Opinion paper

Bad Science: The instrumental data in the Floyd Landis case

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A R T I C L E   I N F O

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A B S T R A C T

Background: In 2006 Floyd Landis won the world’s most prestigious bicycle race, the Tour de France. However, not many days after the race’s conclusion it was released to the press that the Laboratoire National de Dépistage du Dopage (LNDD) had found Landis’ urine after stage 17 positive for synthetic testosterone.

Methods: This review examines the instrumental data and methodology used by LNDD in the Landis case. The conclusions reached by LNDD were based on results of 2 separate instrumental methods. Subsequent to urine extraction and possibly derivatization, samples were initially screened via gas chromatography/mass spectrometry (GC/MS) using selected ion monitoring (SIM) to measure the ratio of testosterone to epitestosterone (T/E). Final confirmation of exogenous testosterone was determined by measuring the $^{13}\text{C}/^{12}\text{C}$ stable isotope ratios in 4 metabolites of testosterone via gas chromatography combustion stable isotope ratio mass spectrometry (GC-C-IRMS).

Conclusion: T/E ratios determined by LNDD in Landis’ stage 17 urine were unreliable due to the combined factors of an unsatisfactory extraction, high GC background, failure to obtain baseline peak separation for epitestosterone, unreliable quantitation of the epitestosterone peak due to both peak overlap and because it was barely above background noise, and because only a single ion mass (432) rather than a minimum of 3 was used for SIM (in violation of both LNDD’s SOP and WADA procedures). GC-C-IRMS methodology is less well known to the analytical chemistry community, but here too the results obtained by LNDD were unreliable. GC-C-IRMS errors can be briefly summarized as uncertain peak identification, unsuitable standards, and unreliable (and possibly biased) calculation of $^{13}\text{C}/^{12}\text{C}$ ratios due to peak overlap as well as LNDD’s usage of manual peak integration rather than use of the instrument system software.

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1. Introduction

In 2006 Floyd Landis won the world’s most prestigious bicycle race, the Tour de France. However, not many days after the race’s conclusion it was leaked to the press that the Laboratoire National de Dépistage du Dopage (LNDD) had found Landis’ urine specimen obtained from Landis after stage 17 to be positive for synthetic testosterone. Landis denied doping and his strategy in fighting these charges has been to generate public support and to make all of the documentation of the LNDD tests available to the public. This information was available through his website [1]. At this website one could download files including copies of the chain of custody documents, instrumental data, and correspondence.

Landis’ defense team twice had the opportunity to present their case. First, during the week of May 14–23, 2007 before a 3-man arbitration panel of the American Arbitration Association - North American Court of Arbitration for Sport convened on the campus of Pepperdine University in Malibu, California. Panel members were selected under the American Arbitration Association’s rules from a pool of independent arbitrators of the North American Court of Arbitration for Sport residing either in Canada or the US. That panel by a margin of 2:1 ruled against Landis [2].

Landis’ last and final hearing was held in March 2008 in New York City before a 3-man panel of the Court of Arbitration for Sport (CAS). This hearing was closed to the public. At the end of June the CAS announced a unanimous finding against Landis.

The World Anti-Doping Agency (WADA) has guidelines for determining which athletes must provide urine specimens, policies to insure against specimen tampering, chain of custody protocols, and cutoff concentrations for various drugs above which they consider doping indicated. Normally an athlete’s urine specimen is split into A and B specimens. Initially only the A specimen is examined and the B specimen is reserved for any challenges. In the initial drug screen of an A specimen by gas chromatography-mass spectrometry (GC-MS), a long list of various drugs are investigated. These data from LNDD are easy to follow since they use a similar Agilent 6000 series GC with a 5000 series Mass Selective Detector found in many analytical laboratories. Also, the data printouts are in English. Since no other drugs were found in Landis’ urine, only considered will be the protocols for testing of testosterone.

Testosterone is normally produced in the body (both males and females). LNDD and other labs accredited by WADA are looking for indications that the testosterone concentration in an athlete has been augmented from sources outside the body, that is, an exogenous source.
Epitestosterone is also normally produced in both males and females. However, the biological pathway for production of testosterone is independent of that for production of epitestosterone. Therefore, should an athlete administer testosterone it will have no effect on their epitestosterone concentration. In the initial screening of A specimens for exogenous testosterone, epitestosterone is used like an internal standard. Quantitatively, the ratio of testosterone/epitestosterone (T/E) is obtained. If the T/E ratio is above a certain value (previously it was 6, but has been lowered to 4), the specimen is considered to be presumptively positive for exogenous testosterone and the analysis proceeds to the confirmatory test.

Stable isotope ratio mass spectrometry (IRMS) is considered by WADA to be the “gold standard” for the determination of exogenous testosterone. The A specimen is not initially subjected to carbon 13 stable isotope ratio testing. Only if preliminary tests produce testosterone to epitestosterone profiles above cutoff concentrations do they then proceed with IRMS.

2. Methods

2.1. Focus

The transcripts of the 2 Landis arbitration hearings involve thousands of pages of testimony. The majority of this testimony is unsupported by actual chemical data provided by LND to the Landis defense team. In an actual US court of law rather than an arbitration hearing, much of this testimony would be ruled hearsay and inadmissible. To prevent this critical review from becoming a “he said/she said” polemic, only instrumental data and instrument conditions supported by actual LND printouts are considered.

2.2. T/E ratio determination

To determine the T/E ratio in a specimen LND uses selected ion monitoring (SIM) from the GC-MS run and divides the area under the testosterone peak (computer generated) by the area under the epitestosterone peak (computer generated). To obtain reliable results by this method the peaks must be well-separated from their nearest neighbors. If peaks overlap, the computer program will take this into consideration, but assay accuracy and precision will suffer. Also, if a peak is too small from the measured area under it has high uncertainty (if the relative error in a measurement is ±1 and your measured value is “5”, there is far more relative uncertainty than if your value was “50”). Any uncertainty in the E value can greatly skew the T/E ratio. Fig. 1 is the SIM plot for the testosterone and epitestosterone peaks for one GC-MS run of Landis’s specimen (USADA page 0280 vial 5). According to LND the peak at 19.37 min is testosterone and the peak at 18.57 min is epitestosterone. The noisy chromatogram suggests a rudimentary problem with the extraction, especially when one compares the above chromatogram with those routinely produced at the University of California at Los Angeles (UCLA) and Montreal doping laboratories. In addition, in terms of both peak separation and peak size, the epitestosterone peak is clearly unsatisfactory. How can this be used to accurately determine the T/E ratio?

![Fig. 1. GC/MS single ion mass chromatogram for m/e 432.40 (432.10 to 433.10) for Landis urine sample A from stage 17. According to LND the peak at 19.37 min is testosterone and the peak at 18.57 min is epitestosterone.](image)

Additionally, WADA requires that a minimum of 3 ions be used for SIM analysis and the ions must be analyzed and evaluated, not discarded. In the Landis case, LND technicians claim they acquired 3 ions, but there is no data supporting their claim. Why is this important? A single SIM peak at the right retention time is untrustworthy as an identification of a specific compound. It’s like using a flame ionization detector on your GC, rather than an MS. You know there is a peak there at the right retention time, but you really have no information about its molecular composition. Unfortunately, by chance, some other compound could have the same retention time under those conditions. Using a single SIM peak is especially untrustworthy if you are using it as a basis for quantization (determining the T/E ratio). How do you know that some other compound also having that ion (m/z 432) isn’t co-eluting with either T or E? With 3 or more SIM ions you can look at the relative intensities of the peaks compared to your standard of T or E. If there is no co-elution the relative intensities should agree with the standard and this should be true whether you are looking towards the front, middle, or back of the peak. Also, if you display a stacked plot of the 3 or more SIM ions, they should all line up one above another if there is no co-elution of other compounds. This is especially necessary if one is dealing with a complex biological matrix such as urine. As an example, Fig. 2 is a stacked SIM plot from a case examined at the UCLA lab [3]. LND has a rate of detecting exogenous testosterone that is ~300% that of other certified WADA labs and over 6 times that of the UCLA lab. Why? Also, it seems logical that if an athlete were trying to gain an unfair advantage by taking an artificial form of testosterone, then their total testosterone concentration should be elevated. If not, how has the athlete gained an advantage? If one had knowledge of WADA guidelines and LND testing protocols he might reason that if he took a mixture of testosterone and epitestosterone he could benefit from the exogenous testosterone but it wouldn’t be detected because his T/E ratio would remain within normal ratios. However, in that case his total testosterone and epitestosterone should be elevated. LND test results show an approximate testosterone concentration for Landis of 45 ng/ml, while an average testosterone concentration is roughly 100 ng/ml and a reading of 200 ng/ml is considered elevated.

2.3. Gas chromatography combustion stable isotope ratio mass spectrometry

In sports doping investigations the basic assumption is that the range of values for the ratio of $^{13}$C/$^{12}$C for testosterone from endogenous sources will be different from that of testosterone originating from exogenous sources (outside the

![Fig. 2. A GC/MS selected ion monitoring (SIM) stacked plot of three selected fragment ions of testosterone. This is from page 37 of a positive testosterone doping report from the UCLA Olympic Analytical Laboratory (sample name: SC503 TE A Confirmation LIN) and was used by the Landis defense team at the hearing at Pepperdine [3]. The relative retention times (all three fragments ions peak at 13.44 min) are in agreement with those of the testosterone standard (shown on page 36 of the report); the relative abundances of the fragment ion peaks are in agreement with that of a testosterone standard, and all three fragment ions display symmetrical peak shapes suggesting no overlapping elution of other molecular species.](image)

| Table 1: Delta/delta$^*$ values obtained from GC-C-IRMS of Landis’ stage 17 urine. |
|----------------------------------|----------------------------------|
| Delta/delta$^*$ value            | Testosterone metabolite          |
| -2.02                            | Androsterone                     |
| -3.51                            | Androsterone                     |
| -2.65                            | 5α androstanediol                |
| -6.39                            | 5α androstanediol                |

$^*$ The delta/delta value is the difference between the C$^{13}$/C$^{12}$ delta value for a non-steroid internal standard and the value obtained for the metabolite.
CO2 is ionized. Once ionized, the singly charged ions come under the influence of the isotope ratio mass spectrometer (IRMS). There the CO2 continues on and enters the IRMS. Next, this vapor stream passes through a membrane or a cryogenic trap and the water is removed but the carbon dioxide, how does one “identify” (the original molecular composition before combustion) the different peaks? And how do you know that for a given peak you had complete baseline separation (i.e. – the peak only represents the analyte you are interested in) and there is no overlap with anything eluting slightly before or after? LNDD uses an endogenous internal standard and injects the same specimen into a GC-MS. In theory, from the MS fragmentation patterns one can identify the peak that represents the internal standard as well as the peaks representing the 4 different testosterone metabolites. LNDD knows that the absolute retention time values on the GC-MS and the GC-C-IRMS will not be identical, but they figure that they can nevertheless identify the peaks from the GC-C-IRMS if they use the endogenous internal standard to create relative retention times. However, the technicians at LNDD do not have a clear understanding of the underlying scientific requirements.

LNDD makes at least 3 errors in trying to identify the peaks in their GC-C-IRMS data.

1. Calculation and use of relative retention times. LNDD calculates the relative retention times in the GC-MS by measuring the time from sample injection into the GC-MS until peak detection. This does not take into account the inevitable dead volume in any system. One must introduce a non-retained analyte (example, butane gas) and determine the time from injection to peak detection. For this system under these conditions this time is then subtracted from the various peak retention times to get an adjusted retention time. It is the adjusted retention time for a given analyte peak that is divided by the adjusted retention time of the internal standard to give you the relative retention. Then for the GC-C-IRMS you must again introduce a non-retained analyte and determine the time from injection to peak detection. Because of the presence of additional dead volume due to the combustion furnace and the membrane filter, this value will be different from that obtained for the GC-MS even if both systems are using the same GC column and temperature program.

2. Different column stationary phases and different temperature ramps. Even if calculated correctly, relative retention times are only reliable if the system they are compared with has the same type of GC column and the same temperature program.

According to LNDD protocols, carbon stable isotope ratios are determined for 4 testosterone breakdown products. What constitutes a positive test (proof of sports doping)? LNDD considers the test is positive if any one of the ratios for the 4 metabolites is abnormal. But WADA-certified labs at UCLA and in Australia require that at least 2 metabolites be abnormal. How can these labs all be certified by WADA and yet not have the same criteria for what constitutes a positive test?

According to LNDD SOP a value of above −3.0±0.8 is considered to be beyond the range of normal values. In Table 1 are the LNDD results for the 4 testosterone metabolites from the Landis specimen.

Using the −3.0±0.8 criterion, only 1 of the 4 metabolites is beyond the normal range. Had the lab at UCLA run the IRMS tests and come up with these values a positive finding would not have been reported. When compared to LNDD’s SOP for quality control, to conclude that doping is indicated if the Δ/Δ value for any one of the 4 testosterone metabolites is outside range totally defies logic. For a blank (negative) urine sample according to LNDD quality control it is sufficient if the Δ values obtained for 3 of the 4 metabolites are within 0.8 Δ units of initial values. In essence LNDD is saying that for quality control purposes it’s okay to screw up on 1 of the 4 measured values for a blank sample, but if one of 4 values on an athlete’s sample is outside range then he is guilty!

However, there are additional factors that make the IRMS values obtained by LNDD for the 4 testosterone metabolites untrustworthy. In the IRMS test procedure, a specimen of the athlete’s urine (there may have first been some chemical processing) is injected into a capillary column GC. Ideally, the GC separates this complex mixture into individual components that elute from the GC at different retention times (time from injection to elution and detection). Pushed along by a continuous stream of helium gas, the individual components that elute from the GC at different retention times (time from injection to peak detection). Because of the additional dead volume due to the combustion furnace and the membrane filter, this value will be different from that obtained for the GC-MS even if both systems are using the same GC column and temperature program.

Since everything entering the mass spectrometer has been converted to carbon dioxide, how does one “identify” (the original molecular composition before combustion) the different peaks? And how do you know that for a given peak you had complete baseline separation (i.e. – the peak only represents the analyte you are interested in) and there is no overlap with anything eluting slightly before or after? LNDD uses an endogenous internal standard and injects the same specimen into a GC-MS. In theory, from the MS fragmentation patterns one can identify the peak that represents the internal standard as well as the peaks representing the 4 different testosterone metabolites. LNDD knows that the absolute retention time values on the GC-MS and the GC-C-IRMS will not be identical, but they figure that they can nevertheless identify the peaks from the GC-C-IRMS if they use the endogenous internal standard to create relative retention times. However, the technicians at LNDD do not have a clear understanding of the underlying scientific requirements.

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2. Different column stationary phases and different temperature ramps. Even if calculated correctly, relative retention times are only reliable if the system they are compared with has the same type of GC column and the same temperature program.

Fig. 3. GC/MS TIC for the same Landis urine fraction whose GC-C-IRMS plot is shown in Fig. 4.
For their GC-MS system LNDD uses an AGILENT 19091s-433 column. The stationary phase is 5% phenyl methyl polysiloxane and 95% methyl polysiloxane. It is considered to be a non-polar column. For the LNDD’s GC-C-IRMS system used for the Landis specimen they used a DB17-MS column that has a stationary phase of 50% phenyl methyl polysiloxane and 50% methyl polysiloxane. This column is considered to be a midpolarity column. To make a bad situation worse, in the two systems they used different temperature ramps (temperature programs). With different stationary phases and different temperature ramps it is not unusual for the order of elution of the various components of a mixture to change.

3. Calibration standard used for GC-C-IRMS lacked 3 of the 4 analytes of interest. With both systems LNDD injected a calibration standard. However, they used different calibration mixtures for the 2 systems. For the GC-MS they used “Mix Cal Acetate.” It contained endogenous internal standards and all of the targeted analytes (testosterone metabolites). However, for GC-C-IRMS they used “Mix Cal Acetate.” It contained endogenous internal standards but only one of the 4 testosterone metabolites (and it wasn’t the one that LNDD claimed exceeded the limit).

In the majority finding of the arbitration panel, to support LNDD’s IRMS analysis they say (Point 186): “The lab compares the peaks and the sequence of peaks from the GC/MS and the GC-C-IRMS to identify metabolites and the endogenous reference compounds. Specifically, to identify the substances in question, one would compare the pattern of peak heights and retention times in the GC-C-IRMS chromatograms, anchored by the internal standard with a known RT, with the pattern of peak heights and RIs in the GC/MS chromatogram obtained from the same aliquot of the sample.” In this case, it appears that the relative retention times were incorrectly used. Not only do we have different GC and different temperature ramps, but the 2 systems use entirely different technology for peak detection (detector response will not be the same for the 2 systems).

There is another aspect of IRMS that makes Landis’ stage 17 urine specimen interesting (due to the GC or LC process) from the front of your peaks of interest (internal standard and metabolites of testosterone) to their trailing edges. This slight fractionation will be maintained when the components eluting from the GC or LC are then converted into $^{13}$CO$_2$/$^{12}$CO$_2$ and water. The result is that even with perfect baseline separation of your peaks of interest the stable isotope ratio values obtained will be in error if integration errors are made in selecting the beginning and ending of the peak. Because in GC-C-IRMS the eluant from the GC must pass through transfer zones (combustion furnace and cryogenic trap) before entering the MS, there will inevitably be more peak broadening before reaching the MS detector than with GC-MS under the same conditions. In other words, if peak separation is just barely acceptable with GC-MS, it will not be acceptable for GC-C-IRMS.

Although LNDD technicians were unable to provide documentation for their GC-C-IRMS analysis, they say they had a clear understanding of GC-C-IRMS. When using SIM for determining the T/E ratio via GC-MS, those compounds whose elution overlaps with either the T or E peak will not interfere as long as their fragmentation patterns contain insignificant amounts of the chosen SIM ions. This is a major reason for using SIM to determine the T/E ratio. However, for GC-C-IRMS any carbon-containing molecules whose elution from the GC overlaps either the internal standard or any of the 4 testosterone metabolites will contribute to the IRMS results.

Fig. 3 is from USADA 0342 page 113. It is the TIC of a full scan of Landis’ specimen run on GC-MS in order to identify the IRMS analyte peaks. Compared to the single ion SIM plot used for T/E, its baseline is far less noisy and peak separation is much better.

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**Fig. 4.** GC-C-IRMS TIC for the same Landis urine fraction in Fig. 3. The peaks at each end are for the CO$_2$ calibration gas. Values above peaks are the delta values for each peak (C$^{13}$/C$^{12}$ ratio compared to a standard). The values shown in Table 1 are delta–delta values (these values subtracted from the delta value of an internal standard). Notice the difference in patterns between Figs. 3 and 4. Were the same sample fraction injected onto virtually similar capillary GC columns (same length, same diameter, and same liquid phase with same thickness) and had both the GC/MS and the GC-C-IRMS instruments used the same temperature programs you would expect the TICs from the two systems to be quite similar. Are they? What caused the sudden rise in background at about 760 s?
Most analyte peaks still do not have baseline separation, but that is not the point. Because LNDD used a different temperature ramp and a column with a different stationary phase, this TIC is unsuitable for identifying either the peaks in the GC-C-IRMS of the same sample or even for determining if there is adequate peak separation for the IRMS results to be trustworthy.

For example, Fig. 4 is one of the IRMS mass chromatograms obtained for Landis’ specimen. Bear in mind that all of the peaks represent the detection of just carbon dioxide. The 3 peaks at either end are from the injection of CO₂ calibrant gas and in between is the sample mass chromatogram. The numbers by each peak are the [¹³C/¹²C] values obtained for each peak. Obtaining these values is more complicated than just selecting an integration starting point for the front of the peak and an integration ending point for the tail of the peak. Since the [¹³C/¹²C] values gradually change from the front to the tail of each peak (due to the fractionation that occurred as those molecules passed down the GC column), the peak integration must include both the isotope ratio at each integration point under the peak and multiply that by the amplitude of the peak at that point. Rather than use the software for peak integration (including selection of peak starting and ending points) provided with the IRMS instrument system (a method that would be free of operator bias), LNDD technicians elected to integrate the peaks of interest manually. Note the sudden rise in background at a retention time around 760 s. Although there is no annotation, it would appear that at this point the sensitivity (y axis scale) was greatly increased, and without that change the signal between 800 and 2000 s would have been buried in background noise. Not only is the background high, but for most of the peaks of interest there is no baseline separation. By contrast, in Fig. 5 notice the dramatic improvement when LNDD injected a calibration standard (USADA 0361 page 132).

How important is this? Until recently, Don Caitlin was head of the WADA-certified UCLA Olympic Analytical Laboratory in Los Angeles. In a paper he co-authored it stated: “The quality of GC-C-IRMS measurements depends first on chromatographic peak purity.” [4] Under LNDD’s policy, an error in the calculation of the [¹³C/¹²C] ratio for just 1 of the 4 testosterone metabolites could lead to a false guilty finding. If the chromatography of Landis’ stage 17 urine specimen was unacceptable for obtaining a reliable T/E ratio via GC-MS, it would be even more unacceptable for GC-C-IRMS.

Linearity is a test of the instrument’s response as the total amount of an individual component changes. Although precision may suffer as lesser amounts of a specific molecule are introduced into the IRMS, the [¹³C/¹²C] ratio determined for that molecule should not appreciably change. Simon Davis, PhD, helped write the operational manual for the IsoPrime®-1, the GC-C-IRMS system used by LNDD. As a member of the Landis defense team, Davis was present when the Landis B sample was examined at LNDD. Davis was surprised that the LNDD SOP only required that linearity checks be run on a monthly basis. That the instrument used OS2 software dating back to 1987 was also surprising. When queried at the first arbitration hearing, an LNDD technician explained that the IRMS peaks were integrated manually because the instrument software was unreliable. “Manual integration is biased” observed Russell Grant in his plenary presentation, “Mass Spectrometry in Clinical Diagnostics – David versus Goliath”, at MSACL ’08 on Monday, 03 Nov. 2008. Oh, but WADA rules and the LNDD SOP insures the anonymity to the analyst of the urine samples being examined. Not necessarily. Because Landis had a severely arthritic hip (he had hip replacement surgery shortly after the completion of the race), he was authorized to take cortisone. Prior to stage 17 Landis was required to provide a urine specimen after stages 9, 11, 12, and 15, and each time GC/MS would have shown the mass spectrum for cortisone. And of course, when LNDD examined the Landis B specimen they obviously knew it was from Landis.

Wolfram Meier-Augenstein, PhD, is one of the world’s foremost authorities on IRMS. He is a Senior Lecturer at Queens University in Belfast. The research lab that he runs has roughly 14–15 IRMS instruments (quite possibly the most of any lab in the world). He has authored an excellent review, “Applied gas chromatography coupled to isotope ratio mass spectrometry” [5].

Meier-Augenstein’s testimony left no doubt that in his opinion LNDD results for IRMS on the Landis specimen was untrustworthy. One of his responses on direct was especially telling:

A. Even cheaters have the right to a fair hearing and to have data used against them that are sound and can be proven. Here we don’t even know what these peaks are. I just have to go back to the point I made earlier. I actually don’t know what these peaks are. I refer to them under the names as identified by the lab. But, given the discrepancies in the relative retention times, I – – – –

The author has over thirty-five years experience in forensic science. In this time period he has seen the advent of The American Society of Crime Laboratory Directors [6]. ASCLD is the sponsor of a system for crime laboratory inspection and accreditation [7]. There can be no doubt that laboratory accreditation has significantly improved the quality of service provided by crime labs. However, one area of concern is the tendency to unthinkingly apply validated protocols to an examination of evidence without using critical thinking to consider the special circumstances involved [8].

Fig. 5. GC-C-IRMS TIC for the Mix Cal Acetate standard. Notice that there is no sudden rise in background around 760 s, and the far better peak shape and peak separation compared to Fig. 4. However, the Mix Cal Acetate standard contains only one of the four testosterone metabolites and it’s not the one (5α-androstenediol) that LNDD claimed was outside of range.
Had the LNDD technicians instead used critical thinking, they would have realized that not only was the specimen too degraded, the GC baseline far too noisy, and peak size and separation unacceptable to provide a reliable T/E ratio, they would have realized that these same problems could only exacerbate any attempt at IRMS.

While the purpose of this article is to raise the scientific community’s awareness of the complex analytical issues related to the Tour de France anti-doping measures and their case against Floyd Landis, it is hoped that the community of analytical chemists and toxicologists use this situation to examine the current WADA practices. Many resources were spent (and wasted) to prosecute and defend this case.

Acknowledgements

Without the instrumental data provide by LNDD to the Landis defense team and posted on the Floyd Landis webpage, this article would not have been possible. Much additional background was obtained from an exchange of e-mails with Arnie Baker, MD, as well as from his webpage, Trust But Verify http://trustbut.blogspot.com/index.html?com.

For those desiring a more in-depth examination of this case, Dr. Baker has published a book, The Wiki Defense, which is available for free at: http://arniebakercycling.com/books/wiki.htm.

The author obtained additional information from Bruce A. Goldberger, Ph.D., who testified on behalf of Landis at both hearings. I am also indebted to Wolfram Meier-Augenstein, Ph.D., for information regarding the capillary GC columns used in the GC/MS and GC-C-IRMS instruments at LNDD as well as how LNDD calculated relative retention times and the temperature programs used in the two instrument systems. And many thanks to James Ehleringer, Ph.D., Department of Biology, University of Utah, Salt Lake City, Utah, for background information on GC-C-IRMS.

References

[1] Although the Landis website, www.floydlandis.com, is no longer up, all of the original data as well as video clips from the hearing at Pepperdine University may be found at: http://www.archive.org/search.php?query=floyd%20landis [Accessed 24 Nov. 2008].


[3] To find the SIM plot used in Fig. 2 go to: http://www.archive.org/details/Floyd_Landis_Case_Documents_Exhibits Then along the left side of the page you will see ‘View the book’ and in line below it a list of numerous PDF files. Select the next to the last file [PDF (216 MB)] and scroll down to page 1803 of 2114 pages. This should be page 37 of the Testosterone Confirmation Report for Sample Name: 9CS03 from the UCLA Olympic Analytical Laboratory. [Accessed 16 Jan. 2009].


Further Reading


Website of the Court of Arbitration for Sport: http://www.tas-cas.org/.

The announcement of the CAS findings in the Landis hearing is at: http://www.tas-cas.org/dzw/files/document/1418/5048/0/Award%20Final%20Landis%202008.06.30.pdf.

http://blog.environmentalchemistry.com/ Scroll down and look at the listings along the right until you see: Floyd Landis: Prosecuted on Bad Science. Below are several hypertext links to related articles. [Accessed 16 Jan. 2009].

Berry Dr. The science of doping, Nature 2008; 454:692–693.