

EDITORIAL

How hemp got high

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If *Genome Biology* had been launched today, instead of 11 years ago, it might well have been given the alternative title of “*Transcriptome Biology*”.

While *Genome Biology* captured the millennial zeitgeist of genomics brought about by the project(s) to sequence the human genome, the breathtaking progress of this field in the intervening decade has brought us to a new frontier: the transcriptome.

The development of RNA-seq, which applies high-throughput next-generation sequencing technology to cDNA generated from RNA samples, has resulted in an explosion of transcriptome sequences. Not only does RNA-seq benefit from higher sensitivity than microarrays, it also does not require the *a priori* knowledge needed for constructing chips; this flexibility has infused the transcriptome explosion with a biologically diverse character and encompassed many species not well covered by commercially available microarrays.

Species such as *Cannabis sativa*, a plant with a ‘split personality’, whose Dr Jekyll, hemp, is an innocent source of textiles, but whose Mr Hyde, marijuana, is chiefly used to alter the mind. Until now, *Cannabis sativa* was not one of the many species whose genome had been published during *Genome Biology*’s lifetime. In common with many plants, genome assembly of cannabis DNA sequence is technically challenging, and so the publication of a 534 Mbp [1] draft genome in this month’s issue is in itself a landmark achievement.

However, a comparison of the draft genome, which is that of the Purple Kush marijuana strain, with genes in the cannabinoid biosynthetic pathway in hemp strains did not point to any variants likely to result in a functional difference in the production of THCA - the chemical underlying marijuana’s psychoactivity. But, as with *Genome Biology*’s recent article on the kangaroo [2], a fruitful decision was made to analyze cannabis’s transcriptome while completing its genome project.

Gene expression levels observed in the plant’s flower made the likely reason for phenotypic differences between hemp and marijuana strikingly apparent. While transcripts for the THCA synthase enzyme were abundant in marijuana, they were barely detectable in hemp. Similarly, an enzyme that removes a precursor from the THCA synthesis pathway was highly expressed in hemp but not detectable in marijuana.

So it seems that the transcriptome is how hemp got high - or maybe how marijuana came ‘down.’ Either way, it is clear that without complementing a genome with functional information, such as the transcriptome, the true meaning of a DNA sequence will largely remain unknown.

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References

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