Academie des Sciences

Honorary Permanent Secretary

Paris 3 May 2018 Registered

letter with AR

Dear Director General, Mr High Commissioner, Mr Director,

The CEA commissioned me, a few months ago, to chair a committee of hearing to examine five articles published by Anne Peyroche. These articles had been the subject of allegations of scientific misconduct on the Pub Peer website. The committee's mission was to analyze the reality of these allegations and to confront the main authors of the articles. The committee has met five times and has just completed its report, which is attached.

It is, however, only a stage report because it was not possible to audition Mrs. Peyroche, who is prevented for medical reasons. It goes without saying that if Madam Peyroche could be heard, the committee would receive her and could possibly amend its report.

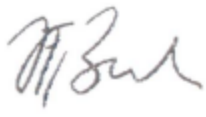
Let me mention, as usual, the volume of work done by the members of the committee: eighty hours by Valérie Lallemand and Joël Bockaert and one hundred and twenty hours by Jean-Marc Egly.

I am ready, if you wish, to meet you, possibly in the presence of some members of the committee to the extent that they can be released because two of them do not live in the Paris region.

Please believe, Sir, the High Commissioner, Mr. Director, in the assurance of my best feelings.

Jean-François Bach

Academy of Sciences - 23, quai de Conti - 75006 Paris



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PROGRESS REPORT ON FIVE ARTICLES PUBLISHED BY MRS ANNE PEYROCHE

03/05/2018

The Atomic Energy Commission (CEA) has recently been concerned about anonymous allegations, errors or misconduct appearing on the Pub Peer website concerning five articles published under the aegis of Mrs. Anne Peyroche (AP). In order to form an opinion on the reality of these allegations, the CEA commissioned two groups of experts. The first of these consisted of four senior scientists who expressed themselves through deliberately anonymous reports. In a second step, the CEA set up a hearing committee whose purpose was to study the incriminated articles in greater depth and also to give the authors of these articles the opportunity to provide all the necessary explanations and answers.

The latter committee heard the first authors and the corresponding authors of each of the five articles except, unfortunately, from PA prevented for medical reasons. The committee delayed the writing of its report by more than two months in order to give AP the opportunity to appear, but that was not enough. The committee therefore decided to submit its report in the current state of the elements that were in its possession by giving AP the opportunity to speak later, and then, of course, to amend this report.

The hearing committee set itself the task: 1) to draw up a list of questions allowing co-authors to express themselves; 2) to identify the respective responsibilities of the authors in the realization of the experiments, the writing of the articles and, especially, the assembly of the figures; 3) identify any misconduct and qualify it; 4) to identify the responsibilities in the anomalies observed. This was done by separate auditions of each author with recording of the auditions to ensure that the speech of the auditioned was not distorted.

The Hearing Panel met five times and provided a progress report on May 3, 2018.

Each of the figures studied in depth first gave rise to a discussion within the committee. In a second step, the comments resulting from this work were presented to the auditioned authors asking them their reaction but also the context in which the work corresponding to these figures had been realized: Who had carried out experiments? Who had written the report? Who had prepared the figures? To what extent did the prepared figures have been discussed and reviewed by the different members of the group? Did the authors, whether they were the first author, the corresponding author, or the author of the experiments, checked the accuracy of the published figures?

At the end of these hearings, for each of the figures, the anomaly found resulted in a classification into five categories of increasing severity. Some anomalies observed in the figures or the text of a scientific article may be due to simple errors, whether errors in the design or execution of experiments, errors in the recording of results or transcription or errors in the preparation of figures, but such errors do not represent misconduct from the point of view of ethics or ethics. They translate or may reflect a certain level of negligence or incompetence.

Scientific misconduct is very different in nature and much more serious. We chose to classify them into five levels of increasing severity.

Level 1. Embellishment is a term often used. It gathers in fact various faults and of variable gravity. It includes the addition or omission of parts of figures or the excessive choice of so-called representative figures when they are not.

Level 2. Manipulation consists of using existing data, but presenting it in such a way as to give it an appearance that it did not originally have. A typical example is to collect figure elements from different experiments that make one believe that it's the same experiment.

Levels 3 and 4. Falsification consists of modifying some results, for example by removing a band in a gel or more generally by making significant changes to the raw data. Hiding results in positive or negative way to show the presence or absence of certain biomolecules in protein fractions is also a form of forgery. We propose to differentiate level 3 falsification that does not change the interpretation of a text figure or sentence, regardless of the overall scientific message, and level 4 falsification that corresponds to falsifications that alter the interpretation of the figure or text.

Level 5. Manufacturing is the ultimate stage. It consists in creating de novo results that have not been obtained in the laboratory, whether whole experiments or parts of experiment.

In addition, it should be remembered that the committee decided not to question whether the observed misconduct changed the general scientific message provided by the articles in question. This was not the question we were asked. This would be an expertise of a different nature.

Article: J. Cell Science, 2001;

Peyroche A., Corbeyrette R., Rambourg A. Jackson C.

Title: The ARF exchange factors Geatp and Gea2p regulates the Golgi structure and function in yeast

First author: A. Peyroche

Corresponding author: C. Jackson.

Authors auditioned: Catherine Jackson.

C. Jackson assumes the editing of the figures was done "to show representative images of the results". The figures were made by her.

Analysis of Figures:

Figures 2C-D:

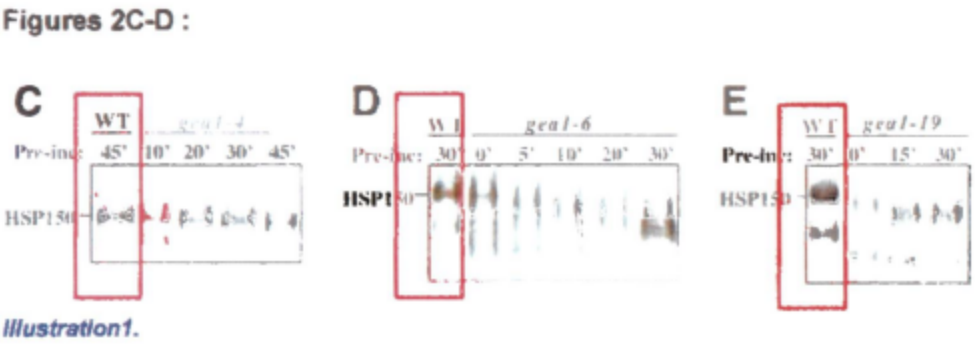

Illustration1.

The WT track was joined to the others without indication (illustration 1). According to the paper description, this control should have migrated at the same time as the other samples since their electrophoretic mobility is examined. Potential deficiencies of glycosylation due to the genetic modifications introduced into the yeast strains can thus be evaluated. The comparison with the wild control (WT) if it comes from another migration, then lose its strength of conviction.

It is the same for Figure 3A, or the first track was contiguous without further explanation. This way of proceeding, as indicated previously, weakens the experimental quality.

Level I / II.

Figure 4D:

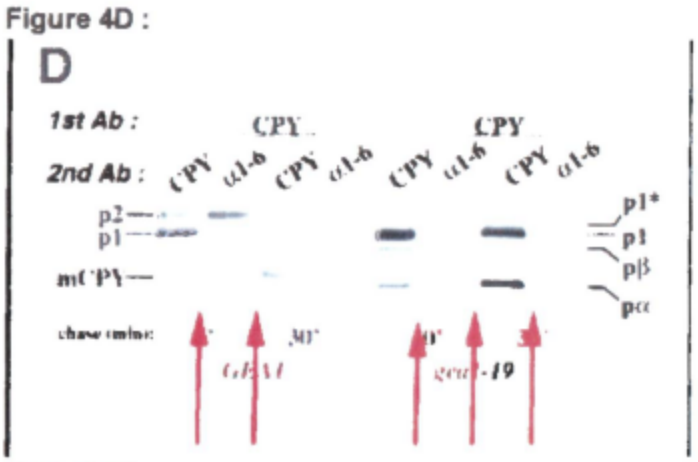

Illustration2.

This figure represents immuno - purifications whose compounds are identified by Western-blot.It has 8 tracks from 5 different divisions (illustration 2) .Whatever the origin of these cuts (from one or more experiments), it is good to remember: The principle is that polyacrylamide gels (known as SDS-PAGE) and electrophoretic migrations are usually made under standard experimental conditions, which makes it possible to compare different protein gels of the SDS-PAGE type (made denaturing and stained by Coomassie Blue) knowing that these gels are often made with molecular weight markers that make it possible to locate (or even identify) each colored protein band, but it would be difficult to compare them to Western-blots quantitatively and therefore to join them. Indeed, the membrane transfer (Western-blot) must take into account the membrane itself (type, batch, pore size, ...), electrophoretic transfer conditions (buffer, transfer time, temperature ,. ..) and also the type of antibody used (origin, batch, contact time, washing mode and exposure time for autoradiography). All of these parameters (difficult to standardize at the same time) demonstrate the difficulty of comparing tracks from various Western blots. In the case which concerns us, or if the binding took into account the protein markers not presented in the figure, one can be astonished by this relatively complex assembly of protein profiles resulting from 6 cuttings. The fact remains that to repeat the gel migration experiment, followed by a possible Western-blot would have been much simpler and more convincing technically, especially since the starting protein material seems to be readily available.

Level I / II

Figures 6 AB:

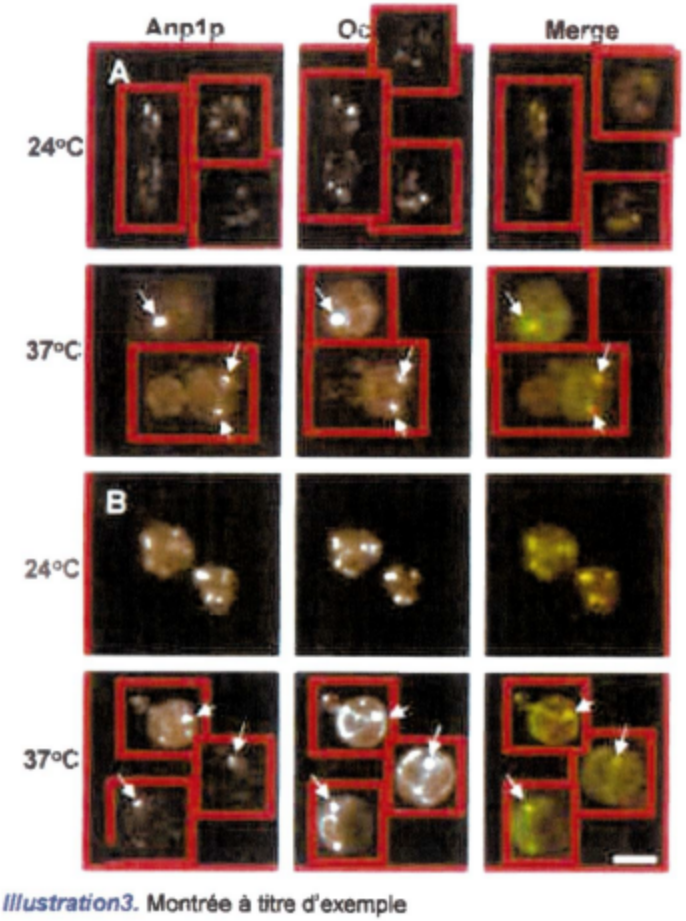

Illustration 3. Shown as an example

These figures do not correspond to a single field of microscopy (Illustration 3). This is a kind of montage of images (red boxes) assembled on a black background and from several different shots to show the location of proteins expressed in different strains having grown at different temperatures (24 ° C and 37 ° C). In several publications that we have reviewed, we find this unconventional way of proceeding.

This same way of operating is found in the establishment of Figure 5A-C.

The documents in our possession as well as the various auditions we were able to undertake, did not allow us to know if the editing was made from shots from a single experiment or independent experiments.

Level II

C. Jackson told us that this was a common practice at the time the paper was written. Inquiry made, and to the knowledge of the members of our committee, this kind of practice was never done. To convince of the reality of the results, it would have been enough to show a single field with possibly a statistical study concerning cells presenting the same profiles under the experimental conditions described. One could also delimit the shots proposed in the figure and mention it in the legend.

Article: Molecular Biology of the Cell, 2003

Chantalat, Sophie, Régis Courbeyrette, Francesca Senic-Matuglia, Catherine L Jackson, Bruno Goud, and Anne Peyroche.

Title: A Novel Golgi Membrane Protein is a Partner of the ARF Factors Exchange Geap and Gea2p.

First author: Sophie Chantalat

Corresponding author: Anne Peyroche

Authors auditioned: Catherine Jackson and Sophie Chantalat

Catherine Jackson auditioned on February 21, 2018 indicates that it was Anne Peyroche who began this work, under her direction at the end of her thesis. The job was to look for multicopy deletions of mutations in gea1 and gea2. C. Jackson being part of the USA (NIH) for 5 years, it is Sophie Chantalat who finished this work under the direction of A. Peyroche. It was part of her thesis work. According to C. Jackson, it would be A. Peyroche who would have prepared the figures and would have begun writing. The hearing of S. Chantalat on April 16, 2018 confirms that this work was started by A. Peyroche and that she finished it under the direction of A. Peyroche. She testified that the figures below, which are problematic, were not prepared by her. It assumes the preparation of FIGS. 7A-C as well as FIGS. 8C and 9B. She declared herself surprised and upset when she examined the other contested figures.

Analysis figures:

Figure 1A

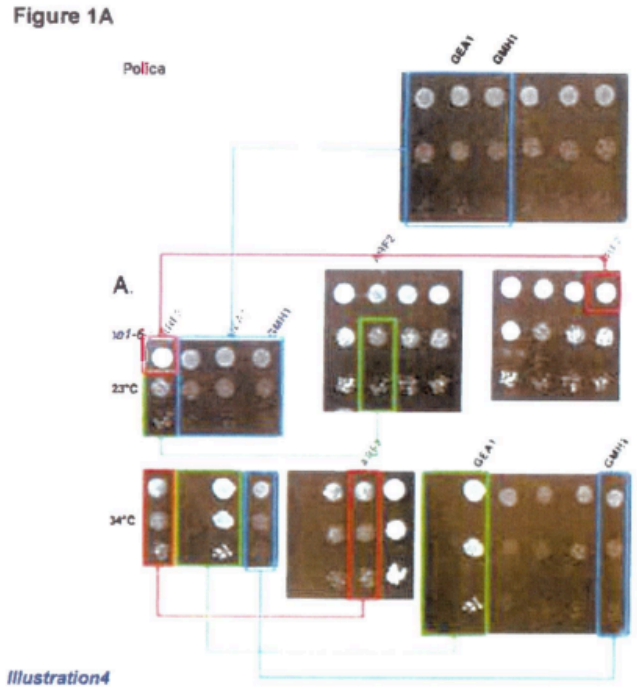

Illustration 4

In this type of experiments comparing the yeast growth capabilities depending dilutions and temperatures must be on the same Petri dish to ensure a correct comparison between different strains and experimental conditions. It appears after "unbundling" (dissociation of the figure) that 5 different plates were used to build the final figure (illustration 4). This figure is therefore a "recomposition of spots" from the experiments presented in these 5 boards.

For example, we see that in plate 23o, spot ARF2 (low dilution, red box, illustration 4) comes from an experiment while the other 2 dilutions of this strain (green square, illustration 4) comes from another experiment. For specialists, this is not done because we do not "break" a dilution of yeast. Without commenting on all the other montages, we see that the final figure is a patchwork of spots, taken on several experiments, which also concludes S. Chantalat. Jury question to S. Chantalat: "Do you think this way of doing things is common?

S. Chantalat.-" Of course not. I did a lot of dilutions of this kind during my thesis and it would not occur to me to do it. It's so simple, it's basic. We only do this on one box to compare. We do not break a dilution".

Level III

Figure 4A

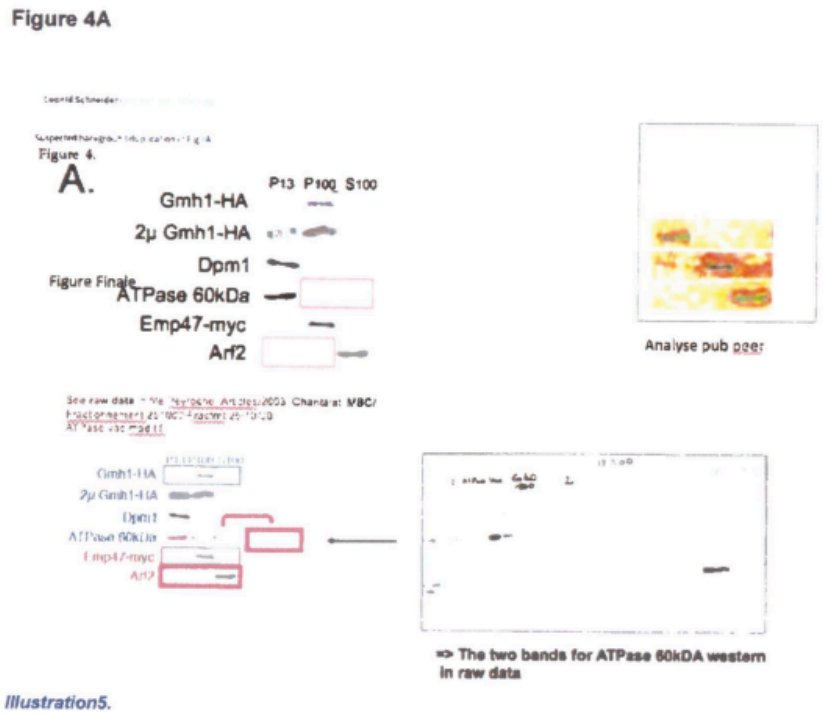

Illustration5.

Illustration 5.

The purpose of this experiment is to detect the subcellular localization of Gmh-HA by differential centrifugation. Centrifugation is a technique that separates organelles or very large complexes of lesser and sometimes more soluble biological compounds.

The figure of the paper is at the top left (illustration 5). It can be seen that the Western blot of ATPase 60kDa indicates that this enzyme is present only in the P13 fraction and that the Arf2 protein is present only in the S100 fraction. It has been detected that a cache (surrounded by red on illustration 5) has been added to mask the presence of the ATPase 60kDa in the well-visible P100 and S100 fractions.

This cache is therefore a copy-paste as shown in the figure Peer Pub (top right).

There is therefore here a voluntary band masking of a Western which modifies the raw data, namely that the ATPase is not exclusively in the P13 fraction and does not coincide with Arf2. C. Jackson and S. Chantalat say they have not noticed these maskings they disapprove.

Level IV

Figure 6

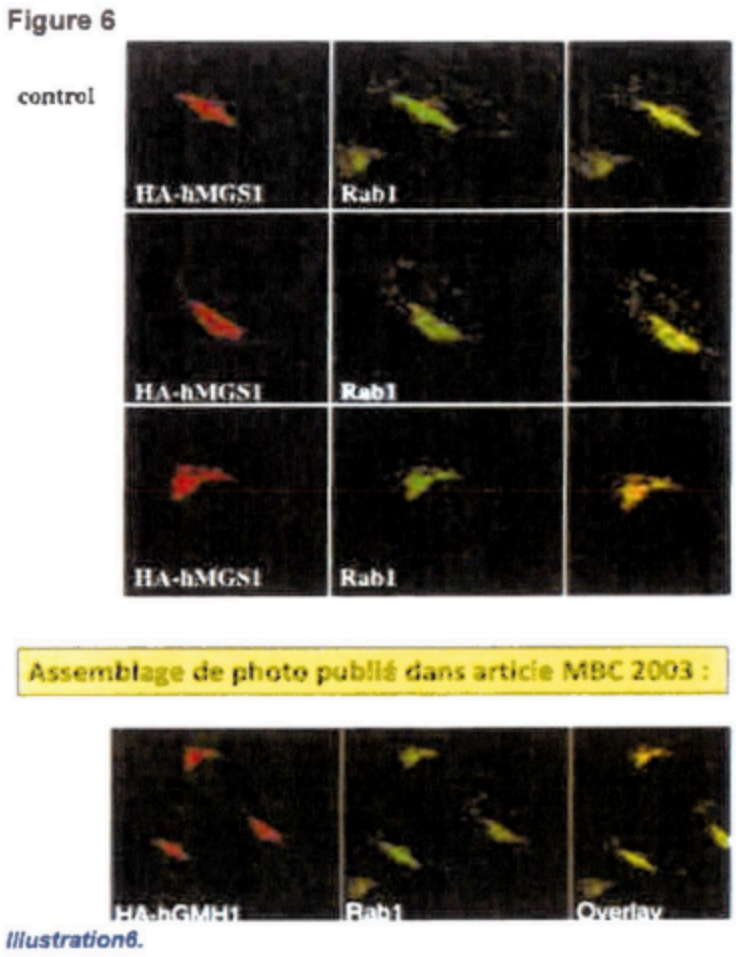

Illustration 6.

The immunofluorescence experiments were intended to visualize the co-localization of the hMGS1-tagged (tagged) -HA and Rab1, Rab6 or GMAP-210 proteins. We see (Figure 6), for line 1, that the 3 cells that the reader thinks to be photographed in a single field of microscopy actually correspond to 3 cells of different fields that have been arranged so as to "virtually reconstitute Only one (illustration 6, bottom images). It is the same for the immunofluorescence of lines 2 and 3. The good practice would have been to show a field of microscopy containing several cells in order to convince the reader of the homogeneity of the results or to show in a box the detail of the co -marking on one or more cells.

Level I/II

Figure 8

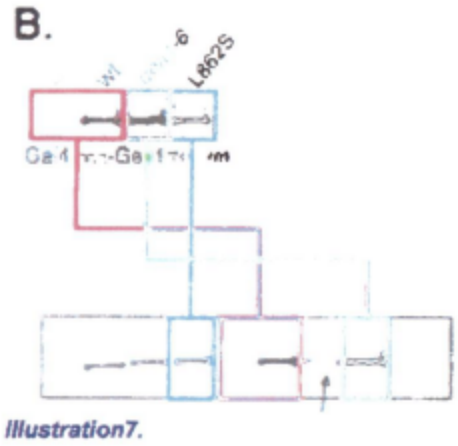

Illustration 7.

This Western-blot experiment is intended to verify that the level of expression of the WT and mutant Gea 1p proteins were identical. By "ungrouping" Figure 8B, it appears that the latter has been "recomposed" (Figure 7) from an image (bottom) provided by the CEA which has no legend. The cut strips should have been separated by bars and the legend should have indicated that they came from a single gel if this was the case. This questions the reality of Gea1p expression levels in all three strains.

Level II

Article: 2007 MOLECULAR CELL, Volume 27, 660-674

Le Tallec Benoit, Barrault Marie-Benedicte, Courbeyrette Regis, Guerois Raphael, Marsolier-Kergoat Marie-Claude, and Peyroche Anne

Title: 20S proteasome assembly is orchestrated by two distinct pairs of chaperones in yeast and in mammals

Author: Benoit Le Tallec

Corresponding author: Anne Peyroche

Authors auditioned: Benoit Le Tallec and Marie-Bénédicte Barrault

B. Le Tallec and MB. Barrault auditioned on February 21, 2018 indicate that frequent exchanges took place between them and Anne Peyroche throughout the phase of obtaining the results. This work consisted of characterizing the chaperone function of POC1 proteins at 4 for the 19S proteasome. A sieve identified POC1-4 as necessary for the yeast's response to DNA damage. B. Le Tallec was then a student in these under the direction of A. Peyroche, MB. Barrault was a technician, she was then promoted to engineer. MB. Barrault and B. Le Tallec states that A. Peyroche alone would have done the construction of the figures and the writing of the text. M-8. Barraut says, "I claim my work and the integrity of my work." MB Barrault performed immuno-precipitation, gel filtration, Western blot analysis; B. Le Tallec, genetic screening, sequencing, establishment of mutant yeast strains and growth tests. According to B. Le Tallec, A. Peyroche could also have made some Western bots.

FIGS Analysis: Figure 2A

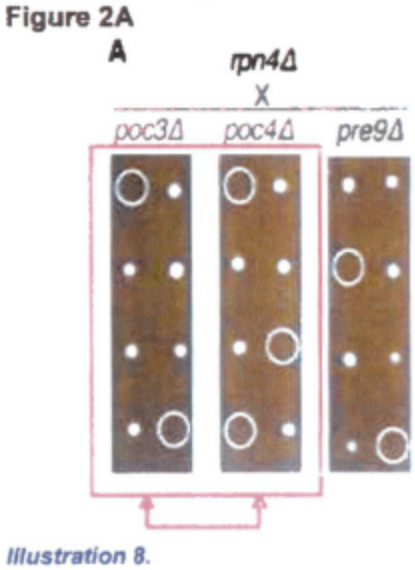

Illustration 8.

Various elements noted on previous articles led us to focus on Figure 2A above. The analysis of files prior to that of the final version of the figures showed a difference with the final version. On examining the original photographs of the yeast boxes, an inversion has been observed: the tetrads denoted POC3A are in fact POCA4 (Illustration. 8).

Level II

Several figures in this article show proteins analyzed by Western blot from total cell extracts, immuno-precipitations or fractions obtained after separation on gel filtration. Many are copied and pasted.

Figure 3C, top panel

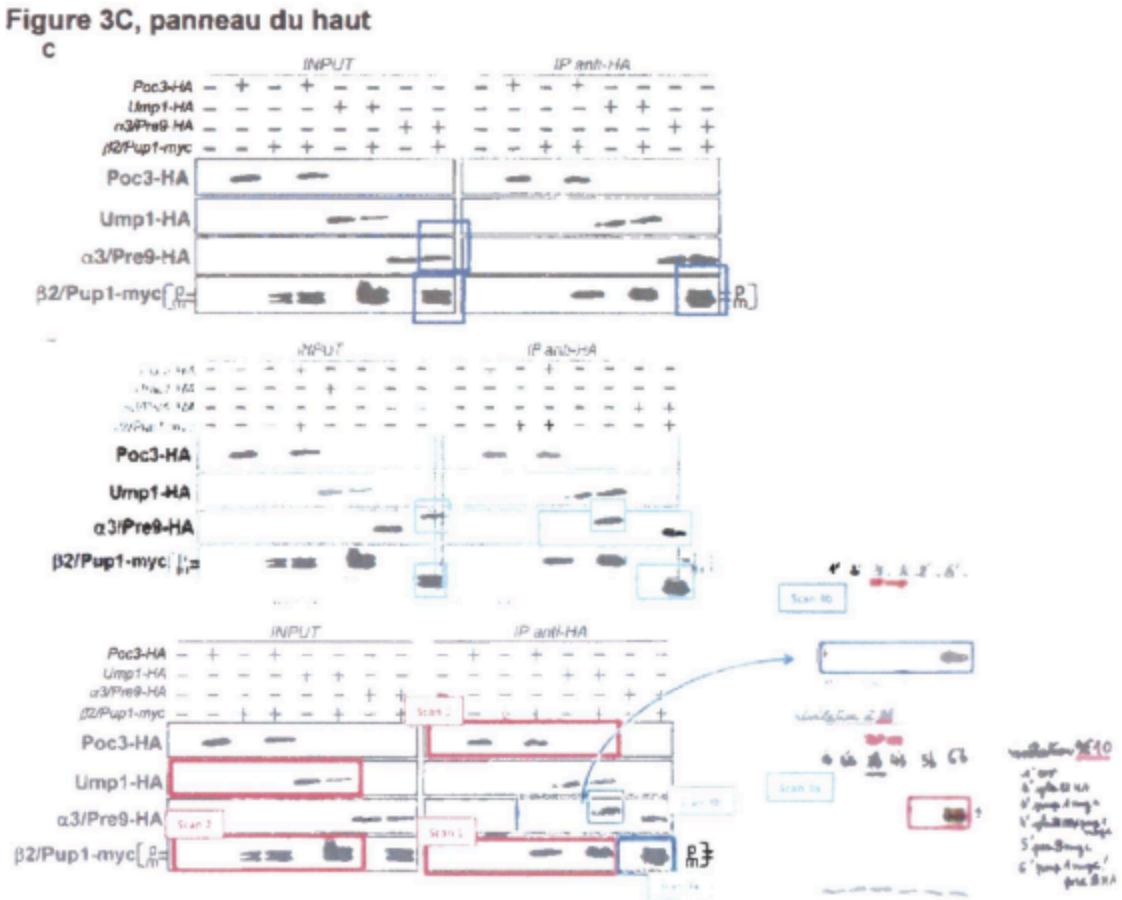

Illustration9. *Les différentes étapes de dégroupages ainsi que 2 Western blots originaux sont représentés*

Illustration 9. the different stages of unbundling and 2 Western blots are shown original

Immunoaffinity préciptation experiments (IP) designed to determine whether there is an interaction between the subunit B2 proteasome and POC3 in the various yeast strains Two positive controls for interaction with B2 are used: Ump1 and a3 These experiments are presented in the article as if they had all been analyzed by Western blotting on the same gels (Figure 9) The starting fractions (INPUTS) must be compared with each other to check that the same quantities of material were initially used. The rigor would have them analyzed from the same gel (see comment on Western blot p.4). The same is true for IP products. In view of the original images, this is not the case (illustration 9, red and blue boxes). Another representation would have been more adequate to indicate that these Western blots correspond to different gels. All the authors should have noticed this point.

Level I / II

Furthermore, the a3-HA band shown as corresponding to the product of the IP a3-HA actually appears to correspond to an anti-myc IP (Figure 9, compare large blue box bottom panel and right panel scan 4b).

Level IV

Figure 3C, bottom panel

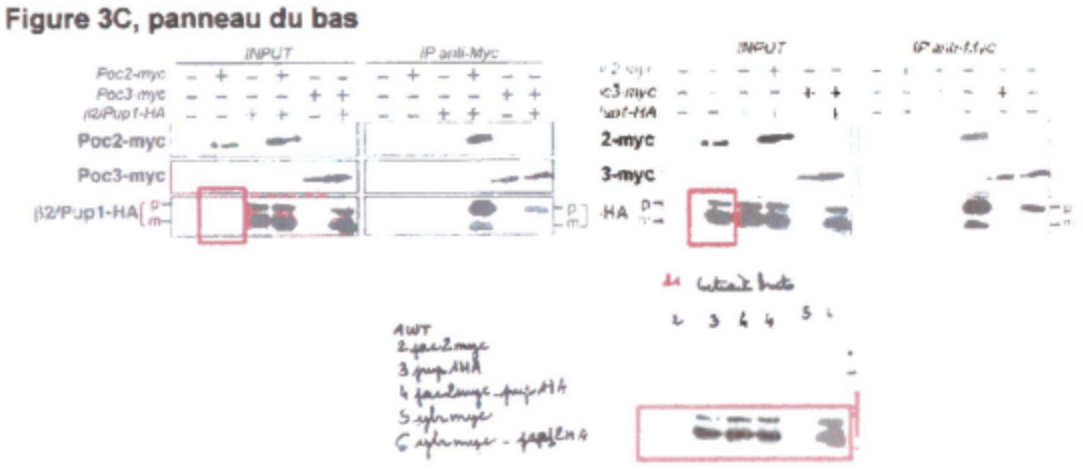

Illustration 10.

Illustration 10

The purpose of this Western blot on the INPUT samples is to give indications of migration profile and quantity of proteins, especially here the molecular weights of the precursor and mature form of B2-HA. It has been noted the hiding of a double band (illustration 10, red box). The analysis of the original data in the presence of B. Le Tallec shows that the same sample was deposited in duplicate: crude yeast extracts expressing B2-HA with POC2-myc Figure 10, wells 4 split on the original figure, large red box). The band was masked in the sample corresponding in fact to B2-HA alone and the true negative sample POC2-myc without B2-HA was not shown, just like the B2-HA control which is missing in the end. B. Tallec does not understand the reason and MB. Barrault and B. Le Tallec say they did not notice the manipulation since the real negative control was produced.

Level II/III

Figure 3

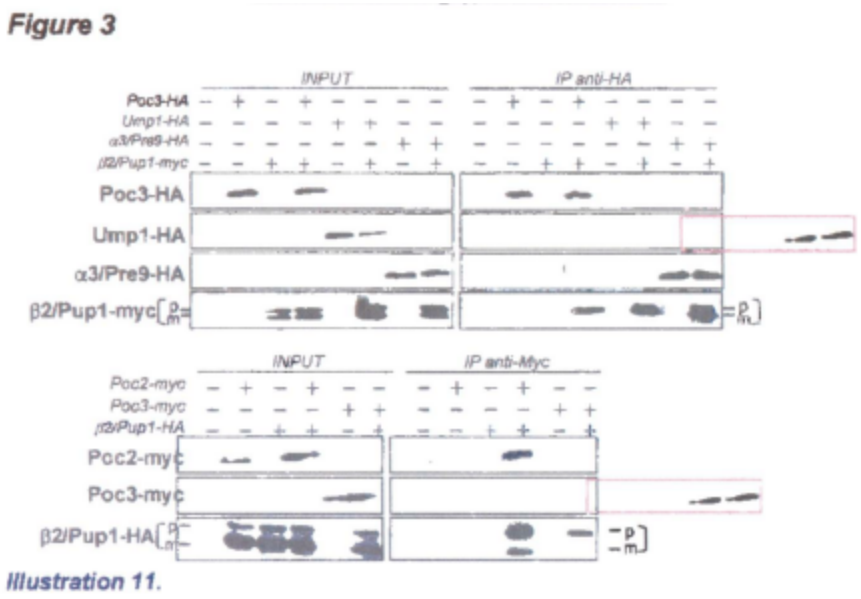

Illustration 11.

There are two identical blots in the top and bottom panels, representing respectively Ump1 protein and POC3 protein (illustration 11, red boxes). MB. Barrault says he does not understand. B. Le Tallec says, "I did not notice this when I corrected the figures," "By the time things went out on PubPeer, I checked the article, and when I having seen that, I wondered how it was possible not to have seen it. "" When I saw that, I was rather shaken.

Level IV

Figure 3D

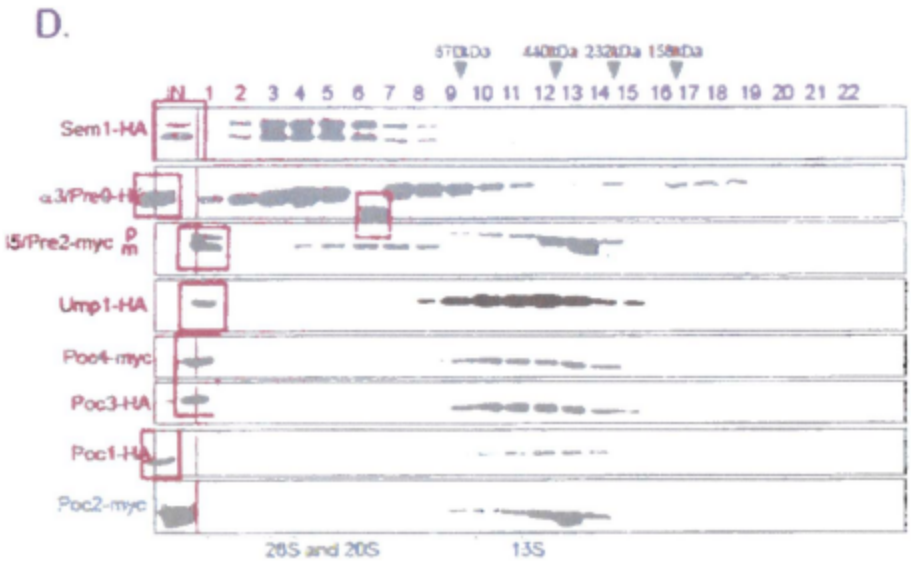

Illustration12.

Illustration 12.

This is a Western blot analysis of proteins separated by gel filtration (the principle of the technique is detailed below in the analysis of the publication of Le Tallec 2009). One band was added to Western blot with the anti-HA antibody on the well corresponding to fraction 6 (Figure 12, red box), which does not correspond to the original well. According to the original blot, the latter contained only a small amount of protein and corresponds to a fraction that was obviously not collected correctly during the gel filtration experiment. The inputs (deposits-controls) as indicated (illustration 12, red boxes) come from different electrophoresis experiments.

Level II/III

Figure 5C

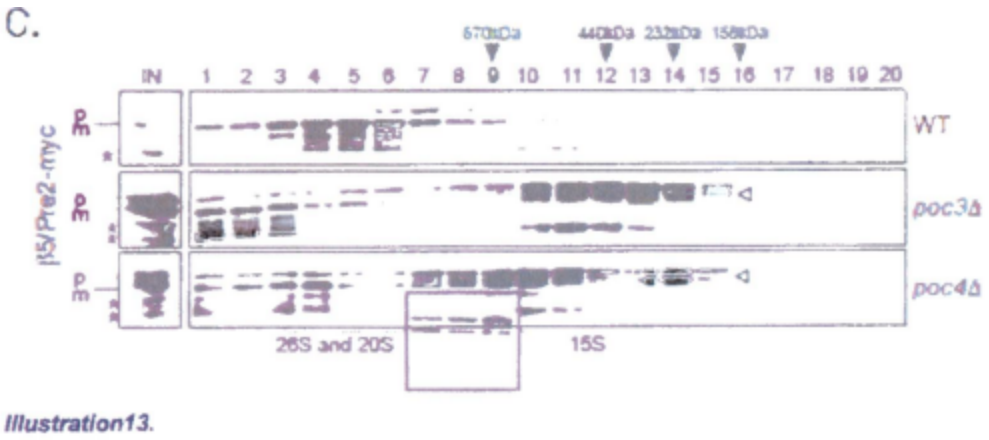

Illustration13.

Illustration 13.

The objective of the experiment is to compare the elution profiles of the B5-Myc subunit of the 19S proteasome in 3 yeast genetic backgrounds (WT, mutated for POC3 or POC4), in order to know the effect of the mutations. on the maturation of the 19S proteasome. There will be more than beta5-myc eluted with low molecular weight fractions if the proteasome is immature, ie when the assembly is not complete. Three bands corresponding to fractions 7, 8, 9 were glued to the 35-myc Western blot of the gel filtration experiment from the yeasts poc4delta (FIG. 13, red box). The originals showed a more intense beta5 marking and the copy and paste attenuates and modifies the elution profile by shifting the fractions containing the beta5 protein. Poc4delta will thus present a migration profile similar to that of poc3delta but different from that observed in the wild-type strain (WT). This manipulation would like to show more strongly the lack of maturation of the proteasome in these poc4delta strains. Not only is it a mixture of 2 different experiments, but in addition the glued strips do not correspond to the same yeast strains. Indeed, these 3 bands come from the gel filtration analysis of the POC3delta strains (according to the original data). There is therefore a mixture of the POC3delta and POC4delta samples.

Level IV

Figure 7D

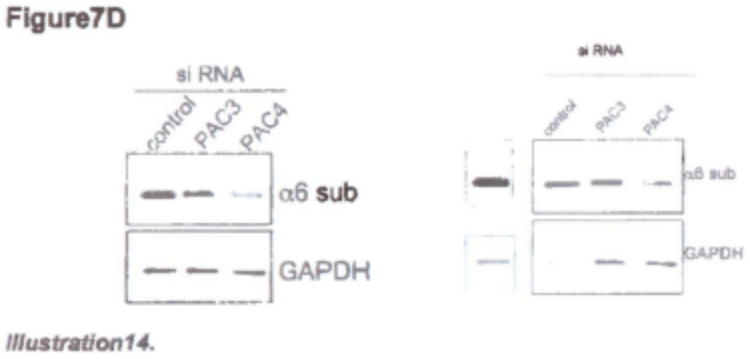

Figure 14.

B. Le Tallec indicates that this experiment (Figure 14) was done by him, but the figure presented in the paper would come from a Western blot made by A. Peyroche; the results of this experiment would have been assembled in figure form by her. There is a modification according to the wells of the intensities of the ab and GAPDH proteins; the latter having been used as a control. Indeed, it seems that the copy and paste control well come from different exposure time.

Level: II / III

Article Molecular Cell, 2009

Benoit Tallec, Barrault Marie-Benedicte, Raphael Guerois, Carré Thibault and Peyroche Anne.

Title: Hsm3/S5b participate in the assembly pathway of the 19S regulatory particle of the proteasome

First author: Le Tallec B.

Corresponding author: Peyroche A.

Authors auditioned: Benoit Le Tallec and Marie-Bénédicte Barrault

This article as the previous one contains many manipulations / collages / assemblies. MB Barrault who was the master of the purely biochemical part, she tells us, transmitted to A. Peyroche the raw data (western-blots identifying the various proteins eluted by gel filtration). The latter was busy doing the tricks, a step in which MB Barrault was not involved.

Analysis of the figures:

FIGS. 2A and 2B: There are numerous collages, in particular at the level of immunoprecipitation (IP myc) in the fraction indicated Rpn10 in red (FIG. 15, left panel), the origin of which is unknown. The Rpn2 protein (red box) was added in the immuno-precipitation Rpn1 and Rpn9 (right panel) on the original Western blot.

Tallec et al., Fig. 2

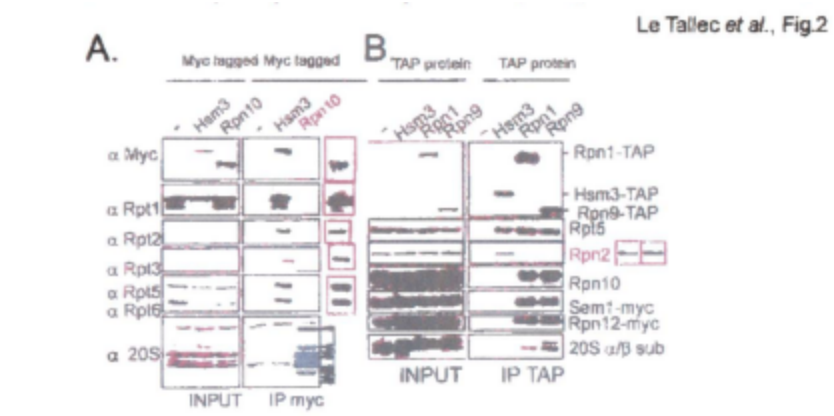

Illustration15.

Figure 2E Gel filtration is a method of separating biomolecules according to their size (mass). Thus the highest molecular weight protein molecules or complexes will be eluted first, the smallest will be eluted last. This technique is used to determine in addition to the molecular weight of these complexes, and following complementary experiments the co-elution of various proteins. In the case which concerns us, the authors have manufactured a chromatography column for "gel filtration" and they have standardized the experimental conditions namely type of elution buffer, flow of the column and elution temperature. In addition, with molecular weight markers they were able to estimate the molecular mass of interest complexes identified by immuno-detection.

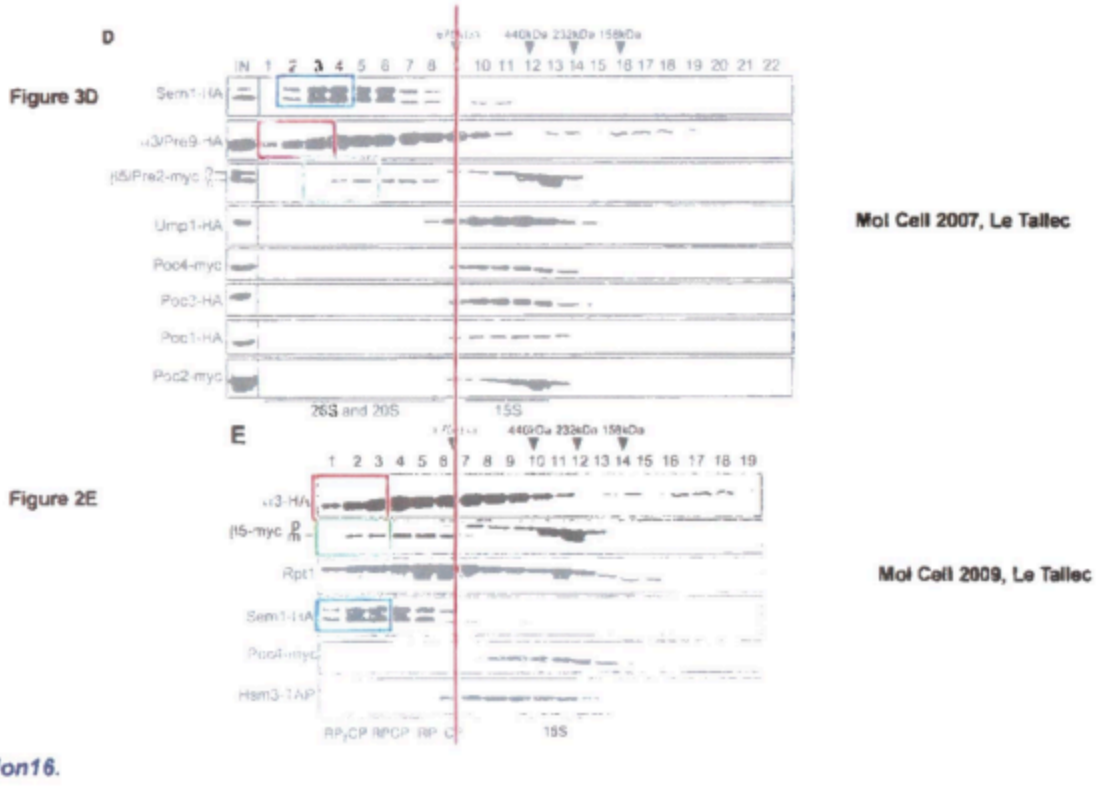

Illustration 16.

It can be seen that some of the results of the Mol Cell 2007 article are reused, especially with regard to Figure 3D to produce Figure 2E (Figure 16). These come from a figure already used in the paper Le Tallec 2007: gel filtration elution profiles of alpha3-HA (or there was already bonding of a band at fraction 6 level), of beta5-myc and from sem1-HA.

There is also a numbering of the fractions and a position of the molecular weight

markers presented in Figure 2E, very different from those observed in the 3D figure of the publication Le Tallec 2007. We also note the sliding of the elution profiles to 3 -HA (illustration 16, red box), beta5-myc (illustration 16, green box) and sem1-HA (illustration 16, blue box) which considerably modifies on the one hand the molecular weight evaluations to which the proteins can belong revealed, and on the other hand the possibilities of conclusion as to a co-elution see a membership in the same protein complex.

Level IV

Figure 5C

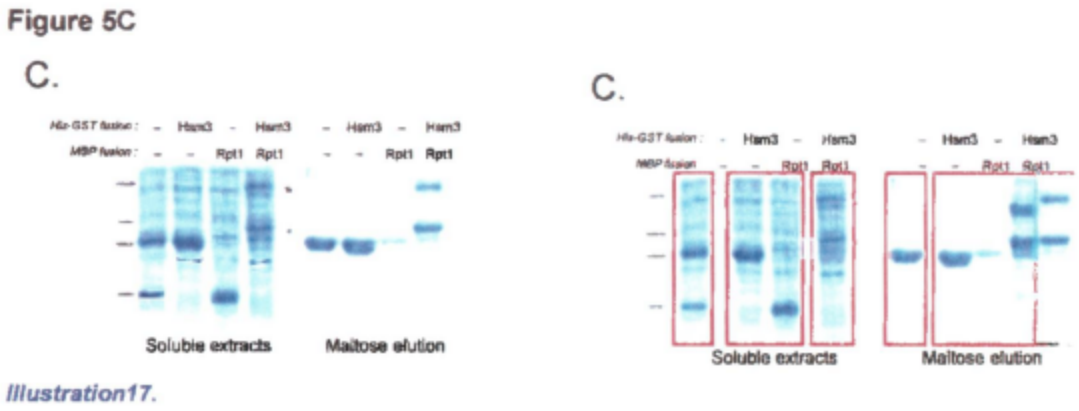

Illustration 17.

As previously described, this figure assembles several tracks probably from several experiments. There is also a superposition of images letting a certain ambiguity (illustration 17, left panel, red and green boxes).

Level I / II

Figure 5D:

This figure shows the behavior of 3 yeast wild type (WT) or mutated strains (hsm3D and cim5-1) in which HSM3 or RPT1 gene expression vectors were introduced (Illustration 19, top) . The plates on which various dilutions would have been deposited were then incubated at different temperatures and treated with the inhibitor 4NQO, as indicated at the bottom of FIG. 5D presented in the article Le Tallec 2009 (FIGS. 18 and 19).

The boxes represent the picks made on the original plates also annotated on the bottom panels (which are the results of the original experiments carried out under

specific conditions (dilutions and temperature) and made in triplicates). the final Figure 5D does not represent the results of the

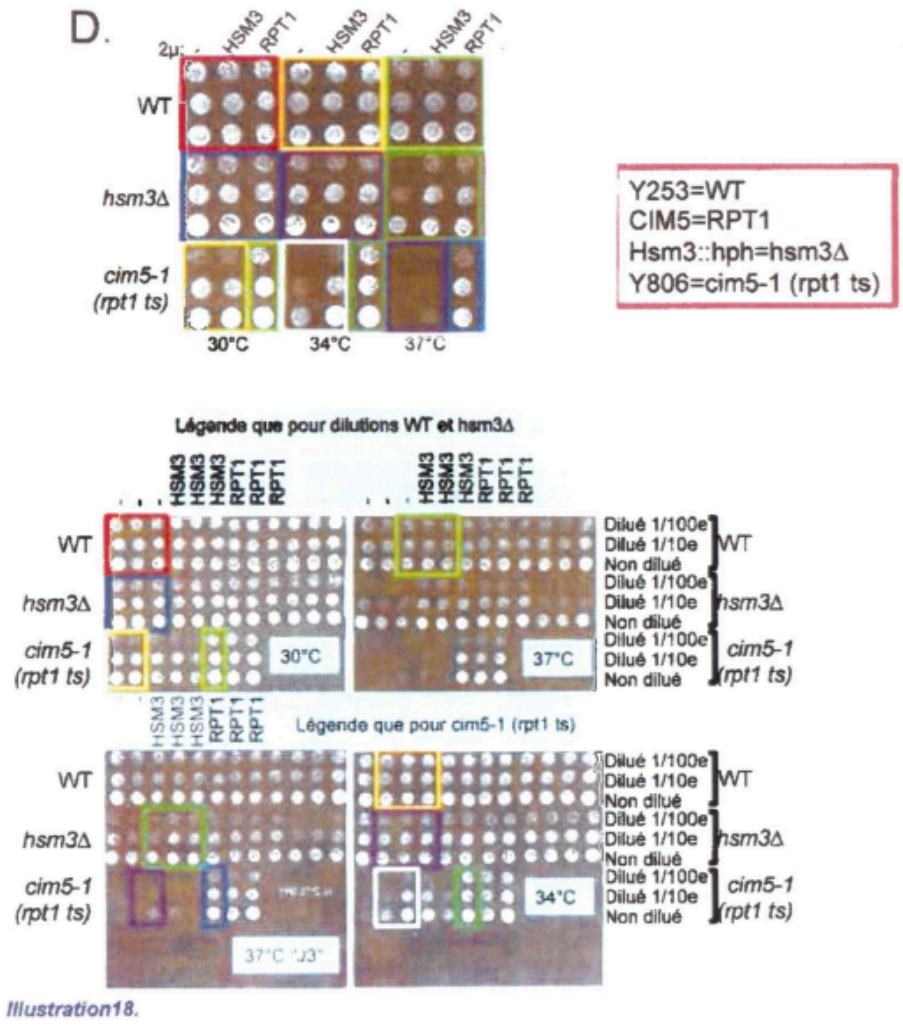

Illustration18.

For example,

1) red frame of Figure 5D section (Figure 18, top panel) showing three dilutions of wild strain or not transfected by the vectors and HSM3 RPT1, is actually the triplicate of the wild strain untransfected (Illustration 19, bottom panel, red box). The cim5-1 panel (FIG. 18, top panel in yellow and light green) of FIG. 5D showing 3 dilutions of this non-transfected strain (incubated at 30 ° C.) and then transfected with HSM3 and RPT1, is in fact the arrangement of the first two duplicates of the untransfected wild cim-1 pick, arranged with HSM3 transfected cim5-1 (Fig. 19, bottom panel, yellow and green boxes). In the figure of the paper (top panel), it becomes the cim5-1 strain transfected by RPT1. The hsm3A panel (FIG. 19, green box) of FIG. 5D, representing the growth of this strain at 37 ° C., either untransfected or transfected with HSM3 or RPT1, is in fact the triplicate of this same HSM3 transfected strain only (illustration 19, bottom panel, light green box).

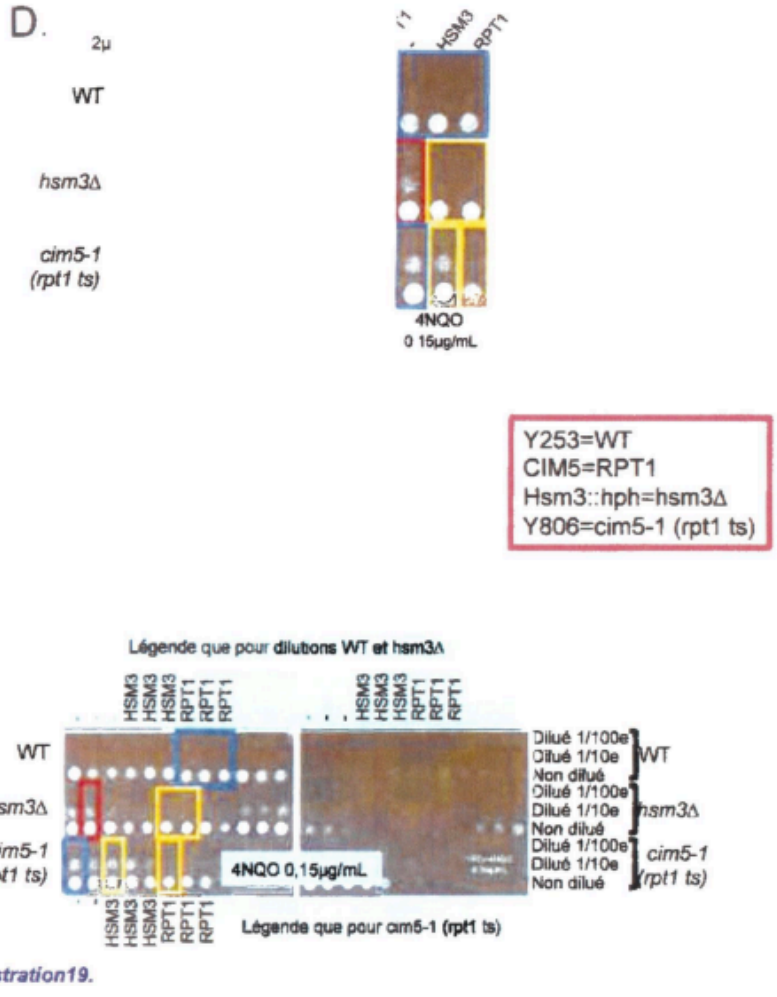

Illustration19.

Illustration 19.

2) The analysis of the second part of the figure, will be built according to the same process as before without taking into account the original experiment (illustration 19). None of the other five panels in the published figure (Figure 5D) reflect the results observed on the original plate shown on the bottom panel. In this figure, one could give other examples where none of the panels represented in the published figure relate to the original experiment. In view of these figures, B. Le Tallec said he was "dismayed". According to him, he was not at all kept informed of these arrangements of figure, he who was at the origin of these experiments. Moreover, the figure 5D presented on the publication as one would have wanted, could have been redone without any problem in a few days. It should be noted that the latter only dealt with the genetic part of transformation of the various yeast strains. The biochemical part being realized by MB Barrault. The presentation part of the figures for the publication being, according to him, reserved exclusively to Mrs. A. Peyroche.

Level IV

Figure 6C

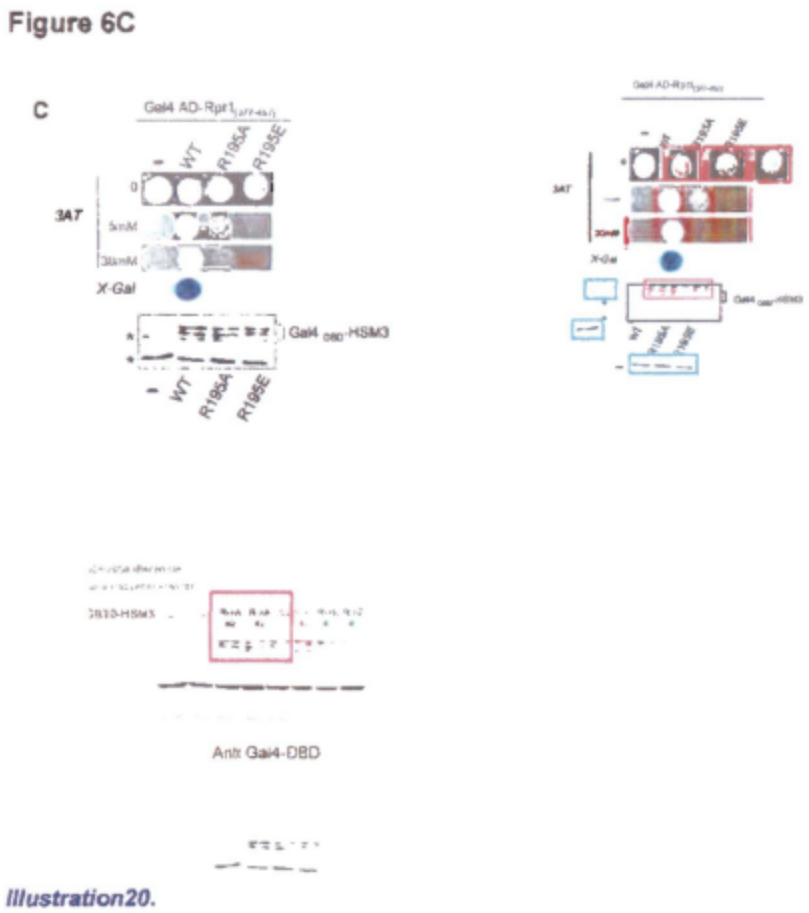

Illustration20.

The top panel representing the growth levels of various strains mutated or not at the level of RPT1, is also the result of a montage (illustration 20, various red boxes) made from first results which we did not have the pictures of the original experimental plates. -. The bottom panel of Figure 6C is an experiment showing following electrophoresis and immuno-detection that the different mutations made on the RPT1 protein do not affect their level of expression. However, we notice that the Western blot is the result of an assembly where the tracks (-), WT, R195A, R195E shown in the figure (illustration 20, black framed panel of the figure of the article and red box), represent respectively tracks (-), R195A, R195A and WT of the original Western blot (bottom panel, red box figure). None of them reflect the original results.

Level III

Article PNAS, 2011

Barrault Marie-Benedicte., Nicolas Richet, Chloe Godard, Brice Murciano, Benoit Le Tallec, Erwann Rousseau, Pierre Legrand, Jean Baptiste Charbonnier, Marie Helene Le Du, Raphael Guerois, Francoise Ochsenbein and Peyroche Anne.

Title: Dual functions of the Hsm3 protein in chaperoning and scaffolding regulatory particles subunits during proteasome assembly

First author: Barrault Marie-Benedicte

Corresponding author: Anne Peyroche and Françoise Ochsenbein Authors auditioned: Françoise Ochsenbein

F. Ochsenbein indicates that his responsibility as an author correspondent concerned only the structural part.

Analysis of Figures:

Figure 6B

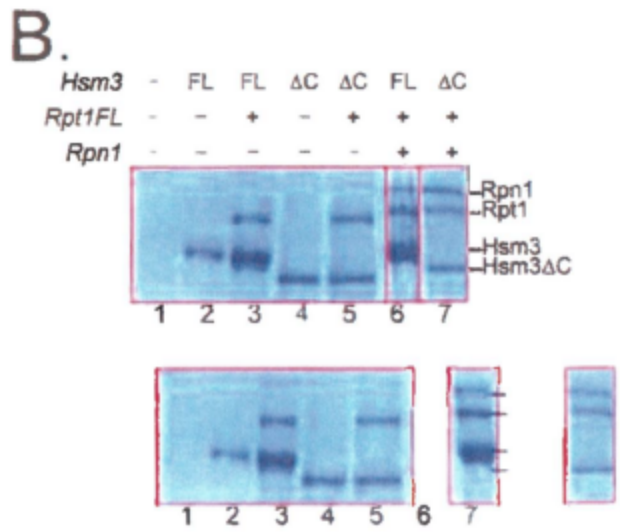

Illustration21.

Illustration 21, The last two tracks of the Coomassie Blue gel have been contiguous to the first 5 (illustration 21, red box). In view of migration patterns, it seems that this comes from several gels and / or perhaps from different experiments.

Level I /II

Figure 6C-D:

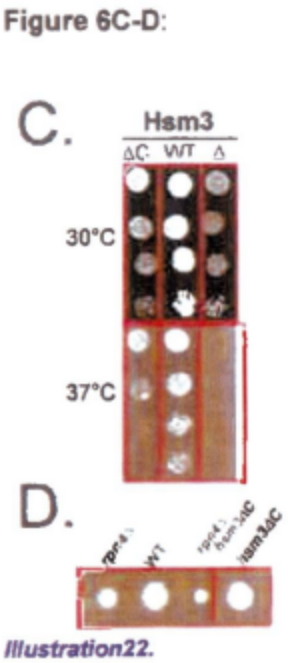

Illustration 22.

The growth results of various yeast strains were pasted in columns (Figure 22, red box), suggesting that these experiments were not performed under the same experimental conditions.

Level II

Figure 6F-G:

Figure 6F-G :

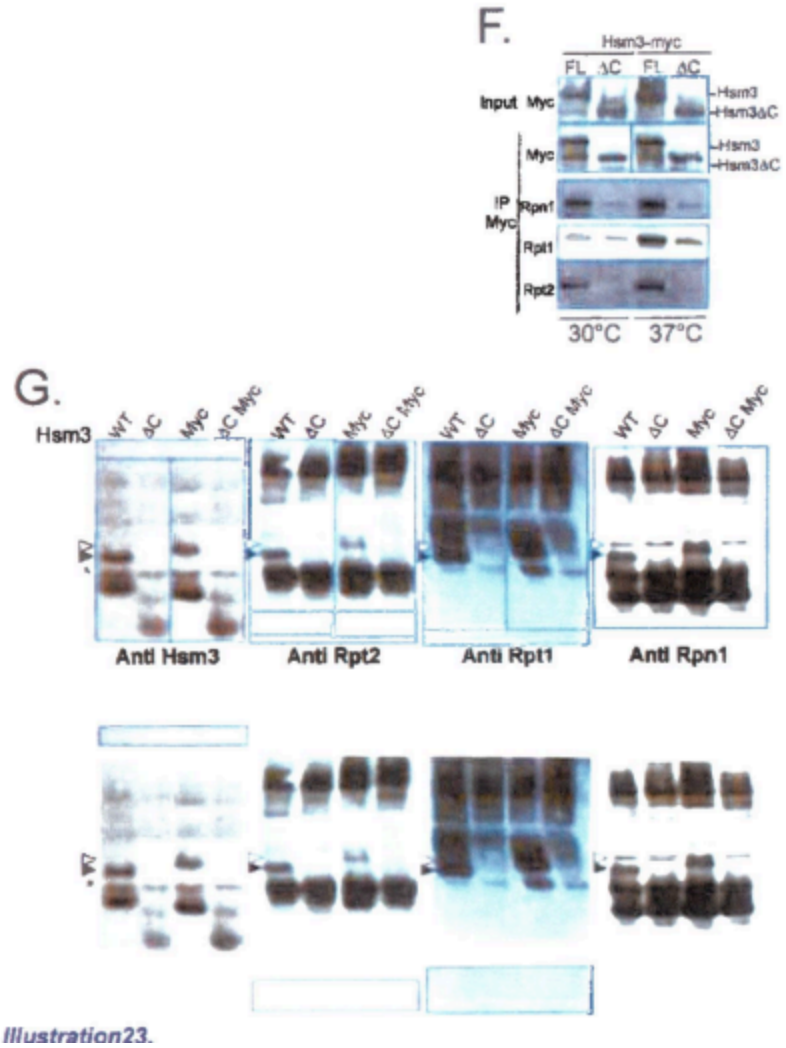

Illustration23.

Illustration 23.

Several tracks of this figure have been joined together (illustration 23, blue boxes) suggesting different origins of experiments. We also note size adjustments by adding several funds.

F. Ochsenbein would, she said, have proceeded differently with regard to the assemblies of Figure 6 mentioned above: "redo a single protein migration gel and repeat the growth experiment of the yeast strains on a single support “

Level I/ II

CONCLUSIONS

The in-depth analysis of the five articles signed by A. Peyroche and which led to allegations of scientific misconduct by the PubPeer site led us to make the following conclusions.

Many misconduct marks were found in the five offending articles. The anomalies found were of variable severity depending on the figures and articles, ranging from embellishment to forgery altering the interpretation of the data.

The findings of the hearing panel are consistent with those made by the panel of foreign experts, with the understanding that the Hearing Panel considered a larger number of figures than these experts had done.

An essential point was to hear the authors of the articles to give them the opportunity to explain the anomalies observed and to listen to their answers, particularly as regards their personal responsibility. The five authors interviewed, who were either first-time authors or corresponding authors, independently and controllably on the recordings, said that the responsibility for the figures fell entirely to A. Peyroche, with the exception of Cathy Jackson in 2001 Article of which she is the author. They all said that they had not followed the preparation of the figures throughout the process of preparation of the publication and only surprisingly noted the anomalies observed in the dissemination of the allegations of PubPeer. We must mention that we could not listen to the version of A. Peyroche, which could leave some doubts about the veracity of the statements of the coauthors.

The problem is whether some of these items should be subject to erratum or retraction. This is, in the opinion of the Hearing Panel, the case of the articles of 2003, 2007 and 2009.

In conclusion, there seems little doubt that improperly acceptable misconduct was committed in the drafting of the five incriminated articles. The partial or total responsibility of Mrs A. Peyroche is clear, even if one wonders how the first authors or corresponding authors had had such a furtive look at publications in which they had a major responsibility.