Multi-laboratory experiment PME11 for the standardization of phosphoproteome analysis

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Many aspects of cell biology are regulated by reversible protein phosphorylation networks that involve thousands of phosphorylation events. In the last decade multiple methods have been developed to identify and quantify involved phosphorylation sites, and their modulation and dynamics under physiological and pathological conditions. Global post-translational modification analysis based on cutting edge mass spectrometry technology has emerged as the premier tool in many laboratories worldwide to investigate the complexity of signaling pathways and their crosstalk [1–3].

In 2016 the Spanish Proteomics Network ProteoRed-ISCI proposed the PME11 multi-laboratory experiment as part of the EuPA Standardization Initiative. The aim was to evaluate the performance and reproducibility of phosphopeptide enrichment procedures and to test the usefulness of phosphopeptide mixture standards to set up, monitor, and troubleshoot phosphopeptide analysis pipelines. The reference samples analyzed in the study (PME11-A1, A2, A3) consisted of a yeast tryptic digest (125 μg of a C-18 purified peptide digest), spiked-in with three different concentrations (100, 250 and 500 fmol) of a mixture of 20 human phosphopeptide standards (Phosphomix 1 and 2 from Sigma-Aldrich, (product reference MSP1L and MSP2L, Table 1), containing light isotopes. Each participant laboratory received two aliquots of each of the three samples (SUPP INFO 1&2), that were distributed in dry ice, lyophilized from a water-acetonitrile mixture. One additional vial PME11-B, containing 2 pmol of each of the corresponding isotopically labeled heavy Phosphomix standard peptides (Sigma-Aldrich MSP1H and MSP2H) was distributed in dried form for ulterior quantitative analysis. Upon reception participants were indicated to re-dissolve the samples in the appropriate buffer for the enrichment procedure selected. Then, enriched phosphopeptides were analyzed by LC-MS/MS (three replicates) following the recommended guidelines (10 to 30% of the enriched sample and 60 min 0–35% acetonitrile gradient). Analysis of pre-enriched samples was also recommended. Detailed descriptions of the experimental settings, reference sample and analysis guidelines were provided to the participants (SUPP INFO 1&2).

Recently, a related study conducted by several laboratories in the frame of the MS Resource Pillar of the HUPO Human Proteome Project has been reported [4]. In this study, a standard set of 94 phosphopeptides and their nonphosphorylated counterparts, mixed in a neat sample and a yeast background were analyzed. Unlike the HUPO study samples, the samples proposed in the present study allowed for the assessment of the enrichment of the endogenous yeast phosphopeptides, in conditions and amounts similar to a real sample. Besides, the spiked-in phosphopeptide standards were provided in isotopically labeled and unlabeled form, allowing for assessment not only of targeted phosphopeptide analysis, but also to estimate the yield of the enrichment procedures used.

Under the coordination of ProteoRed-ISCI, 36 datasets were received from 23 laboratories (Table 2) distributed across Europe -Spain, France, Switzerland, United Kingdom, and Sweden- and USA. Individual reports including experimental details and results were prepared by each participant in the template specifically design for this experiment. Additionally, MS/MS files (mgf format) were also submitted to the coordination unit for their centralized processing and integration, which will be described elsewhere. Some laboratories provided various datasets that corresponded to different analytical pipelines, which allowed the specific evaluation of the experimental conditions tested as the user and instrument used in these cases were the same. Shotgun analysis results were used to evaluate the general performance of each laboratory in terms of number of yeast phosphopeptides identified, efficiency of the enrichment procedure (phosphopeptides/total peptides ratio) and detection of spiked-in phosphopeptide standards.

In light of the dispersion of the analytical conditions used by the participating labs, a comprehensive statistical analysis may have limitations. Nevertheless, several outcomes are worth to be discussed taking into consideration the interlaboratory nature of the present experiment. Samples were processed following different protocols in eight different mass spectrometers as summarized in Table 2 and supplementary information.

A first clear outcome is that intra-laboratory reproducibility is in general very good, as shown by the error bars in the graph in Fig. 1A, with a median %CV between triplicate analysis of 9.16% (Table 2). It has to be remarked that these correspond to triplicate experiments, including the enrichment step and the LC-MS analysis.

Regarding inter-laboratory comparison, the number of
phosphopeptides identified in the different experiments spans a wide range, with an average value of 1026, (Fig. 1A, B and Table 2). One of the main factors that explains this wide range is of course the technical capability of the different instruments used. To roughly estimate the contribution of this factor, normalized values have been calculated (black points in the graph) using as normalization factor the ratio between the reported number of total peptides in the analysis of the pre-enrichment sample for each experiment (Table 2), and the average values for all the experiments. Using this normalization to compensate for instrument performance, the inter-laboratory %CV for the number of phosphopeptides decreases from 66% to 36% (Fig. 1B).

Other factors accounting for this variability would certainly include the enrichment protocol used, as well as the parameters used for data processing and database searches, but also reflect the different expertise of the different laboratories. This is apparent when comparing the results from laboratories using the same type of enrichment and identical processing and database searches, but also reflect the different expertise used for data processing and database searches, but also reflect the different expertise.

The enrichment chromatography format did not have any systematic effect either in the number of phosphopeptides detected or in the enrichment capacity; the observed variations result from inter-operator variability.

Detection of phosphopeptide standards relied on an enrichment step, no matter the amount of standard spiked on the yeast extract (approx. 100, 50 or 20 fmol on column). The frequency of detection defined as the proportion of laboratories detecting a given peptide in three samples, was above 60% for most phosphopeptides (12/20 labs), around 50% in five cases while three phosphopeptides were not detected in any lab, likely due to their small size and highly hydrophilic nature, preventing their retention in the C18 precolumn (Fig. 1A and B).

The enrichment selectivity (Fig. 1C) spans from 15 to 90%. Overall, there is no clear correlation between the observed selectivity and the number of phosphopeptides identified in each of the experiments, influenced, as discussed, by many other factors.

| Sequence | PhosphoMix # | phosphosite 1 | phosphosite 2 |
|----------|--------------|---------------|---------------|
| ADPSSESDLEIDK | 1,6 | S5 | |
| ADPSSESDLEIDK | 1,7 | S6 | S9 |
| ADPSSESDLEIDK | 2,6 | S9 | S14 |
| ELNSPLRENSFGPLEFR | 1,9 | S5 | S3 |
| ELNSPLRENSFGPLEFR | 2,9 | S3 | |
| EQQFQVYK | 2,3 | T2 | |
| EVQAEQPSSSSPR | 1,5 | S10 | |
| FEDEGAFESSETGDYEEK | 1,8 | S12 | |
| HQVSDYDYSSEKEK | 2,7 | Y8 | S12 |
| LGGRPLPFTPTSECTSDVEPDT | 2,10 | T12 | |
| LQFQAR | 2,1 | T5 | |
| NTFSQHSSISQHSPER | 2,8 | S4 | S9 |
| RDSLGTYSSR | 1,3 | T6 | |
| RSYSSSR | 1,2 | Y3 | S4 |
| RSYSRSSR | 2,2 | S3 | S4 |
| SPTEYEHVYANFYBPTTPQR | 1,10 | Y10 | T19 |
| SRPSSPELNNK | 2,5 | S1 | S5 |
| TKLITQLRDAK | 1,4 | T1 | T5 |
| VIEDNYFAR | 2,4 | Y7 | |
| VLHSGSR | 1,1 | S6 | |

Table 1 Phosphopeptide standard description.
In conclusion, the use of different protocols, instruments and operators provides a wide scenario of experimental conditions that is optimal to prove the suitability of the reference material here described for inter- and intra-lab protocol benchmarking, indicating strengths, weaknesses, and guidance for optimization (Stage-Tip vs batch, sample/medium ratio). Overall, we propose that the use of a standardized reference material in a multi-lab study is a useful resource for technology testing as has been extensively demonstrated [7–10] and provide excellent references to set up protocols and rank the performance of individual labs, contributing to the democratization of sophisticated proteomics pipelines under standardized conditions. We think that the results here

| CODE | Affinity type | Support | Ratio TiO2/ sample w/w | MS instrument | Enriched sample amount loaded in LCMS (%) | # peptides Pre-enriched sample | # Phospho-peptides | Std Dev. # Phospho-peptides | %CV # Phospho-peptides |
|------|---------------|---------|------------------------|---------------|-------------------------------------------|-------------------------------|------------------|--------------------------|------------------------|
| L06  | TiO2          | Stage Tip | 6                      | 5600 TTOF     | 30                                         | 5755                          | 823              | 59.2                     | 7.2                    |
| L12  | TiO2          | SpinTip  | N/A                    | 5600 TTOF     | 25                                         | 5666                          | 679              | 28.4                     | 4.2                    |
| L07  | TiO2          | Stage Tip | 6                      | 5600 TTOF     | 25                                         | 11,008                        | 741              | 199.3                    | 26.9                   |
| L16  | TiO2          | SpinTip  | 8                      | Speed ETD     | 20                                         | 1461                          | 141              | 19.1                     | 13.5                   |
| L21_1| TiO2          | Stage Tip | 6                      | Orbitrap XL   | 30                                         | 606                           | 101.9            | 16.8                     |                        |
| L23_1| TiO2          | SpinTip  | 6                      | Orbitrap XL   | 10                                         | 539                           | 39.7             | 7.4                      |                        |
| L14_1| TiO2          | Stage Tip | 6                      | OT Fusion     | 15                                         | 9073                          | 856              | 112.8                    | 13.2                   |
| L14_2| TiO2          | Batch    | 24                     | OT Fusion     | 15                                         | 9024                          | 716              | 150.9                    | 21.1                   |
| L09  | TiO2          | SpinTip  | N/A                    | OT Fusion     | 20                                         | 102                           | 24.5             | 24.0                     |                        |
| L28_1| TiO2          | Batch    | 0.3                    | OT Fusion     | 17                                         | 23,851                        | 2675             |                          |                        |
| L23_3| TiO2          | SpinTip  | 6                      | OT Fusion     | 20                                         | 12,402                        | 2486             | 83.8                     | 3.4                    |
| L19  | TiO2          | SpinTip  | N/A                    | OT Fusion     | 20                                         | 16,524                        | 2295             | 54.7                     | 2.4                    |
| L28_2| TiO2          | Batch    | 40                     | OT Fusion     | 17                                         | 23,851                        | 2184             |                          |                        |
| L28_3| TiO2          | Batch    | 6                      | OT Fusion     | 17                                         | 23,851                        | 2161             |                          |                        |
| L10  | TiO2          | SpinTip  | 6                      | OT Fusion     | 20                                         | 17,286                        | 2062             | 57.4                     | 2.8                    |
| L23_2| TiO2          | SpinTip  | 6                      | OT Fusion     | 2                                          | 10,181                        | 1104             | 26.7                     | 2.4                    |
| L15  | TiO2          | SpinTip  | 6                      | OT Fusion     | 10                                         | 5636                          | 768              | 34.9                     | 4.6                    |
| L02_2| TiO2          | Stage Tip-Gly | 5                         | OT Velos  | 25                                         | 5813                          | 1333             | 144.7                    | 10.9                   |
| L13_1| TiO2          | Stage Tip | 6                      | OT Velos     | 20                                         | 5299                          | 1184             | 56.7                     | 4.8                    |
| L05  | TiO2          | Stage Tip | 24                     | OT Velos     | 30                                         | 6846                          | 1051             | 136.6                    | 13.0                   |
| L04  | TiO2          | Stage Tip | 8                      | OT Velos     | 30                                         | 599                           | 67.6             | 11.3                     |                        |
| L03  | TiO2          | Stage Tip | 6                      | OT Velos     | 20                                         | 4194                          | 586              | 206.0                    | 35.1                   |
| L02_1| TiO2          | Stage Tip-DHB | 2                         | OT Velos  | 25                                         | 5813                          | 549              | 92.9                     | 16.9                   |
| L20  | TiO2          | Magnetic Beads | N/A                       | OT Velos  | 10                                         | 4527                          | 427              | 57.8                     | 13.5                   |
| L108_1| TiO2         | Stage Tip | 5                      | Q-Exactive    | 25                                         | 6231                          | 1412             | 26.4                     | 1.9                    |
| L108_2| TiO2         | Stage Tip | 5                      | Q-Exactive    | 25                                         | 6231                          | 1407             | 56.6                     | 4.0                    |
| L29  | TiO2          | Batch    | 24                     | Q-Exactive    | 16                                         | 4774                          | 647              | 56.1                     | 8.7                    |
| L30  | TiO2          | Stage Tip | 6                      | Synapt G2     | 10                                         | 930                           | 92.6             | 10.0                     |                        |
| L21_2| TiO2          | Stage Tip | 6                      | Synapt       | 30                                         | 437                           | 3.1              | 0.7                      |                        |
| L25_1| TiO2/TiO2    | Batch    | 6                      | 5600 TTOF     | 25                                         | 5271                          | 623              | 58.5                     | 9.4                    |
| L25_2| TiO2/IMAC    | Select   | 6                      | 5600 TTOF     | 25                                         | 5271                          | 830              | 74.1                     | 8.9                    |
| L17  | IMAC          | Fe       | 30                     | OT Velos     | 30                                         | 7653                          | 667              | 175.2                    | 26.3                   |
| L13_3| IMAC          | Phos Select | 20                       | OT Velos  | 20                                         | 5299                          | 476              | 39.1                     | 8.2                    |
| L13_2| IMAC          | Phos Select | 20                       | OT Velos  | 20                                         | 5299                          | 408              | 15.9                     | 3.9                    |
| L23_4| IMAC          | Phos Select | 10                       | Orbitrap XL  | 10                                         | 366                           | 20.4             | 5.6                      |                        |
| L23_6| IMAC          | Phos Select | 20                       | OT Fusion    | 20                                         | 12,402                        | 2114             | 236.5                    | 11.2                   |
| L23_5| IMAC          | Phos Select | 2                       | OT Fusion    | 2                                          | 10,181                        | 972              | 110.8                    | 11.4                   |

1- Number of phosphopeptides identified in the enriched sample. Average of triplicate analysis, Std. Dev. and %CV shown when available.
Fig. 1. Results of the analysis of PME11 samples reported by the different laboratories participating in the study. A) Number of phosphopeptides from each analysis. Each bar represents the average number reported, the error bars being the standard deviation of triplicate analysis performed in the same laboratory (when available). Columns are colored according to the MS instrument used for the analysis, as indicated in the legend. Results are grouped by the type of affinity enrichment used (TiO₂, IMAC). L25–2 corresponds to a two step sequential enrichment TiO₂-IMAC. The black points indicate the corrected number of phosphopeptides weighed by instrument performance (see text). B) Box and whisker plot summarizing the raw and weighed number of phosphopeptides data. C) Selectivity of the phosphopeptide enrichment measured as the % of phosphopeptides in the enriched sample. Results are shown in the same order as in Fig. 1A.
described demonstrate that the standard proposed in this study is a suitable reference material for the assessment and optimization of phosphoproteomic analysis and certainly provide valuable information to dig deeper into the pros and cons of phosphoproteomics workflows.

Data availability

No

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jprot.2021.104409.

References

[1] M.A. Jünger, R. Aebersold, Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic, Wiley Interdiscip. Rev. Dev. Biol. 3 (1) (2014 Jan-Feb) 83–112, https://doi.org/10.1002/wdev.121. Epub 2013 Jul 2, 24902836.
[2] J.V. Olsen, M. Mann, Status of large-scale analysis of post-translational modifications by mass spectrometry, Mol. Cell. Proteomics 12 (12) (2013 Dec), https://doi.org/10.1074/mcp.M113.034181, 3444-52. Epub 2013 Nov 1, 24187339. PMC3861698.
[3] W. Qiu, C.A. Evans, A. Landels, T.K. Pham, P.C. Wright, Phosphoprotein enrichment for phosphoproteomic analysis - a tutorial and review of novel materials, Anal. Chem. Acta 1129 (2020 Sep 8) 158–180, https://doi.org/10.1016/j.aca.2020.04.053. Epub 2020 Apr 28, 32891386.
[4] M.R. Hoopmann, U. Kusebauch, M. Palmblad, N. Bandeira, D.D. Stheyenberg, L. He, B. Xia, S.H. Stoychev, G.S. Omenn, S.T. Weintraub, R.L. Moritz, Insights from the first phosphopeptide challenge of the MS resource pillar of the HUPO human proteome project, J. Proteome Res. 19 (12) (2020 Dec 4) 4754–4765, https://doi.org/10.1021/acs.jproteome.0c00648. Epub 2020 Nov 9. PMID: 33166149; PMCID: PMC8204901.
[5] X. Yue, A. Schunter, A.B. Hummon, Comparing multistep immobilized metal affinity chromatography and multistep TiO2 methods for phosphopeptide enrichment, Anal. Chem. 87 (17) (2015 Sep 1) 8837–8844, https://doi.org/10.1021/acs.analchem.5b01855. Epub 2015 Aug 11, 26237447. PMC4766865.
[6] T.E. Thingholm, M.R. Larsen, Sequential elution from IMAC (SIMAC): an efficient method for enrichment and separation of mono- and multi-phosphorylated peptides, Methods Mol. Biol. 1355 (2016) 147–160, https://doi.org/10.1007/978-1-4939-3049-4_10. 26584924.
[7] V. Vialas, N. Colomé-Calls, J. Abian, K. Aloria, G. Alvarez-Llamas, O. Antúnez, J. M. Arizmendi, M. Azkargorta, S. Barceló-Batlori, M.G. Bardeno, F. Blanco, J. I. Casal, V. Casas, C. de la Torre, E. Chichano-Galvez, F. Elortza, G. Espadas, J. M. Estanyol, J. Fernandez-Irijoyoy, P. Fernandez-Fuente, M.J. Fidalgo, M. Fuentes, M. Gay, C. Gil, A. Hainard, M.L. Hernaez, N. Barrola, A.T. Kopylov, A. Lario, J. A. Lopez, M. Lopez-Lucardo, M. Marcilla, A. Marina-Ramírez, G. Marko-Varga, L. Martin, M.I. Mora, E. Morato-Lopez, J. Muñoz, M.A. Odena, E. de Oliveira, I. Oren, I. Orteo, C. Pasquazuelo, K.B. Ray, M. Rezeli, I. Ruppen, E. Sabidó, M.M. S. Del Pino, J. Sancho, E. Santamaría, J. Vazquez, M. Vilaseca, F. Vivanco, J. J. Walters, V.G. Zgoda, F.J. Corrales, F. Canals, A. Paradela, A multicentric study to evaluate the use of relative retention times in targeted proteomics, J. Proteome 152 (2017 Jan 30) 136–149, https://doi.org/10.1016/j.jprot.2016.10.014. Epub 2016 Oct 29, 27989941.
[8] A. Campos, R. Díaz, S. Martínez-Bartolomé, J. Sierra, O. Gallardo, E. Sabidó, M. López-Lucardo, J. Ignacio Canal, C. Pasquazuelo, A. Scherl, C. Chiva, E. Borras, A. Odena, F. Elortza, M. Azkargorta, N. Barrola, F. Canals, J.P. Albar, E. Oliveira, Multicenter experiment for quality control of peptide-centric LC-MS/MS analysis - A longitudinal performance assessment with nLC coupled to orbitrap MS analyzers, J. Proteome Res. 19 (12) (2020 Dec 4) 4754–4765, https://doi.org/10.1021/acs.jproteome.0c00648. Epub 2020 Nov 9. PMID: 33166149; PMCID: PMC8204901.
[9] J.P. Albar, F. Canals, Standardization and quality control in proteomics, J. Proteome Res. 19 (3) (2020 Dec 1) 1–12, https://doi.org/10.1021/acs.jprot.10.002. 24275454.
[10] S.M. Mische, N.C. Fisher, S.M. Meyn, K. Sol-Church, R.L. Hegstad-Davies, F. Weis- Garcia, M. Adams, J.M. Ashton, K.M. Delventhal, J.A. Dragon, L. Holmes, P. Jagtap, K.E. Kubow, C.E. Mason, M. Palmblad, B.C. Searle, C.W. Turk, K. L. Knudtson, A review of the scientific rigor, reproducibility, and transparency studies conducted by the ABRF research groups, J. Biomed. Tech. 31 (1) (2020) Apr 11–26, https://doi.org/10.7171/jbt.20-3101-003. PMID: 31969795; PMCID: PMC6959150.