Reply to Comment on ‘Analysis of decay chains of superheavy nuclei produced in the $^{249}$Bk + $^{48}$Ca and $^{243}$Am + $^{48}$Ca reactions’

To cite this article: V B Zlokazov and V K Utyonkov 2019 J. Phys. G: Nucl. Part. Phys. 46 018002

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Reply to Comment on ‘Analysis of decay chains of superheavy nuclei produced in the $^{249}$Bk + $^{48}$Ca and $^{243}$Am + $^{48}$Ca reactions’

V B Zlokazov and V K Utyonkov

Joint Institute for Nuclear Research, RU-141980 Dubna, Russian Federation

E-mail: utyonkov@jinr.ru

Received 2 August 2018, revised 5 October 2018
Accepted for publication 14 November 2018
Published 22 November 2018

Abstract

Forsberg and Leino (2019 J. Phys. G: Nucl Part Phys 46 018001) question the validity of criticism (2017 J. Phys. G: Nucl. Part. Phys. 44 075107) of the method proposed by Forsberg et al (2016 Nucl. Phys. A 953 117). In this reply, we show that this method is based on unclear principles and its implementation leads to the results that contradict the conclusions following from mathematical statistics.

In a paper by Forsberg et al [1], a new method was suggested for statistical treatment of decay times of nuclei in the decay chains arising in the decay of parent nucleus. A Figure-of-Merit (FoM) was proposed as a probability density function for the decay times of nuclei:

$$f(t) = t(N - 1) \frac{(N\tau)^{N-1}}{\Gamma(N\tau + t)^N} \sim t/(N\tau + t)^N,$$

where $t$ stands for individual decay times observed in $N$ decays of nucleus ($N > 1$) and $\tau$ is an average lifetime determined from $N$ measured values of $t$ [1]. Function $f(t)$ reaches maximum at $t \approx \tau$ and $f(t) \to 0$ at $t \to 0$ and at $t \to \infty$. In an attempt to analyze simultaneously the decay times of all of the nuclei in the chain, the authors calculate the FoM$_{1-3}$ values which correspond to individual decay times of nuclei in the three-step decay chain. From the calculated FoM$_{1-3}$ values, their geometrical mean values FoM$_{\text{geom}}$ were calculated for each chain. Then, the arithmetic mean of FoM$_{\text{geom}}$ (FoM$_{\text{ar}}$) over all of the $N$ chains was calculated for the total data set.
To compare the FoMar value, calculated from experimental data, with at least some a priori unknown value, the same procedure was repeatedly performed for simulated decays that were generated using the Monte Carlo method with lifetimes calculated from the experiment. The resulting distribution of FoMar values from such simulation was used to determine the interval within which the simulated values are located with a probability of 90%. Thus, 5% of chains with the lowest FoMar values and 5% of chains with the highest ones are rejected.

We have doubts about the applicability of this method for several reasons:

1. Most important, the results of application of the method of [1] disagree with conclusions (see [2]) following from traditional methods of mathematical statistics whose reliability was proven for many decades. In these methods, the decays of each nucleus in chains are treated separately because decay times of parent and descendant nuclei do not depend on each other.

2. Physical and mathematical principles of the FoM value construction are not clarified; this raises questions on the validity of steps chosen in [1, 3] for calculating the final FoMar value: Why is the chosen order of calculating firstly geometric mean for each chain and then arithmetic mean of FoM values better than any other combination of these values, for example, geometric and arithmetic means in reverse order or calculating only geometric (or arithmetic) mean in both steps of data treatment?

3. The principal rule of the radioactive decay of nuclei is that the decay time of the daughter nucleus does not depend on the decay time of the mother nucleus (Markov property). However, multiplying the probabilities of observing the decay times of nuclei, in the calculation of geometrical mean, and analyzing only their (smoothed) product violates the principle of independence of the decay times of each of the nuclei in a chain. For example, a decay chain may match the confidence interval if it begins with, e.g., decay time of nucleus leading to high FoM \(t_1 \approx \tau_1\), but is followed by nuclei with decay times substantially different from their lifetimes which results in low FoM values \(t_2 \gg \tau_2\) or \(t_2 \ll \tau_2\), see (1)).

4. The largest FoM values which correspond to the most likely decay times are outside the interval proposed in [1]. Questions arise again: Why the most probable decay time values \(t \approx \tau\) do not fall into the chosen confidence interval? Why the upper limit of the FoMar interval is not determined by its maximum possible value but is chosen from the 5% part of the FoMar distribution?

5. Forsberg and Leino dispute doubts we express concerning their method which doubts are based on the fact that only 2 of the 38 FoM_{1-3} values fall within the 90% confidence interval (CI) [1]. In response, one can make simple calculations. The arithmetic mean of FoM_{geometric} values and one standard deviation (SD) are 0.162 and 0.101, respectively (CI is 0.061–0.262); 7 of the 14 individual FoM_{geometric} values fall into this interval. On the contrary, according to the method [1], only 4 out of the 14 values fall into the CI of 0.181–0.255 which corresponds to the 90% confidence level. For data obtained independently at TASCA and BGS, FoMar = 0.177, one SD = 0.101, CI = 0.075–0.278; again 50% of the FoM_{geometric} values satisfy this CI, however, only 2 of the 10 values fall into the CI calculated for 90% confidence level in [1]. These calculations demonstrate a discrepancy between the method [1] and the above values FoMar which are based on experimental decay times.

6. Application of the same method in [3] results in a conclusion by Forsberg et al.: ‘the evaluation of the congruence of the first four short element 115 chains fails the hypothesis of a single radioactive source with >95% confidence level’, ‘adding the three short chains from the LBNL experiment and, further, the seven short chains from the GSI
experiment into the statistical analysis, the hypothesis of a common origin of all 14 chains can be rejected on a >99% confidence level’, ‘the hypothesis that the ten short element 117 chains form one common sequence must also be rejected on a >95% confidence level’, ‘the ten element 117 chains together with the four element 115 chains from Dubna do not, on a close to 100% confidence level, form a common ensemble’, ‘adding the [three Dubna] chains, to the ten element 117 chains does not, with a confidence level of >99%, produce a congruent data set’. However, examining the relations shown in figure 2 of [2] is enough to be sufficiently convinced in the ambiguity of all of the above statements.

Finally, the sentence by Forsberg and Leino reads ‘The non-congruence is seen only when entire decay chains are considered’. However, it seems to us that without a strong justification of the initial basic principles of the method and its reliability, the discussion of the results of its use does not make sense.

Acknowledgments

We acknowledge the support by the JINR Directorate grant and the RFBR Grant No. 16-52-55002.

ORCID iDs

V K Utyonkov © https://orcid.org/0000-0003-2766-4766

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