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Heidelberg Plenary Lecture Tuesday August 30, 1994.

Angiostatin: A novel protein by which primary tumors

suppress growth of metastases.

This well organized meeting with its many very exciting titles to be presented, symbolizes one of the unique distinctions of the field of vascular biology in general and of angiogenesis research in particular:

. there is an immense collegiality among ar researchers in these fiel

And one hears in the coffee breaks and at meals, . . . a certain shared enthusiasm for someone else's new finding: "A ha! So that's the explanation!"

There are explanation!"

One include few scientific fields with the comraderie of this one, with the possible exception of those happy souls who study

C. elegans, and chatter to each other in their weekly "Worm Lover's Journal," about their latest discoveries.



So, in that spirit, I wish to tell you about a new finding, in fact on the eve of its publication, . I one that I began to think about 4 years ago, followed by 3 years of experimental work with Michael O'Reilly who came as a post-doc. I presented the outlines of this work in an unfinished form, at a Keystone meeting last February, and now wish to show you how it turned out.

Virtually all solid tumors are angiogenic and neovascularized by the time they are detectable in animals and humans. But, when they first originate, most tumors are not angiogenic, and in humans, carcinoma in situ angiogenic for months to years!

Thus, a central problem in tumor growth is how tumor cells switch to the angiogenic phenotype!

In the early 1980s, when the first POSITIVE regulators of angiogenesis were purified, it was thought that the "switching problem" could be understood solely in terms of the behavior of these polypeptides, puch (FGF, and later VEGF, etc).

For example, If one just knew <u>enough</u> about how bFGF was exported out of cells etc, one would eventually know how tumors switched ON angiognesis and <u>kept</u> it ON, when <u>normally</u> it was such a rare and

Slide 34: (diagram of sequence)

Bill Lawret flared

Microsequence analysis revealed that the protein is homologous to an internal <u>fragment</u> of **plasminogen**, specifically a fragment of the A-chain of plasmin with an N-terminus at amino acid 98 and a carboxy terminus at approximately amino acid 440.

-(This fragment inhibits endothelial cells, but full-length plasminogen does not). We named it "ANGIOSTATIN")

[These results were obtained for 2 separate purifications by N-terminal analysis and by analysis after tryptic digest, by Bill Lane at Harvard's dept of biochemistry)

Slide 35: Angiostatin includes the first 4 triple loop structures, or "kringle" regions, of plasminogen].

[V = valine; Y = tyrosine; L = leucine; S = serine; E = glutamine; X = ? K = lysine].

Slide 36: (Commercial human plasminogen on SDS-PAGE)

When this was purified by several cycles of HPLC, it revealed 3