

Dimer versus tetramer

Dear Sir:

We see no convincing evidence in favor of an aggregational model for the gramicidin channel, and find the evidence in favor of a (generalized) dimer model to be overwhelming. Many of the arguments were summarized or discussed by Cifu et al. (1992); here we wish to make three points.

(a) From the distribution of single-channel current transition amplitudes it can be concluded that gramicidin channels have a single predominant conformation, i.e., being either dimers or tetramers (or another oligomer of defined molecular-ity) but not some less defined aggregate (cf. Andersen et al., 1987; Sawyer et al., 1989; Cifu et al., 1992).

(b) In hybrid channel experiments, one sees at most two hybrid channel types (Apell et al., 1977; Veatch and Stryer, 1977; Andersen et al., 1988; Cifu et al., 1992), and the hybrid channel appearance rates and energetics are consistent with the formation of dimers but not with the formation of tetramers (Veatch and Stryer, 1977; Durkin et al., 1990). These results can only, with serious difficulties, be reconciled with any type of lateral aggregation model.

(c) Both the relaxation kinetics and the sequence-dependent changes in channel-forming potency can be accounted for by a generalized dimer model (Becker et al., 1991; Cifu et al., 1992). In contrast, it is not clear how to reconcile the very different single-channel durations of [Val¹]gramicidin A and malonyl-bis-gramicidin channels (cf. Bamberg and Janko, 1977) with similar relaxation behaviors reported by Stark et al. (1986). That the malonyl-bis-gramicidin sample used by Stark et al. gave rise to several classes of channel events suggests contamination.

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