Reply to "Comment on 'Pre-equilibrium particle emission and critical exponent analysis'"

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We reply to the preceding comment. [S0556-2813(97)02001-3]

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The preceding Comment criticizes our paper [1], pointing out that the two branches for \( \ln M_2 \) vs \( \ln |m - 26| \) are not exactly parallel in our model (see Fig. 2 in [1] and Fig. 1 in the preceding Comment). This is indeed true. However, the authors of the Comment then claim that the only meaningful comparison to their data can be made by using their \( \gamma \)-matching procedure to determine \( m_c \). There we disagree. We show below that the assumptions entering the \( \gamma \)-matching procedure are questionable and not supported by the data. This is why we did not use this procedure in our paper [1], but instead used the cut value of \( m_c = 26 \) used by Gilkes et al. [2].

Let us look at all available data of the average value of the second moment of the charge distribution, \( M_2 \), for each total charged particle multiplicity bin \( m \). This is done in Fig. 1, where the data [2–4] are represented by circles with their statistical error bars indicated. The upper branch is obtained by computing \( M_2 \) for all fragments, and the lower one by ignoring the largest fragment in each event.

Attempting to extract signatures of critical behavior, the authors of the preceding Comment and of Ref. [2] now assume that there is one unique value of the total multiplicity \( m_c \) which corresponds to the critical temperature. In inclusive data where different remnant sizes are present in different events, this assumption probably is not correct, and it is also not supported by our calculations.

Since for infinite systems in the vicinity of the critical point the second moment of the cluster size distribution scales as \( M_2 = N(T - T_c)^{-\gamma} \), Gilkes et al. fit power laws to their data of \( M_2 \) vs \( |m - m_c| \). Studies based on the percolation model [5] indicate that values of \( m \) too close to \( m_c \) are contaminated by finite size effects. Therefore the authors of [2] use lower and upper boundaries in multiplicity on the "gas" and on the "liquid" sides for their two fit intervals. We will call these parameters \( m_{g1}, m_{g2}, m_{l1}, \) and \( m_{l2} \) (compare Fig. 1). In addition, the normalization of the power laws on the "liquid" and the "gas" sides, \( N_l \) and \( N_g \), are also free parameters of the fit. They then adjust these seven fit parameters \( (m_c, m_{g1}, m_{g2}, m_{l1}, m_{l2}, N_l, \) and \( N_g) \) for their power laws in such a way that the exponents on the "liquid" and the "gas" sides have equal value. The result of this fit is indicated by the solid line in Fig. 1.

In our papers [1,6] we have tried to point out that there are several problems associated with this fitting procedure. The most obvious, however, can be directly seen from Fig. 1: The functional form of the data is really not a power law. Only in the (very limited) multiplicity intervals that the power law is fit to can one get a somewhat reasonable reproduction of the data with this fit.

We also note that scaling should only hold in the vicinity of the critical point, and not far away from it. By using the fit boundaries above and summing the counts in each multiplicity interval [3], we find that 53% of all events were considered close enough to the critical point by the authors of Ref. [2]. This seems highly unlikely.

The insistence of the authors of the preceding Comment...
and of [2] on the power-law shape is not borne out by their data, but comes from theoretical prejudices. Some of these have been formed, by the way, by using a percolation model [5]. However, in [5] a percolation lattice of 216 sites is used. This is not adequate here, because only between 78 and fewer than 50 charges are in the decaying remnant. In our work, by contrast, we use an ensemble of different numbers of percolation sites, obtained from the number of charges in the remnant as calculated from an intranuclear cascade [1]. This mixing of different remnant sizes is essential.

The histograms in Fig. 1 show the result of our INC/percolation model [1]. As can be seen, the agreement between theory and experiment is rather astonishing. In particular, the histogram for the upper branch is almost completely covered by the data points.

In the preceding Comment the authors argue that any theoretical analysis that does not adhere to the power-law fitting procedure employed in [2] is irrelevant for the description of the data. In [1] and in this present reply we believe to have shown that this fitting procedure itself is not adequate. It seems to us that the reader can decide from Fig. 1 which leads to a more accurate representation of the data, our model calculation (histogram) or the power-law fit of Gilkes et al. (solid line).

Finally, we would like to stress that we agree with the authors of the preceding Comment on one extremely important point: The data set shown in Fig. 1 contains a subset of events which have probed the critical point of a second-order multifragmentation phase transition. This gives much hope for future excitement in this field.