161b The Intellectual Property Landscape of the Human Genome

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During the the past decade, the development of a handful of technologies --- mainly EST sequencing, DNA microarrays, and high-throughput sequencing --- drastically increased the pace of gene discovery. The ensuing patenting of genes is often compared to a gold rush: a genomic "land grab". Critics argue that these gene patents will stifle downstream innovation and slow the development of new medicines, producing a genomic anti-commons effect. Supporters of gene patents argue that strong intellectual property protection is crucial to downstream investment. However, both sides of this debate seem to draw from evidence that is largely anecdotal and non-quantitative. A comprehensive review of the literature reveals that, despite the public accessibility of both U.S. patents and the human genome, no study has analyzed patenting trends in the human genome. Here we will present a quantitative mapping of the intellectual property landscape of the human genome. We will answer a number of basic questions such as, What fraction of human genes are patented? What type of genes are patented? and Which institutions own the most gene patents? This work, we hope, will enable empirical studies on the effects of human gene patents, leading to informed policy decisions based on quantitative data.