The state of Illinois has a grand tradition of corrupt politicians (Re: Former governor Rod Blagojevich.)

Ex-Gov. Ryan of Illinois Reports to Prison

By CATRIN EINHORN
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CHICAGO, Nov. 7 — Former Gov. George Ryan, who drew international attention for halting the death penalty in this state, reported to a federal prison in Wisconsin on Wednesday to begin his six-and-a-half-year sentence for racketeering and fraud.

Justice John Paul Stevens of the Supreme Court on Tuesday denied Mr. Ryan’s request to remain free on bail while he continued his appeal.

Mr. Ryan, 73, told reporters that he faced prison with a clear conscience.

“I have said since the beginning of this 10-year ordeal that I am innocent,” he said. “And I intend to prove that.”

Mr. Ryan, who in 40 years in public office became one of the most powerful Republicans in the Midwest, was convicted last year of a long list of corruption charges stemming from his tenure as secretary of state and governor of Illinois, including using public money for campaign work and exchanging state business for money and gifts, among them an island vacation.

Outside Illinois, he was better known for his moratorium on the death penalty and commuting more than 160 death sentences to life in prison just before leaving office after one term, in 2003. To some, Mr. Ryan’s prison term should be cautionary in a state where making deals and giving favors have long been viewed as politics as usual. He is the third former Illinois governor convicted of wrongdoing.
Justice for Death Row

Published: Thursday, November 21, 2002

Gov. George Ryan of Illinois, whose state has a bad record of sentencing innocent people to death, declared a moratorium on executions a few years back. Now, in his final months in office, he is considering commuting the sentences of everyone on death row. His willingness to do so may have been tested last month, by televised hearings that underscored the horror of the crimes for which these inmates were sentenced. But despite the bad publicity, Governor Ryan should do the right thing, and commute all the sentences to life in prison.

Illinois has been at the center of the death penalty debate since it was revealed, through DNA evidence, that 13 of the people sent to its death row since capital punishment was restored in 1977 had been wrongly convicted. That's more than the 12 people who were actually executed. The co-chairman of a blue-ribbon commission appointed to study the system noted that it was unlikely that any doctor "could get it wrong over 50 percent of the time and still stay in business." In one case, a convicted murderer who had spent 16 years on death row was exonerated just two days before his scheduled execution.

The investigations into the Illinois exonerations have made it clear how a person who is innocent of a capital crime could nevertheless wind up on death row. Witnesses, from jailhouse snitches to police officers, have testified falsely. Prosecutors, whether out of incompetence or bad motives, have ignored evidence that they were trying the wrong person. Lawyers assigned to represent capital defendants were often not qualified, or failed to conduct investigations that could have cleared their clients.

Governor Ryan, a conservative Republican who voted for the death penalty as a legislator, has said repeatedly that he is considering a blanket commutation, which would reduce death sentences to life in prison. But last month's hearings, which received wide attention across the state, appear to have slowed the momentum. The testimony, much of it from
Innocence Project

http://www.innocenceproject.org/know/

• To date, there have been over 250 post-conviction DNA exonerations in the United States.
• And in almost 40 percent of the cases profiled on the Innocence Project site (link above), the actual perpetrator has been identified by DNA testing.

After serving 14 years in prison, a DNA fingerprinting test showed that Thomas Webb had been wrongly convicted of rape.
What is so compelling about the science underlying DNA fingerprinting that it can be used to overturn a conviction of an individual? Or to unequivocally convict an individual of a serious crime?

To address this question, we need to consider

• the structure of our genome
• how to use PCR to genotype highly polymorphic sites
• basic issues in population genetics

Good web sites on DNA forensics
http://www.dnai.org/d/
Chromosome 11 “Flyover”

http://www.dnalc.org/ddnalc/resources/chr11.html
The human genome provides a rich source of genetic variability especially in non-coding regions

*(See also last page of these notes)*

**Single nucleotide polymorphisms (SNP’s)**
Frequency in genome: \( \sim 1/1250 \) base pairs
Number per genome: \( \sim 2-3 \) million
Mutation rate per site per gamete: \( 1 \times 10^{-9} \)

*Compare to Gene mutation rate: \( 10^{-4} - 10^{-5} \) per gene per gamete*

98% of genetic diversity is in this category [but SNP’s have fewer possible alleles than micro and mini satellites]

**Microsatellites aka STR (simple tandem repeats)**
repeat unit: typically 2-5 bp (up to 10 bps)
up to \(~25\) tandem repeats
Mutation rate per site per gamete: \( 1 \times 10^{-3} \)

Also called: *Simple Sequence Repeats* or *Simple Tandem Repeats*  
*Nature 409: 888 2/15/01*

**Minisatellites aka VNTR = variable number of tandem repeats**
repeat unit: 10-100 bp in length
up to about 50 tandem repeats
Mutation rate per site per gamete: \( 1 \times 10^{-3} \)
An example of a microsatellite or STR polymorphism

* STRs are short sequences of DNA, normally of length 2-5 base pairs, that are repeated numerous times in a head-tail manner.

* The 16 bp sequence of "gatagatagatagata" would represent 4 head-tail copies of the tetramer "gata".

* Example: D7S280

    1 aatattttgta ttttttttag agacggggtt tcaccatgtt ggtcaggctg actatggagt
    61 tatatttaagg ttaatatata taaaggttat gatagaacac ttgctatagt ttagaaccgaa
   121 ctaacgtag atagatagat agatagatag atagatagat agatagatag atagacagat
   181 tgatagtttt ttttatctc actaaatagt ctatagtaaa catttaatta ccaatatattg
   241 gtgcaattct gtcaatgagg ataatgtgg aatcgttata attcttaaga atatatatttc
   301 cctctgagtt tttgatacct cagatttttaa ggcc

* The polymorphisms in STRs are due to the different number of copies of the repeat element that can occur in a population of individuals.
Polymorphisms in mini and microsatellites are used for DNA profiles
• easy to assay using PCR
• highly polymorphic*
• under no obvious selection pressure -- “anonymous site”
• codominant Mendelian alleles

Estimated mutation rate at a given mini/microsatellite site is $1 \times 10^{-3}$ per gamete
• This means ~1 change in a given site in every 1000 gametes
• Results in lots of variation between unrelated individuals in a population
• But mutation rate is low enough that within a family allele changes do not occur readily
• Why are micro-satellite regions so mutable? What mechanisms of mutation could explain this?

The D1S80 repeat unit is 16 base pairs (bp) in length and there are dozens of known alleles.

<table>
<thead>
<tr>
<th>ALLELE* (no. of core units)</th>
<th>FREQUENCY IN</th>
<th>Unrelated Finns (n = 140)</th>
<th>U.S. Caucasian (n = 94)</th>
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<tbody>
<tr>
<td>1 (18)</td>
<td></td>
<td>.307</td>
<td>.293</td>
</tr>
<tr>
<td>2 (19)</td>
<td></td>
<td>.011</td>
<td>.011</td>
</tr>
<tr>
<td>3 (20)</td>
<td></td>
<td>.032</td>
<td>.021</td>
</tr>
<tr>
<td>4 (21)</td>
<td></td>
<td>.018</td>
<td>.032</td>
</tr>
<tr>
<td>5 (22)</td>
<td></td>
<td>.014</td>
<td>.043</td>
</tr>
<tr>
<td>6 (23)</td>
<td></td>
<td>.014</td>
<td>.016</td>
</tr>
<tr>
<td>7 (24)</td>
<td></td>
<td>.311</td>
<td>.335</td>
</tr>
<tr>
<td>8 (25)</td>
<td></td>
<td>.075</td>
<td>.037</td>
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<tr>
<td>9 (26)</td>
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<td>.011</td>
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<td>10 (27)</td>
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<td>.007</td>
<td>.000</td>
</tr>
<tr>
<td>11 (28)</td>
<td></td>
<td>.068</td>
<td>.059</td>
</tr>
<tr>
<td>12 (29)</td>
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<td>20 (37)</td>
<td></td>
<td>.007</td>
<td>.000</td>
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</tbody>
</table>

* Nomenclature is that of Budowle et al. (1991).
Using PCR to determine the genotype at the D1S80 STR locus

The D1S80 repeat unit is 16 base pairs (bp) in length and there are dozens of known alleles ranging from approximately 350 to 1,000 bp.

Alleles are distinguished by the size of PCR products generated with primers that match unique (single-copy) sequences that flank the repeat units.
STR typically loci used for DNA profiling

FBI CODIS = Combined DNA Index System
http://www.fbi.gov/hq/lab/html/codis1.htm
http://www.cstl.nist.gov/biotech/strbase/str_fact.htm

Typically 13 core CODIS loci plus Amelogenin to determine sex of individual

13 CODIS Core STR Loci with Chromosomal Positions
automated capillary electrophoresis
How are DNA profiles produced, analysed and displayed?

Three different sites are examined simultaneously in one PCR reaction. By carefully adjusting the positions of the primers relative to the repeat sequence, amplification products from different sites will not overlap during gel electrophoresis.

Three or four different polymorphisms are labeled with each of four fluorescent dyes.


http://www.dnai.org/d/

Black in display below
**Multiplex STR (simple tandem repeat) profile including X and Y specific products as analyzed by capillary gel electrophoresis**

- Multiplex means that a single PCR reaction is performed with more than one set of primers -- 11 primer pairs in this case.
- Numbers below STR peaks indicate allele sizes in repeat units.
- The primer pairs are tagged with one of three fluorescent dyes -- yellow, blue or green.
- The STR profile is displayed in the green, blue and yellow channels of a four-color fluorescent system with the red channel being used for size markers (not shown).
- Amelogenin is found on both the X & the Y chromosomes. But, the Y linked copy results in a
- Standard number of PCR cycles used is 28.
- 34 cycles are used when little DNA is available: typically <100 pg or < 17 diploid genomes!
- Note, a different primer/dye mixture was used for this profile.
DNA fingerprint (or profile): the multi-locus* pattern produced by the detection of genotype at a group of unlinked, highly polymorphic loci

Comparing two DNA fingerprints to determine if they represent the same person:

**Exclusion:** if the patterns do not match at every micro/minisatellite locus tested, then the DNA must have come from different individuals

**Inclusion:** if the pattern of bands match at every locus, then the DNA may have come from the same source
**Exclusion:** if the patterns do not match at every micro/minisatellite locus tested, then the DNA must have come from different individuals

http://www.dnai.org/d/

*click on Innocence project*

<table>
<thead>
<tr>
<th>Sample</th>
<th>Sex</th>
<th>D8S1179</th>
<th>D21S11</th>
<th>D18S51</th>
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<tr>
<td>Anderson</td>
<td>XY</td>
<td>13, 16</td>
<td>28, 30</td>
<td>14, 15</td>
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<tr>
<td>Crime Scene</td>
<td>XY</td>
<td>13, 14</td>
<td>30</td>
<td>14, 15</td>
</tr>
</tbody>
</table>
**Inclusion:** if the pattern of bands match at every locus, then the DNA *may* have come from the same source.

Are the data sufficient to conclude identity between the suspect and the forensic sample?

If matches appear in multiple tests*, a statistical conclusion can be reached by calculating the *probability of a chance match.*

See web site for info on sample calculations

Short tandem repeats are thought to be particularly prone to slipped strand mispairing, i.e. mispairing of the complementary DNA strands of a single DNA double helix. The examples show how slipped strand mispairing can occur during replication, with the lower strand representing a parental DNA strand and the upper blue strand representing the newly synthesized complementary strand. In such cases, slippage involves a region of nonpairing (shown as a bubble) containing one or more repeats of the newly synthesized strand (backward slippage) or of the parental strand (forward slippage), causing, respectively, an insertion or a deletion on the newly synthesized strand.
HVS, hypervariable site; Mb = megabase; mtDNA, mitochondrial DNA; SGM, second generation multiplex; STR, short tandem repeat.

Figure 1 | Sources of human genetic variation used in forensic analysis. Further details of the properties of different loci can be found in the text.

Heteroplasmy describes the presence of two or more different mitochondrial DNA sequences in the same cell, or individual. FBI CODIS, US Federal Bureau of Investigation Combined DNA Index System;