons in miniature) and LARDs (large retrotransposon derivatives) that are both recently described non-autonomous elements derived from LTR retrotransposons [48,49]. SINEs (short interspersed elements) are non-autonomous, non-LTR retrotransposons that occur in large numbers in a wide variety of vertebrate genomes [14,50–53]. Class II non-autonomous mobile elements include the MITEs (minature inverted terminal repeat elements), Mers, and Acrobat elements among others [54–56].

This review will focus on SINEs. The widespread presence of SINEs in eukaryotes [14,50] and their relatively small size (usually between 100 and 500 bp) make them useful for a variety of different forensic approaches. Below, we will discuss some of them. The approaches that have been attempted include the simple identification of the taxon present in an unknown DNA sample to the identification of ancestry within a specific taxon.

## 2. Identification and quantitation of species-specific DNA

As various SINEs and LINEs expanded throughout the genomes of different organisms, generating over 100,000 mobile elements in many, genome-specific families with characteristic diagnostic mutations have arisen [10]. These large dispersed gene families serve as novel markers that identify the DNA from each species, thus

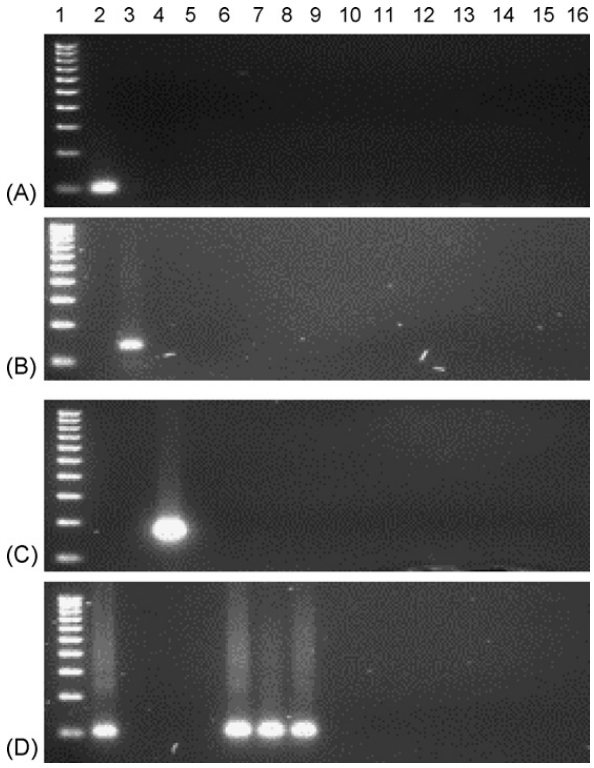


Fig. 2. Species DNA detection using PCR and agarose gel electrophoresis. Lanes: (1) 100 bp ladder, (2) cow, (3) pig, (4) chicken, (5) horse, (6) sheep, (7) deer, (8) antelope, (9) rabbit, (10) duck, (11) dog, (12) cat, (13) rat, (14) mouse, (15) human and (16) NTC (no template control). (A) Cow-specific; (B) pig-specific; (C) chicken-specific; (D) amplifies in all ruminants.

providing specific genomic tags that can be used in conjunction with PCR to amplify specific subsets of genomic sequences unique to the genome or species of interest (for recent reviews see [57,58]). Mobile element-based PCR assays have been developed for the sensitive identification and quantitation of DNA from many different classes, orders and species [59,60]. To date, class-specific intra-element PCR assays are available for birds, order-specific assays are available for primates, ruminants and rodents, and species-specific assays are available for humans, cows, horses, pigs, dogs, cats, hamsters, guinea pigs, rats, rabbits, and chickens (Fig. 2).

## 3. Quantitative detection of species DNA in meats

Documented cases of "mad cow disease" (bovine spongiform encephalopathy) have received high publicity in recent years. The risk associated with infectious transmissible spongiform encephalopathy in humans has discouraged many individuals around the globe from consuming beef. Hindu populations also choose not to eat beef, while Jewish and Muslim populations choose to avoid consumption of pork, even in minute quantities, due to their religious beliefs. Many consumers prefer to include more chicken in their diet instead of beef or pork. In addition to infectious disease and religious concerns, many individuals are altering their eating behavior to include more chicken simply to reduce dietary fat intake in accordance with health trends. Physicians routinely recommend such dietary changes to patients with heart disease, diabetes or obesity, for example.

Previously, species-specific SINE-based and LINE-based PCR assays have been reported for the detection of ruminant-, pig-, and chicken-derived materials [59,60]. Quantitative SINE-based PCR assays have been developed for the sensitive detection and quantitation of bovine, porcine, chicken and ruminant species DNA from mixed sources and food products [60]. For example, the bovine SINE-satellite 1.711B is thought to occupy 7.1% of the bovine genome [61] and the intra-SINE-based PCR assay using this repeat element can detect 0.005% bovine DNA from a mixed DNA sample [60]. The porcine SINE PRE-1 has an estimated 100,000 copies in the pig genome [62] and the intra-PRE-1-based PCR assay is able to detect even trace quantities (0.0005%) of porcine DNA from within a mixed-DNA sample [60]. A randomly selected food product labeled "chicken sausage" was determined to contained about 8% pork [60]. The chicken intra-CR1 SINE-based PCR assay can detect down to 0.05% chicken DNA and the intra-Bov-tA2 SINE-based PCR assay can detect as little as 0.1% ruminant species DNA (cow, sheep, deer, antelope, etc.) from mixed sources [60]. This highly sensitive species specificity makes these assays ideal for identification of beef, pork, chicken, and ruminant materials from human foods and animal feed mixtures.

## 4. Identification and quantitation of animal DNA

In addition to agricultural meat species intended for human consumption, certain situations make determining the source of a tissue, blood or DNA sample a necessity. For example, some violent crime scenes may include blood stains from not only human victims but from our animal companions as well. Other events such as earthquakes, tornadoes, and terrorist attacks create such volatile conditions that the biological evidence available for post-event genomic analysis may include a human and a nonhuman component. Thus, there is a need for sensitive detection and quantitation of other common domestic species from multi-species or unknown DNA samples.

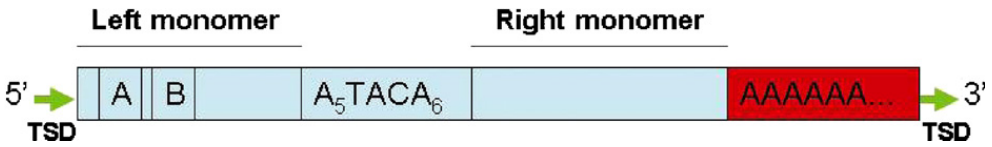


Fig. 3. The typical *Alu* element consists of two monomers, with the right monomer containing an additional 31-bp insertion (not shown) relative to the left monomer. Each *Alu* is ~300 bp, depending on the length of the 3′ poly-A tail. An A-rich central region also exists between the two monomers. The 5′ half of each *Alu* element contains an RNA-polymerase-III promoter (A and B boxes).

To address this need, a series of class-specific (*Aves*), order-specific (*Rodentia*), and species-specific (equine, canine, feline, rat, hamster, guinea pig, and rabbit) PCR-based assays were developed using intra-element amplification of genome-specific SINEs and LINEs [63]. The minimum effective quantitation levels of these assays ranged from 1 to 0.001% in 10 ng of starting DNA template. Thus, even when small amounts of DNA are available, it is possible for forensic investigators to determine "who" may have been present at a scene whether that individual is human or non-human.

## 5. The *Alu* element

The most abundant class of SINE in the human genome is the *Alu* element (Fig. 3). This SINE family is derived from the 7SL gene and is specific to primate genomes. *Alu* elements are only ~300 bp long but, with more than one million copies, they account for more than 10% of the mass of the human genome [1,14]. Most *Alu* elements are "fixed" in the human genome, meaning that all individuals are homozygous for the insertion at a particular locus in the genome in which it resides. The expansion of *Alu* elements throughout primate evolution has created several recently integrated "young" subfamilies that are present in the human genome but are largely absent from nonhuman primates [14]. Some members of these young *Alu* subfamilies have inserted in the human genome recently enough that individuals remain polymorphic for insertion presence/absence [14,64–68]. Both fixed and polymorphic *Alu* elements have been utilized quite successfully as forensic tools for a variety of applications [69,70].

## 6. Mobile element-based human gender identification

One important forensic use for *Alu* elements is human gender identification [70]. Determination of gender from human DNA samples is a common problem in forensic laboratories. The most widely used approach is based on the Amelogenin locus, which yields different-sized PCR (polymerase chain reaction) amplicons for the X and Y chromosome versions of the Amelogenin gene [71]. However, this method can misidentify males as females in some cases due to a deletion in the AMEL Y region [72–74]. While the frequency of the deletion is relatively low, the crucial nature of forensic test results in circumstances such as rape and prenatal gender determination where there is risk for male-specific inherited disorders makes any source of error a legitimate cause for concern. This has led several researchers to recommend that Amelogenin should not be relied upon as the sole determinant of gender [72–75].

Fixed *Alu* insertions on either the X or the Y chromosome provide a way of identifying the respective chromosome. Loci *AluSTXa and AluSTYa* demonstrate 100% accuracy in gender identification (X and Y chromosome identification) in 778 human DNA samples from diverse populations [70]. The combination of these two markers provides added assurance that gender test results are accurate since independent mutations would have to occur in two separate genomic locations to affect the outcome of the test. This *Alu*-based method may also be useful as a precursor to more extensive Y chromosome marker analysis, such as Y-Plex™ 12 (ReliaGene Technologies, Inc., New Orleans, LA). In addition, since *AluSTXa* is fixed on the *X* chromosome and *AluSTYa* is fixed on the Y chromosome, fluorescent-based detection of these markers allows for quantitative resolution of male and female contributions to mixed DNA samples, such as might be found in sexual assault cases.

## 7. Human DNA identification and quantitation

Just as in the examples for other species described above, the identification of human DNA in a complex mix may also be required. The vast majority of human forensic casework involves the analysis of nuclear loci, making the quantitation of human nuclear DNA a paramount issue [76]. *Alu* elements have amplified to a copy number of over 1 million elements throughout primate evolution producing a series of subfamilies of *Alu* elements that appear to be of different ages [14]. Because of their high copy number, *Alu* elements are a rich source of human genetic markers. Several systems have been developed to quantify human DNA using PCR primers designed to amplify the core *Alu* sequence [77–81]. Dur-

ing intra-*Alu* PCR, primers are designed within the core body of the element to amplify multiple target copies of the *Alu* family. Most of these systems are specific to the primate lineage and are not necessarily human specific.

Intra-*Alu*-based PCR assays have been developed for human-specific DNA identification and quantitation based on *Alu* subfamiliesYb8 and Yd6 [69], taking advantage of the large diagnostic insertion or deletion characteristic of these respective subfamilies. The intra-Yb8-based PCR assay has a linear quantitation range of 10–0.001 ng of DNA and is capable of detecting 10 pg of human DNA from a mixed source sample [69]. The intra-Yd6-based PCR assay is less sensitive quantitatively with a detection limit of 100 pg of human DNA. But the intra-Yd6-based PCR assay is specific to humans, no background amplification occurs from non-human primate templates, and has proven useful as an initial screening tool [69]. The collective use of primate specific and human specific *Alu*-based PCR assays in forensic genomics provides a powerful tool for sensitive human DNA identification and quantitation from mixed sources.

## 8. *Alu* insertion polymorphisms and inference of ancestry

Forensic DNA specimens are routinely matched to alleged criminal suspects in modern law enforcement. Frequently however, tools that narrow the potential pool of suspects are essential precursors to a positive identification in investigative forensics. The inferred ancestral origin of a DNA specimen is one type of predictor evidence which can aid a criminal investigation. Polymorphic *Alu* insertions have been widely used to study human genetic variation in world populations [82–103]. These elements are ideal for studying human geographic origins because they are essentially homoplasy free characters [57,104], they are identical by descent [14,57,105], and the ancestral state of a mobile element insertion polymorphism is known to be the absence of the element at a particular genomic location [83]. These features make the analysis of *Alu* elements a robust tool for tracking human geographic ancestry.

The distribution and structure of human genetic diversity has been systematically evaluated in a dataset of 100 *Alu* insertion polymorphisms, mined from existing human genome databases and selected for the greatest allele frequency variation between populations [106]. In this analysis, 710 individuals representing 31 different populations across 4 continents were evaluated for each of the 100 *Alu* insertion polymorphisms [85]. The inferred geographic affiliation of the samples was calculated using the Structure 2.0 software package [107,108]. The Markov Chain Monte Carlo methodology used by Structure 2.0 incorporates a powerful analysis to group all individuals into the selected number of populations and then determine the probability that each individual belongs to any given group. In addition, the software has the ability to detect admixture between populations in individual genotypes going back three generations.

This existing dataset is a powerful forensic tool to ascertain the inferred geographic ancestry of unknown forensic DNA samples. The methodology is simple, requiring only standard thermal cyclers for PCR and the ability to run agarose gel electrophoresis. In a study conducted in collaboration with law enforcement officials, forensic DNA specimens were evaluated using the dataset of 100 *Alu* insertion polymorphisms and Structure 2.0. The system demonstrated accurate assignment of each specimen to the correct geographic affiliation [109].

In addition to existing datasets, *Alu* elements have continued to accumulate in various populations since the human dispersal from Africa estimated to have occurred 156,000 years ago [85]. Many of these "new" *Alu* insertions are likely to be polymorphic and occur in various world populations to different degrees. The presence of these population-specific insertions will allow for subsequent layers of subgroup affiliation tests to be conducted using a cascade-like approach in the analyses. Thus, once the initial Structure 2.0 analysis assigns the DNA specimen to a continental affiliation such as Europe, Africa, Asia or India, subsequent Structure 2.0 analyses, using only insertion loci that are useful within the sub-continental population groups, can be used to further isolate the sub-continental region. The inferred ancestral origin of a DNA specimen narrows the pool of potential suspects and can successfully impact a criminal investigation.

Forensic DNA samples are often only available in trace quantities. This has previously been a limitation to this type of multiple locus approach. Recent advancements in whole genome amplification (WGA) technologies which utilize Φ29 polymerase have virtually eliminated this obstacle. In fact, successful genotypes have been obtained using post-WGA DNA, obtained from residual skin cells salvaged from a fingerprint [110]. Therefore, the inferred ancestral origin of a human DNA sample can even be determined from trace evidence.

## 9. Conclusion

Mobile elements represent novel tools within the increasingly varied armamentarium available to

forensic scientists. Their utility ranges from simple detection schemes, such as gender and species identification, to complex multi-locus systems for inference of human ancestry. Continued development of mobile element-based genetic systems in combination with high-throughput DNA analysis technologies will undoubtedly further the application of these approaches in the future.

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This paper is dedicated to the memory of Tony Carrano. During my (MAB) years at Lawrence Livermore National Laboratory I had the privilege of working in the Human Genome Center under the guidance of Tony. At that time Tony had the foresight to initiate a number of the forensic genomics efforts at Lawrence Livermore National Laboratory in an effort to create future areas of investigation for the Biology and Biotechnology Research Program. These early initiatives proved to be the underpinnings for many subsequent years of fruitful scientific investigations by individuals at Lawrence Livermore National Laboratory and elsewhere including my own laboratory. Tony was an exceptional scientist and was one of the best scientific administrators that I have ever known. His mentoring, dedication, leadership, and enthusiasm will be remembered and missed.

## References

[1] E.S. Lander, L.M. Linton, B. Birren, C. Nusbaum, M.C. Zody, J. Baldwin, K. Devon, K. Dewar, M. Doyle, W. FitzHugh, R. Funke, D. Gage, K. Harris, A. Heaford, J. Howland, L. Kann, J. Lehoczky, R. LeVine, P. McEwan, K. McKernan, J. Meldrim, J.P. Mesirov, C. Miranda, W. Morris, J. Naylor, C. Raymond, M. Rosetti, R. Santos, A. Sheridan, C. Sougnez, N. Stange-Thomann, N. Stojanovic, A. Subramanian, D. Wyman, J. Rogers, J. Sulston, R. Ainscough, S. Beck, D. Bentley, J. Burton, C. Clee, N. Carter, A. Coulson, R. Deadman, P. Deloukas, A. Dunham, I. Dunham, R. Durbin, L. French, D. Grafham, S. Gregory, T. Hubbard, S. Humphray, A. Hunt, M. Jones, C. Lloyd, A. McMurray, L. Matthews, S. Mercer, S. Milne, J.C. Mullikin, A. Mungall, R. Plumb, M. Ross, R. Shownkeen, S. Sims, R.H. Waterston, R.K. Wilson, L.W. Hillier, J.D. McPherson, M.A. Marra, E.R. Mardis, L.A. Fulton, A.T. Chinwalla, K.H. Pepin, W.R. Gish, S.L. Chissoe, M.C. Wendl, K.D. Delehaunty, T.L. Miner, A. Delehaunty, J.B. Kramer, L.L. Cook, R.S. Fulton, D.L. Johnson, P.J. Minx, S.W. Clifton, T. Hawkins, E. Branscomb, P. Predki, P. Richardson, S. Wenning, T. Slezak, N. Doggett, J.F. Cheng, A. Olsen, S. Lucas, C. Elkin, E. Uberbacher, M. Frazier, R.A. Gibbs, D.M. Muzny, S.E. Scherer, J.B. Bouck, E.J. Sodergren, K.C. Worley, C.M. Rives, J.H. Gorrell, M.L. Metzker, S.L. Naylor, R.S. Kucherlapati, D.L. Nelson, G.M. Weinstock, Y. Sakaki, A. Fujiyama, M. Hattori, T. Yada, A. Toyoda, T. Itoh, C. Kawagoe, H. Watanabe, Y. Totoki, T. Taylor, J. Weissenbach, R. Heilig, W. Saurin, F. Artiguenave, P. Brottier, T. Bruls, E. Pelletier, C. Robert, P. Wincker, D.R. Smith, L. Doucette-Stamm, M. Rubenfield, K. Weinstock, H.M. Lee, J. Dubois, A. Rosenthal, M. Platzer, G. Nyakatura, S. Taudien, A. Rump, H. Yang, J. Yu, J. Wang, G. Huang, J. Gu, L. Hood, L. Rowen, A. Madan, S. Qin, R.W. Davis, N.A. Federspiel, A.P. Abola, M.J. Proctor, R.M. Myers, J. Schmutz, M. Dickson, J. Grimwood, D.R. Cox, M.V. Olson, R. Kaul, N. Shimizu, K. Kawasaki, S. Minoshima, G.A. Evans, M. Athanasiou, R. Schultz, B.A. Roe, F. Chen, H. Pan, J. Ramser, H. Lehrach, R. Reinhardt, W.R. McCombie, M. de la Bastide, N. Dedhia, H. Blocker, K. Hornischer, G. Nordsiek, R. Agarwala, L. Aravind, J.A. Bailey, A. Bateman, S. Batzoglou, E. Birney, P. Bork, D.G. Brown, C.B. Burge, L. Cerutti, H.C. Chen, D. Church, M. Clamp, R.R. Copley, T. Doerks, S.R. Eddy, E.E. Eichler, T.S. Furey, J. Galagan, J.G. Gilbert, C. Harmon, Y. Hayashizaki, D. Haussler, H. Hermjakob, K. Hokamp, W. Jang, L.S. Johnson, T.A. Jones, S. Kasif, A. Kaspryzk, S. Kennedy, W.J. Kent, P. Kitts, E.V. Koonin, I. Korf, D. Kulp, D. Lancet, T.M. Lowe, A. McLysaght, T. Mikkelsen, J.V. Moran, N. Mulder, V.J. Pollara, C.P. Ponting, G. Schuler, J. Schultz, G. Slater, A.F. Smit, E. Stupka, J. Szustakowski, D. Thierry-Mieg, J. Thierry-Mieg, L. Wagner, J. Wallis, R. Wheeler, A. Williams, Y.I. Wolf, K.H. Wolfe, S.P. Yang, R.F. Yeh, F. Collins, M.S. Guyer, J. Peterson, A. Felsenfeld, K.A. Wetterstrand, A. Patrinos, M.J. Morgan, J. Szustakowki, P. de Jong, J.J. Catanese, K. Osoegawa, H. Shizuya, S. Choi, Y.J. Chen, Initial sequencing and analysis of the human genome, Nature 409 (2001) 860–921.

[2] R.H. Waterston, K. Lindblad-Toh, E. Birney, J. Rogers, J.F. Abril, P. Agarwal, R. Agarwala, R. Ainscough, M. Alexandersson, P. An, S.E. Antonarakis, J. Attwood, R. Baertsch, J. Bailey, K. Barlow, S. Beck, E. Berry, B. Birren, T. Bloom, P. Bork, M. Botcherby, N. Bray, M.R. Brent, D.G. Brown, S.D. Brown, C. Bult, J. Burton, J. Butler, R.D. Campbell, P. Carninci, S. Cawley, F. Chiaromonte, A.T. Chinwalla, D.M. Church, M. Clamp, C. Clee, F.S. Collins, L.L. Cook, R.R. Copley, A. Coulson, O. Couronne, J. Cuff, V. Curwen, T. Cutts, M. Daly, R. David, J. Davies, K.D. Delehaunty, J. Deri, E.T. Dermitzakis, C. Dewey, N.J. Dickens, M. Diekhans, S. Dodge, I. Dubchak, D.M. Dunn, S.R. Eddy, L. Elnitski, R.D. Emes, P. Eswara, E. Eyras, A. Felsenfeld, G.A. Fewell, P. Flicek, K. Foley, W.N. Frankel, L.A. Fulton, R.S. Fulton, T.S. Furey, D. Gage, R.A. Gibbs, G. Glusman, S. Gnerre, N. Goldman, L. Goodstadt, D. Grafham, T.A. Graves, E.D. Green, S. Gregory, R. Guigo, M. Guyer, R.C. Hardison, D. Haussler, Y. Hayashizaki, L.W. Hillier, A. Hinrichs, W. Hlavina, T. Holzer, F. Hsu, A. Hua, T. Hubbard, A. Hunt, I. Jackson, D.B. Jaffe, L.S. Johnson, M. Jones, T.A. Jones, A. Joy, M. Kamal, E.K. Karlsson, D. Karolchik, A. Kasprzyk, J. Kawai, E. Keibler, C. Kells, W.J. Kent, A. Kirby, D.L. Kolbe, I. Korf, R.S. Kucherlapati, E.J. Kulbokas, D. Kulp, T. Landers, J.P. Leger, S. Leonard, I. Letunic, R. Levine, J. Li, M. Li, C. Lloyd, S. Lucas, B. Ma, D.R. Maglott, E.R. Mardis, L. Matthews, E. Mauceli, J.H. Mayer, M. McCarthy, W.R. McCombie, S. McLaren, K. McLay, J.D. McPherson, J. Meldrim, B. Meredith, J.P. Mesirov, W. Miller, T.L. Miner, E. Mongin, K.T. Montgomery, M. Morgan, R. Mott, J.C. Mullikin, D.M. Muzny, W.E. Nash, J.O. Nelson, M.N. Nhan, R. Nicol,

Z. Ning, C. Nusbaum, M.J. O'Connor, Y. Okazaki, K. Oliver, E. Overton-Larty, L. Pachter, G. Parra, K.H. Pepin, J. Peterson, P. Pevzner, R. Plumb, C.S. Pohl, A. Poliakov, T.C. Ponce, C.P. Ponting, S. Potter, M. Quail, A. Reymond, B.A. Roe, K.M. Roskin, E.M. Rubin, A.G. Rust, R. Santos, V. Sapojnikov, B. Schultz, J. Schultz, M.S. Schwartz, S. Schwartz, C. Scott, S. Seaman, S. Searle, T. Sharpe, A. Sheridan, R. Shownkeen, S. Sims, J.B. Singer, G. Slater, A. Smit, D.R. Smith, B. Spencer, A. Stabenau, N. Stange-Thomann, C. Sugnet, M. Suyama, G. Tesler, J. Thompson, D. Torrents, E. Trevaskis, J. Tromp, C. Ucla, A. Ureta-Vidal, J.P. Vinson, A.C. Von Niederhausern, C.M. Wade, M. Wall, R.J. Weber, R.B. Weiss, M.C. Wendl, A.P. West, K. Wetterstrand, R. Wheeler, S. Whelan, J. Wierzbowski, D. Willey, S. Williams, R.K. Wilson, E. Winter, K.C. Worley, D. Wyman, S. Yang, S.P. Yang, E.M. Zdobnov, M.C. Zody, E.S. Lander, Initial sequencing and comparative analysis of the mouse genome, Nature 420 (2002) 520–562.

[3] J.L. Bennetzen, Transposable element contributions to plant gene and genome evolution, Plant Mol. Biol. 42 (2000) 251–269.

[4] P.L. Deininger, A.M. Roy-Engel, Mobile elements in animal and plant genomes, in: N.L. Craig, R. Craigie, M. Gellert, A.M. Lambowitz (Eds.), Mobile DNA II, ASM Press, Washington, DC, 2002.

[5] M. Labrador, V.G. Corces, Interactions between transposable elements and the host genome, in: N.L. Craig, R. Craigie, M. Gellert, A.M. Lambowitz (Eds.), Mobile DNA II, ASM Press, Washington, DC, 2002.

[6] D. Nouaud, H. Quesneville, D. Anxolabehere, Recurrent exon shuffling between distant P-element families, Mol. Biol. Evol. 20 (2003) 190–199.

[7] H.K. Hamdi, H. Nishio, J. Tavis, R. Zielinski, A. Dugaiczyk, Alu-mediated phylogenetic novelties in gene regulation and development, J. Mol. Biol. 299 (2000) 931–939.

[8] F. Vidal, E. Mougneau, N. Glaichenhaus, P. Vaigot, M. Darmon, F. Cuzin, Coordinated posttranscriptional control of gene expression by modular elements including Alu-like repetitive sequences, Proc. Natl. Acad. Sci. U.S.A. 90 (1993) 208–212.

[9] P.L. Deininger, M.A. Batzer, *Alu* repeats and human disease, Mol. Genet. Metab. 67 (1999) 183–193.

[10] P.L. Deininger, M.A. Batzer, Evolution of retroposons, Evol. Biol. 27 (1993) 157–196.

[11] H.H. Kazazian Jr., Mobile elements: drivers of genome evolution, Science 303 (2004) 1626–1632.

[12] E.M. Ostertag, J.L. Goodier, Y. Zhang, H.H. Kazazian Jr., SVA elements are nonautonomous retrotransposons that cause disease in humans, Am. J. Hum. Genet. 73 (2003) 1444–1451.

[13] C. Baust, G.J. Baillie, D.L. Mager, Insertional polymorphisms of ETn retrotransposons include a disruption of the wiz gene in C57BL/6 mice, Mammal. Genome 13 (2002) 423–428.

[14] M.A. Batzer, P.L. Deininger, *Alu* repeats and human genomic diversity, Nat. Rev. Genet. 3 (2002) 370–379.

[15] M.G. Kidwell, D.R. Lisch, Perspective: transposable elements, parasitic DNA, and genome evolution, Evolution 55 (2001) 1–24.

[16] B. Brouha, J. Schustak, R.M. Badge, S. Lutz-Prigge, A.H. Farley, J.V. Moran, H.H. Kazazian Jr., Hot L1s account for the bulk of retrotransposition in the human population, Proc. Natl. Acad. Sci. U.S.A. 100 (2003) 5280–5285.

[17] N. Gilbert, S. Lutz-Prigge, J.V. Moran, Genomic deletions created upon LINE-1 retrotransposition, Cell 110 (2002) 315–325.

[18] D.E. Symer, C. Connelly, S.T. Szak, E.M. Caputo, G.J. Cost, G. Parmigiani, J.D. Boeke, Human 11 retrotransposition is associated with genetic instability in vivo, Cell 110 (2002) 327–338.

[19] P.A. Callinan, J. Wang, S.W. Herke, R.K. Garber, P. Liang, M.A. Batzer, Alu retrotransposition-mediated deletion, J. Mol. Biol. 348 (2005) 791–800.

[20] K. Han, S.K. Sen, J. Wang, P.A. Callinan, J. Lee, R. Cordaux, P. Liang, M.A. Batzer, Genomic rearrangements by LINE-1 insertion-mediated deletion in the human and chimpanzee lineages, Nucleic Acids Res. 33 (2005) 4040–4052.

[21] O.K. Pickeral, W. Makalowski, M.S. Boguski, J.D. Boeke, Frequent human genomic DNA transduction driven by LINE-1 retrotransposition, Genome Res. 10 (2000) 411–415.

[22] J.L. Goodier, E.M. Ostertag, H.H. Kazazian Jr., Transduction of 3′-flanking sequences is common in L1 retrotransposition, Hum. Mol. Genet. 9 (2000) 653–657.

[23] N. Jiang, Z. Bao, X. Zhang, S.R. Eddy, S.R. Wessler, Pack-MULE transposable elements mediate gene evolution in plants, Nature 431 (2004) 569–573.

[24] J. Xing, H. Wang, V.P. Belancio, R. Cordaux, P.L. Deininger, M.A. Batzer, Emergence of new primate genes by retrotransposon-mediated transduction, Proc. Natl. Acad. Sci. U.S.A. 103 (2006) 17608–17613.

[25] D. Gebow, N. Miselis, H.L. Liber, Homologous and nonhomologous recombination resulting in deletion: effects of p53 status, microhomology, and repetitive DNA length and orientation, Mol. Cell. Biol. 20 (2000) 4028–4035.

[26] S.K. Sen, K. Han, J. Wang, J. Lee, H. Wang, P.A. Callinan, M. Dyer, R. Cordaux, P. Liang, M.A. Batzer, Human genomic deletions mediated by recombination between Alu elements, Am. J. Hum. Genet. 79 (2006) 41–53.

[27] J.A. Bailey, G. Liu, E.E. Eichler, An Alu transposition model for the origin and expansion of human segmental duplications, Am. J. Hum. Genet. 73 (2003) 823–834.

[28] A.M. Roy-Engel, M.L. Carroll, M. El-Sawy, A.H. Salem, R.K. Garber, S.V. Nguyen, P.L. Deininger, M.A. Batzer, Non-traditional *Alu* evolution and primate genomic diversity, J. Mol. Biol. 316 (2002) 1033–1040.

[29] S.E. Fischer, E. Wienholds, R.H. Plasterk, Continuous exchange of sequence information between dispersed Tc1 transposons in the *Caenorhabditis elegans* genome, Genetics 164 (2003) 127–134.

[30] D.H. Kass, M.A. Batzer, P.L. Deininger, Gene conversion as a secondary mechanism of short interspersed element (SINE) evolution, Mol. Cell. Biol. 15 (1995) 19–25.

[31] Y. Ejima, L. Yang, Trans mobilization of genomic DNA as a mechanism for retrotransposon-mediated exon shuffling, Hum. Mol. Genet. 12 (2003) 1321–1328.

[32] Y.H. Gray, It takes two transposons to tango: transposable-element-mediated chromosomal rearrangements, Trends Genet. 16 (2000) 461–468.

[33] D.E. Berg, M.M. Howe (Eds.), Mobile DNA, American Society for Microbiology, Washington, DC, 1989.

[34] D.D. Luan, M.H. Korman, J.L. Jakubczak, T.H. Eickbush, Reverse transcription of R2Bm RNA is primed by a nick at the chromosomal target site: a mechanism for non-LTR retrotransposition, Cell 72 (1993) 595–605.

[35] D.F. Voytas, J.D. Boeke, Ty1 and Ty5 of *Saccharomyces cerevisiae*, in: A.M. Lambowitz (Ed.), Mobile DNAII, American Society for Microbiology, Washington, DC, 2002, pp. 631–662.

[36] V.O. Kolosha, S.L. Martin, High-affinity, non-sequence-specific RNA binding by the open reading frame 1 (ORF1) protein from

long interspersed nuclear element 1 (LINE-1), J. Biol. Chem. 278 (2003) 8112–8117.
[37] V.O. Kolosha, S.L. Martin, In vitro properties of the first ORF protein from mouse LINE-1 support its role in ribonucleoprotein particle formation during retrotransposition, Proc. Natl. Acad. Sci. U.S.A. 94 (1997) 10155–10160.
[38] S.L. Martin, M. Cruceanu, D. Branciforte, P. Wai-Lun Li, S.C. Kwok, R.S. Hodges, M.C. Williams, LINE-1 retrotransposition requires the nucleic acid chaperone activity of the ORF1 protein, J. Mol. Biol. 348 (2005) 549–561.
[39] S.L. Martin, F.D. Bushman, Nucleic acid chaperone activity of the ORF1 protein from the mouse LINE-1 retrotransposon, Mol. Cell. Biol. 21 (2001) 467–475.
[40] Q. Feng, J.V. Moran, H.H. Kazazian Jr., J.D. Boeke, Human L1 retrotransposon encodes a conserved endonuclease required for retrotransposition, Cell 87 (1996) 905–916.
[41] M. Hattori, S. Kuhara, O. Takenaka, Y. Sakaki, L1 family of repetitive DNA sequences in primates may be derived from a sequence encoding a reverse transcriptase-related protein, Nature 321 (1986) 625–628.
[42] J.V. Moran, N. Gilbert, Mammalian LINE-1 retrotransposons and related elements, in: A.M. Lambowitz (Ed.), Mobile DNA II, American Society for Microbiology Press, Washington, DC, 2002, pp. 836–869.
[43] J. Jurka, Sequence patterns indicate an enzymatic involvement in integration of mammalian retroposons, Proc. Natl. Acad. Sci. U.S.A. 94 (1997) 1872–1877.
[44] G.J. Cost, J.D. Boeke, Targeting of human retrotransposon integration is directed by the specificity of the L1 endonuclease for regions of unusual DNA structure, Biochemistry 37 (1998) 18081–18093.
[45] B. McClintock, The Discovery and Characterization of Transposable Elements: The Collected Papers of B. McClintock, Garland, New York, 1987.
[46] M. Kajikawa, N. Okada, LINEs mobilize SINEs in the eel through a shared 3′ sequence, Cell 111 (2002) 433–444.
[47] M. Dewannieux, C. Esnault, T. Heidmann, LINE-mediated retrotransposition of marked *Alu* sequences, Nat. Genet. 35 (2003) 41–48.
[48] R. Kalendar, C.M. Vicient, O. Peleg, K. Anamthawat-Jonsson, A. Bolshoy, A.H. Schulman, Large retrotransposon derivatives: abundant, conserved but nonautonomous retroelements of barley and related genomes, Genetics 166 (2004) 1437–1450.
[49] C.P. Witte, Q.H. Le, T. Bureau, A. Kumar, Terminal-repeat retrotransposons in miniature (TRIM) are involved in restructuring plant genomes, Proc. Natl. Acad. Sci. U.S.A. 98 (2001) 13778–13783.
[50] P.L. Deininger, J.V. Moran, M.A. Batzer, H.H. Kazazian Jr., Mobile elements and mammalian genome evolution, Curr. Opin. Genet. Dev. 13 (2003) 651–658.
[51] N. Okada, SINEs, Curr. Opin. Genet. Dev. 1 (1991) 498–504.
[52] K. Ohshima, M. Hamada, Y. Terai, N. Okada, The 3′ ends of tRNA-derived short interspersed repetitive elements are derived from the 3′ ends of long interspersed repetitive elements, Mol. Cell. Biol. 16 (1996) 3756–3764.
[53] K. Ohshima, N. Okada, SINEs and LINEs: symbionts of eukaryotic genomes with a common tail, Cytogenet. Genome Res. 110 (2005) 475–490.
[54] V.V. Kapitonov, J. Jurka, ACROBAT1, a nonautonomous DNA transposon from zebrafish, Repbase Rep. 2 (2002) 1.
[55] J. Jurka, Novel families of repetitive elements from the human genome, Nucleic Acids Res. 18 (1990) 137–141.
[56] A.F. Smit, A.D. Riggs, Tiggers and DNA transposon fossils in the human genome, Proc. Natl. Acad. Sci. U.S.A. 93 (1996) 1443–1448.
[57] D.A. Ray, J. Xing, A.-H. Salem, M.A. Batzer, SINEs of a *nearly* perfect character, Syst. Biol., in press.
[58] D.A. Ray, SINEs of progress: mobile element applications to molecular ecology, Mol. Ecol., in press.
[59] K. Tajima, O. Enishi, M. Amari, M. Mitsumori, H. Kajikawa, M. Kurihara, S. Yanai, H. Matsue, H. Yasue, T. Mitsuhashi, T. Kawashima, M. Matsumoto, PCR Detection of DNAs of animal origin in feed by primers based on sequences of short and long interspersed repetitive elements, Biosci. Biotechnol. Biochem. 66 (2002) 2247–2250.
[60] J.A. Walker, D.A. Hughes, B.A. Anders, J. Shewale, S.K. Sinha, M.A. Batzer, Quantitative intra-short interspersed element PCR for species-specific DNA identification, Anal. Biochem. 316 (2003) 259–269.
[61] R.E. Streeck, A multicopy insertion sequence in the bovine genome with structural homology to the long terminal repeats of retroviruses, Nature 298 (1982) 767–769.
[62] H. Yasue, Y. Wada, A swine SINE (PRE-1 sequence) distribution in swine-related animal species and its phylogenetic analysis in swine genome, Anim. Genet. 27 (1996) 95–98.
[63] J.A. Walker, D.A. Hughes, D.J. Hedges, B.A. Anders, M.E. Laborde, J. Shewale, S.K. Sinha, M.A. Batzer, Quantitative PCR for DNA identification based on genome-specific interspersed repetitive elements, Genomics 83 (2004) 518–527.
[64] M.L. Carroll, A.M. Roy-Engel, S.V. Nguyen, A.H. Salem, E. Vogel, B. Vincent, J. Myers, Z. Ahmad, L. Nguyen, M. Sammarco, W.S. Watkins, J. Henke, W. Makalowski, L.B. Jorde, P.L. Deininger, M.A. Batzer, Large-scale analysis of the *Alu* Ya5 and Yb8 subfamilies and their contribution to human genomic diversity, J. Mol. Biol. 311 (2001) 17–40.
[65] A.B. Carter, A.H. Salem, D.J.N.K. Hedges, C.B. Kimball, J.A. Walker, W.S. Watkins, L.B. Jorde, M.A. Batzer, Genome wide analysis of the human Alu Yb lineage, Hum. Genomics 1 (2004) 167–178.
[66] A.M. Roy-Engel, M.L. Carroll, E. Vogel, R.K. Garber, S.V. Nguyen, A.H. Salem, M.A. Batzer, P.L. Deininger, *Alu* insertion polymorphisms for the study of human genomic diversity, Genetics 159 (2001) 279–290.
[67] P.A. Callinan, D.J. Hedges, A.H. Salem, J. Xing, J.A. Walker, R.K. Garber, W.S. Watkins, M.J. Bamshad, L.B. Jorde, M.A. Batzer, Comprehensive analysis of *Alu*-associated diversity on the human sex chromosomes, Gene 317 (2003) 103–110.
[68] S.S. Arcot, J.J. Fontius, P.L. Deininger, M.A. Batzer, Identification and analysis of a 'young' polymorphic *Alu* element, Biochim. Biophys. Acta 1263 (1995) 99–102.
[69] J.A. Walker, G.E. Kilroy, J. Xing, J. Shewale, S.K. Sinha, M.A. Batzer, Human DNA quantitation using *Alu* element-based polymerase chain reaction, Anal. Biochem. 315 (2003) 122–128.
[70] D.J. Hedges, J.A. Walker, P.A. Callinan, J.G. Shewale, S.K. Sinha, M.A. Batzer, Mobile element-based assay for human gender determination, Anal. Biochem. 312 (2003) 77–79.
[71] K.M. Sullivan, A. Mannucci, C.P. Kimpton, P. Gill, A rapid and quantitative DNA sex test: fluorescence-based PCR analysis of X-Y homologous gene amelogenin, Biotechniques 15 (1993) 636–638, 640–631.
[72] F.R. Santos, A. Pandya, C. Tyler-Smith, Reliability of DNA-based sex tests, Nat. Genet. 18 (1998) 103.

[73] M. Steinlechner, B. Berger, H. Niederstatter, W. Parson, Rare failures in the amelogenin sex test, Int. J. Legal Med. 116 (2002) 117–120.
[74] K. Thangaraj, A.G. Reddy, L. Singh, Is the amelogenin gene reliable for gender identification in forensic casework and prenatal diagnosis? Int. J. Legal Med. 116 (2002) 121–123.
[75] B. Brinkmann, Is the amelogenin sex test valid? Int. J. Legal Med. 116 (2002) 63.
[76] R. Chakraborty, D.N. Stivers, B. Su, Y. Zhong, B. Budowle, The utility of short tandem repeat loci beyond human identification: implications for development of new DNA typing systems, Electrophoresis 20 (1999) 1682–1696.
[77] M.E. Sifis, K. Both, L.A. Burgoyne, A more sensitive method for the quantitation of genomic DNA by *Alu* amplification, J. Forensic Sci. 47 (2002) 589–592.
[78] J.A. Nicklas, E. Buel, Development of an Alu-based QSY 7-labeled primer PCR method for quantitation of human DNA in forensic samples, J. Forensic Sci. 48 (2003) 1–10.
[79] J.A. Nicklas, E. Buel, Development of an Alu-based, real-time PCR method for quantitation of human DNA in forensic samples, J. Forensic Sci. 48 (2003) 936–944.
[80] J.A. Nicklas, E. Buel, Quantification of DNA in forensic samples, Anal. Bioanal. Chem. 376 (2003) 1160–1167.
[81] J.A. Nicklas, E. Buel, An Alu-based, MGB Eclipse real-time PCR method for quantitation of human DNA in forensic samples, J. Forensic Sci. 50 (2005) 1081–1090.
[82] M.A. Batzer, S.S. Arcot, J.W. Phinney, M. Alegria-Hartman, D.H. Kass, S.M. Milligan, C. Kimpton, P. Gill, M. Hochmeister, P.A. Ioannou, R.J. Herrera, D.A. Boudreau, W.D. Scheer, B.J. Keats, P.L. Deininger, M. Stoneking, Genetic variation of recent *Alu* insertions in human populations, J. Mol. Evol. 42 (1996) 22–29.
[83] M. Stoneking, J.J. Fontius, S.L. Clifford, H. Soodyall, S.S. Arcot, N. Saha, T. Jenkins, M.A. Tahir, P.L. Deininger, M.A. Batzer, *Alu* insertion polymorphisms and human evolution: evidence for a larger population size in Africa, Genome Res. 7 (1997) 1061–1071.
[84] C. Romualdi, D. Balding, I.S. Nasidze, G. Risch, M. Robichaux, S.T. Sherry, M. Stoneking, M.A. Batzer, G. Barbujani, Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms, Genome Res. 12 (2002) 602–612.
[85] W.S. Watkins, A.R. Rogers, C.T. Ostler, S. Wooding, M.J. Bamshad, A.M. Brassington, M.L. Carroll, S.V. Nguyen, J.A. Walker, B.V. Prasad, P.G. Reddy, P.K. Das, M.A. Batzer, L.B. Jorde, Genetic variation among world populations: inferences from 100 *Alu* insertion polymorphisms, Genome Res. 13 (2003) 1607–1618.
[86] M. Bamshad, T. Kivisild, W.S. Watkins, M.E. Dixon, C.E. Ricker, B.B. Rao, J.M. Naidu, B.V. Prasad, P.G. Reddy, A. Rasanayagam, S.S. Papiha, R. Villems, A.J. Redd, M.F. Hammer, S.V. Nguyen, M.L. Carroll, M.A. Batzer, L.B. Jorde, Genetic evidence on the origins of Indian caste populations, Genome Res. 11 (2001) 994–1004.
[87] M.J. Bamshad, S. Wooding, W.S. Watkins, C.T. Ostler, M.A. Batzer, L.B. Jorde, Human population genetic structure and inference of group membership, Am. J. Hum. Genet. 72 (2003) 578–589.
[88] M. Barbalic, M. Pericic, T. Skaric-Juric, N.S. Narancic, Ace Alu insertion polymorphism in Croatia and its isolates, Collegium Antropol. 28 (2004) 603–610.
[89] K. Bulayeva, L.B. Jorde, C. Ostler, S. Watkins, O. Bulayev, H. Harpending, Genetics and population history of Caucasus populations, Hum. Biol. 75 (2003) 837–853.
[90] D. Comas, F. Calafell, N. Benchemsi, A. Helal, G. Lefranc, M. Stoneking, M.A. Batzer, J. Bertranpetit, A. Sajantila, Alu insertion polymorphisms in NW Africa and the Iberian Peninsula: evidence for a strong genetic boundary through the Gibraltar Straits, Hum. Genet. 107 (2000) 312–319.
[91] D. Comas, H. Schmid, S. Braeuer, C. Flaiz, A. Busquets, F. Calafell, J. Bertranpetit, H.G. Scheil, W. Huckenbeck, L. Efremovska, H. Schmidt, Alu insertion polymorphisms in the Balkans and the origins of the Aromuns, Ann. Hum. Genet. 68 (2004) 120–127.
[92] N.H. Cotrim, M.T. Auricchio, J.P. Vicente, P.A. Otto, R.C. Mingroni-Netto, Polymorphic Alu insertions in six Brazilian African-derived populations, Am. J. Hum. Genet. 16 (2004) 264–277.
[93] C.L. Dornelles, J. Battilana, N.J. Fagundes, L.B. Freitas, S.L. Bonatto, F.M. Salzano, Mitochondrial DNA and Alu insertions in a genetically peculiar population: the Ayoreo Indians of Bolivia and Paraguay, Am. J. Hum. Biol. 16 (2004) 479–488.
[94] D.S. Dunn, A.V. Romphruk, C. Leelayuwat, M. Bellgard, J.K. Kulski, Polymorphic Alu insertions and their associations with MHC class I alleles and haplotypes in the northeastern Thais, Ann. Hum. Genet. 69 (2005) 364–372.
[95] E. Gonzalez-Perez, M. Via, E. Esteban, A. Lopez-Alomar, S. Mazieres, N. Harich, M. Kandil, J.M. Dugoujon, P. Moral, Alu insertions in the Iberian Peninsula and north west Africa-genetic boundaries or melting pot? Collegium Antropol. 27 (2003) 491–500.
[96] N. Maca-Meyer, J. Villar, L. Perez-Mendez, A. Cabrera de Leon, C. Flores, A tale of aborigines, conquerors and slaves: Alu insertion polymorphisms and the peopling of Canary Islands, Ann. Hum. Genet. 68 (2004) 600–605.
[97] P.P. Majumder, B. Roy, S. Banerjee, M. Chakraborty, B. Dey, N. Mukherjee, M. Roy, P.G. Thakurta, S.K. Sil, Human-specific insertion/deletion polymorphisms in Indian populations and their possible evolutionary implications, Eur. J. Hum. Genet. 7 (1999) 435–446.
[98] A. Mansoor, K. Mazhar, S. Khaliq, A. Hameed, S. Rehman, S. Siddiqi, M. Papaioannou, L.L. Cavalli-Sforza, S.Q. Mehdi, Q. Ayub, Investigation of the Greek ancestry of populations from northern Pakistan, Hum. Genet. 114 (2004) 484–490.
[99] S. Mastana, D. Lee, P.P. Singh, M. Singh, Molecular genetic variation in the East Midlands, England: analysis of VNTR, STR and Alu insertion/deletion polymorphisms, Ann. Hum. Biol. 30 (2003) 538–550.
[100] I. Nasidze, G.M. Risch, M. Robichaux, S.T. Sherry, M.A. Batzer, M. Stoneking, *Alu* insertion polymorphisms and the genetic structure of human populations from the Caucasus, Eur. J. Hum. Genet. 9 (2001) 267–272.
[101] G.E. Novick, C.C. Novick, J. Yunis, E. Yunis, P. Antunez de Mayolo, W.D. Scheer, P.L. Deininger, M. Stoneking, D.S. York, M.A. Batzer, R.J. Herrera, Polymorphic Alu insertions and the Asian origin of Native American populations, Hum. Biol. 70 (1998) 23–39.
[102] H. Vishwanathan, D. Edwin, M.V. Usharani, P.P. Majumder, Insertion/deletion polymorphisms in tribal populations of southern India and their possible evolutionary implications, Hum. Biol. 75 (2003) 873–887.
[103] F.X. Xiao, J.F. Yang, J.J. Cassiman, R. Decorte, Diversity at eight polymorphic Alu insertion loci in Chinese populations

shows evidence for European admixture in an ethnic minority population from northwest China, Hum. Biol. 74 (2002) 555–568.
[104] B.J. Vincent, J.S. Myers, H.J. Ho, G.E. Kilroy, J.A. Walker, W.S. Watkins, L.B. Jorde, M.A. Batzer, Following the LINEs: an analysis of primate genomic variation at human-specific LINE-1 insertion sites, Mol. Biol. Evol. 20 (2003) 1338–1348.
[105] A.H. Salem, D.A. Ray, M.A. Batzer, Identity by descent and DNA sequence variation of human SINE and LINE elements, Cytogenet. Genome Res. 108 (2005) 63–72.
[106] M.J. Bamshad, S. Wooding, W.S. Watkins, C.T. Ostler, M.A. Batzer, L.B. Jorde, Human population genetic structure and inference of group membership, Am. J. Hum. Genet. 72 (2003) 578–589.
[107] D. Falush, M. Stephens, J.K. Pritchard, Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies, Genetics 164 (2003) 1567–1587.
[108] J.K. Pritchard, M. Stephens, P. Donnelly, Inference of population structure using multilocus genotype data, Genetics 155 (2000) 945–959.
[109] D.A. Ray, J.A. Walker, A. Hall, B. Llewellyn, J. Ballantyne, A.T. Christian, K. Turteltaub, M.A. Batzer, Inference of human geographic origins using Alu insertion polymorphisms, Forensic Sci. Int. 153 (2005) 117–124.
[110] K.J. Sorensen, K. Turteltaub, G. Vrankovich, J. Williams, A.T. Christian, Whole-genome amplification of DNA from residual cells left by incidental contact, Anal. Biochem. 324 (2004) 312–314.