# 生物物理学 II　Handout No. 1

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**Table 3.1**
**Functional classification of voltage-activated calcium channels and corresponding clones of α subunits**

| Type[a] | Threshold[b] | Inactivation | Clone | Alternative designation | Tissue source |
|---|---|---|---|---|---|
| *T* | LV | Yes | — | — | — |
| L | HV | No | S | CaCh1 | Skeletal muscle |
| — | — | — | Ca, Cb[c] | CaCh2a, CaCh2b | Brain and heart |
| — | — | — | D | CaCh3 | Brain |
| P | HV | Slow | A | CaCh4 | Brain |
| Q | HV | Slow | — | — | — |
| N | HV | Yes | B | CaCh5 | Brain |
| R | HV | No | E | CaCh6 | Brain |

[a] Designations T, L, and N originally meant **T**ransient, **L**ong-lasting, and **N**either T nor L; P refers to **P**urkinje cells.
[b] HV and LV indicate high-voltage and low-voltage thresholds for opening.
[c] Lowercase designations a and b indicate splice variants.

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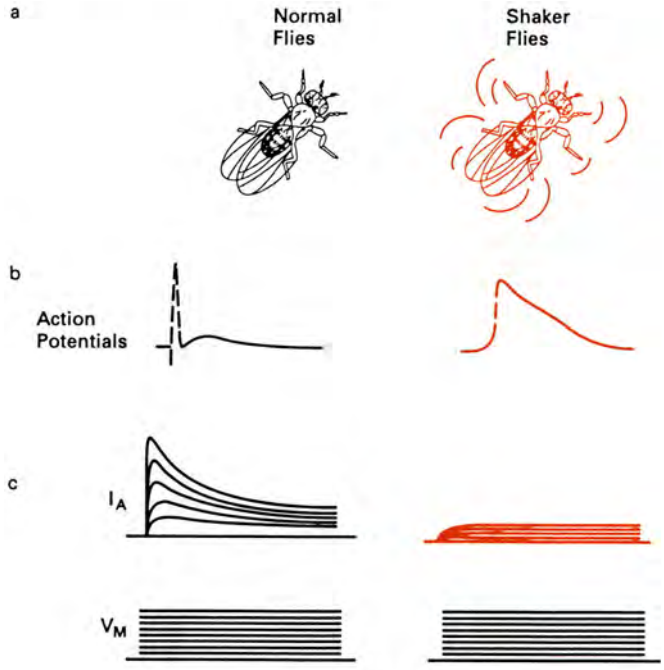


FIGURE 5-7. The Shaker mutation. Action potentials (b) and potassium currents (c) in normal and Shaker flies (a) (from the work of Mark Tanouye, Larry Salkoff, Bob Wyman, and their colleagues).

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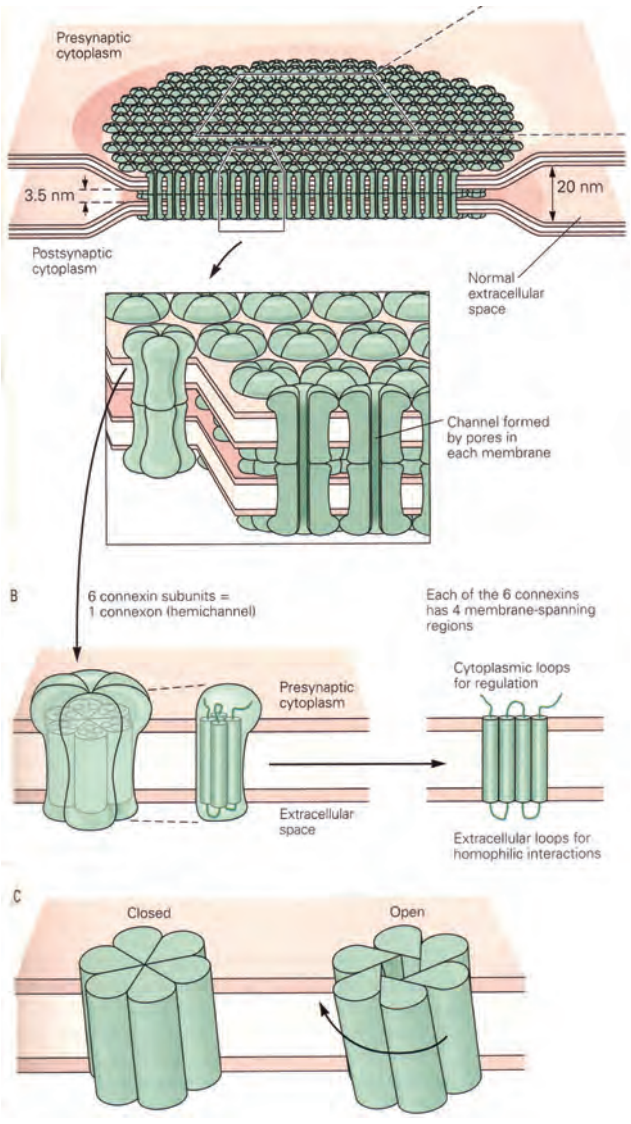


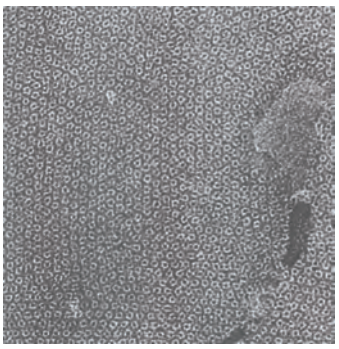

Figure 10-4 A three-dimensional model of the gap-junction channel, based on X-ray and electron diffraction studies.
A. At electrical synapses two cells are structurally connected by gap-junction channels. A gap-junction channel is actually a pair of hemichannels, one in each apposite cell, that match up in the gap junction through homophilic interactions. The channel thus connects the cytoplasm of the two cells and provides a direct means of ion flow between the cells. This bridging of the cells is facilitated by a narrowing of the normal intercellular space (20 nm) to only 3.5 nm at the gap junction. (Adapted from Makowski et al. 1977.) Electron micrograph: The array of channels shown here was isolated from the membrane of a rat liver. The tissue has been negatively stained, a technique that darkens the area around the channels and in the pores. Each channel appears hexagonal in outline. Magnification x 307,800. (Courtesy of N. Gilula.)
B. Each hemichannel, or connexon, is made up of six identical protein subunits called connexins. Each connexin is about 7.5 nm long and spans the cell membrane. A single connexin is thought to have four membrane-spanning regions. The amino acid sequences of gap-junction proteins from many different kinds of tissue all show regions of similarity. In particular, four hydrophobic domains with a high degree of similarity among different tissues are presumed to be the regions of the protein structure that traverse the cell membrane. In addition, two extracellular regions that are also highly conserved in different tissues are thought to be involved in the homophilic matching of apposite hemichannels.
C. The connexins are arranged in such a way that a pore is formed in the center of the structure. The resulting connexon, with an overall diameter of approximately 1.5-2 nm, has a characteristic hexagonal outline, as shown in the electron micrograph in A. The pore is opened when the subunits rotate about 0.9 nm at the cytoplasmic base in a clockwise direction. (From Unwin and Zampighi 1980.)