FLOW CYTOMETRY (FCM) OF TRANSURETHRAL RESECTIONS (TURPS) FROM PROSTATES WITH STAGE A CANCER.

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TURPs from 73 patients were analyzed to determine the technical feasibility and practical value of FCM. Archival specimens stored for up to 9 years were selected from a previous study in which the prostatic chips had been carefully fixed and embedded. Neoplastic and adjacent "normal" tissue from 34 prostatic specimens with stage A carcinoma were separated to create "cancer" and "matched" control groups, respectively. In addition, tissue from 39 TURPs without cancer comprised an "unmatched" control group. Chips containing intraepithelial neoplasia were excluded. Good quality histograms with mean coefficients of variation of 5.7 were obtained from 93% of samples. Abnormal DNA ploidy consisted solely of increased G2M. It occurred in 53% of cancers compared to 25% of matched and 3% of unmatched controls. Knowledge of DNA ploidy doubled the predictive value for progression (P) for clinical stage A2 tumors. The percentage of cells in G2M was statistically higher for "normal" tissue from prostates with cancer than for tissue from prostates without cancer, $p = 0.002$. This suggests that many prostate cancers may arise in an abnormal milieu rather than from a single clone of abnormal cells in a normal gland.

	#	FCM	↑G2M
Unmatched Controls	39	34	1
Matched Controls	34	32	8
Cancer	34	32	17

	#	↑G2M	P	DOD*
Stage A1	15	8	2	0
Stage A2	17	9	10	9

*DOD = dead of disease