

PRELIMINARY NOTE
APPARENT SIMILARITY IN PROTEIN COMPOSITIONS OF MAXIMALLY
DEVIATED CANCER CELLS

GILBERT N. LING and R. C. MURPHY

Department of Molecular Biology, Pennsylvania Hospital, Eighth and Spruce Streets, Philadelphia, Pennsylvania 19107

Using SDS gel electrophoresis, we examined the total protein contents of 14 types of mouse cancer cells (Kreb's, **Reif-Allen**, **P815**, **Hepatoma** 134, **P4132**, LSA, TA3, **L1210**, **P1081**, Ehrlich, Meth. A, 15091A, Sarcoma 180, **T241**) and 5 types of rat cancer cells (Walker 256, Yoshida **hepatoma**, Novikoff, **AS30**, Dunning leukemia). We then compared those contents with the cellular protein contents of normal mouse and rat tissues (brain, muscle, liver, spleen, heart, lung, nerve).

The results show, on the one hand, much similarity in the kinds and amounts of proteins from the various types of cancer cells although they derived originally from widely different tissues. On the other hand, great diversity is seen among the proteins from normal cells, as to be expected. Eight of the major polypeptide bands seen in all cancer cells studied gave apparent molecular weights of 34,000, 36,900, 46,100, 49,800, **57,000**, **59,200**, **69,600** and 92,500 daltons respectively. All the cancer cells were what **Potter**¹ calls "maximally deviated" as indicated by their **very** short transplantation time (i.e., one **week**).

Our findings, to be fully described elsewhere, extend and are in harmony with the **conclusions** of **J. Greenstein**^{2,3} from his studies of one special kind of protein, the enzymes. These he found different in normal tissues but more alike in the cancer cells he studied.

The present results suggest that cancer may indeed represent a cellular change to either a single ontologically earlier totipotent state or to a single new totipotent state. In either case, apparently actively transcribed genes specific to their parent normal tissues are shut off and a specific assembly of genes common to all cancer cells is transcribed to produce highly similar if not identical cancer cells regardless of their ancestry. □

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REFERENCES

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