RESEARCH ARTICLE

Effects of Resveratrol and SIRT1 on PGC-1a Activity and M Biogenesis: A Reevaluation

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Data need to be verified before the bold conclusions of this study can be trusted

Posted by PaulBrookes on **18 Jul 2013** at **17:02 GMT**

I was directed to this study from a NY Times article about "exercise in a pill". Clearly given this degree of news coverage, the work is important. Unfortunately, the standards of data presentation in the paper leave much to be desired. Please consider the following observations...

Fig. 1A, LCAD panel, lanes 2-4, appear identical to Fig. 1B LCAD panel lanes 1-3. Slightly rotated and with different exposure. This is despite thes samples allegedly originating from different experimental treatments. Lots of shared features including the shapes and relative orientations of the bands, and the "kink" in the right most band, the relative shapes and orientations of the bands, and the "streak" emitting from the top right corner o the 3rd band.

Fig. 1A, PGC-1a panel (top one) appears identical to the PGC1a panel in Fig. 1B. They are simply different exposures of the same image, despite allegedly originating from different experimental treatments. Lots of shared features including the white spot in the lower part of the right-most band

The same appears true for the "SUO" blot (3rd from the top) - some "noise" spots added in panel A, but there's no doubt these are the same bands

Fig. 4A (and elsewhere), some blots are used as loading controls for other blots, but cannot possibly have originated from the same gels, because some panels are spliced (as indicated by lines), and others are not. Sometimes it is permissible to run your samples on separate gels at the same time, in the exact same order, and then do the phospho vs. total blots separately and re-unite the data at the end. Here we are asked to believe the gels were run separately and with the samples in different order, then some of the blots were spliced (presumably to remove unwanted samples) bu the others were not. This is not adherent to the usual standards of data presentation for this type of experiment.

Fig. 6B. The CYTO C panel appears to be simply a darker exposure of the one above it (COX IV). Lots of shared features, most notably the bubble above the right lane.

Fig. 3A, compare the band in the right lane of the cyto C panel (2nd blot from the top), with the band in the right lane of the CYTO C blot in Figure They are both of a shape that is too similar to be coincidental.

There are numerous other problems here.... the entire paper contains 85 (!!!) panels of western blotting data, every single one of which is "letter-boxed" to show only the band of interest, and none of which are annotated with molecular weight markers. In addition, despite the common origin o most of the samples, there is variability in the properties of the bands. For example in Fig. 4A, the phospho-ACC blot has 2 bands but the total ACC blot only has one band. Why? In Fig. 5B the ATPase blot has 3 bands, but only a single band in Fig. 3B. In several other cases, enhancing the contrast of the western blots reveals that adjacent bands have completely different color histograms - some are grayscale while others are color. A such, it is difficult to believe that these bands originated from the same scanned blot images (which is a prerequisite for being able to splice togeth blots).

Note... these are NOT allegations of any type of misconduct. I'm just pointing out what appears to be a very sloppy attitude toward data presentatio which seems to have resulted in a number of the "wrong" western blot images ending up in the published paper. Hey, with 85 almost identical lookin images to keep track of, there were bound to be a few that slipped through the net! I'm sure these can easily be attributed to mistakes during electronic figure preparation, and corrected in a manner that in no way affects the conclusions of the paper.

No competing interests declared.

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