Predictive Assays in Radiation Therapy

Radiation Biology

Lecture 4-23-2014

Outline

- Introduction
- Early predictive assays
- Recent trends in predictive assays
- Examples for specific tumors
- Summary

Introduction

- Absolute radioresistance does not exist: if a sufficiently high dose is delivered, all cells can be sterilized
- Radiation therapy objective is to optimize treatment for a higher probability of cure and minimal normal tissue damage
- Predictive assays are needed due to the potential role they could have in selecting individually tailored therapy course

Current clinical practice

- The radiation oncologist writes a prescription for
  - the total radiation dose in Gy
  - the dose per fraction
  - the number of fractions needed to deliver the total dose (and their temporal separation)
- These variables are mostly dictated by the primary site of disease, the histology and the stage of the cancer
- Geometrical factors are of utter importance: target should be fully covered, volume of exposed normal tissues minimized

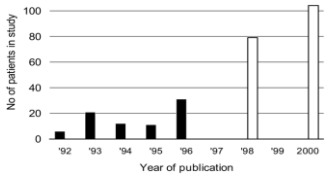
Biological factors determining tumor response to radiotherapy

- There are three widely acknowledged radiobiological factors involved in determining tumor response to radiotherapy:
  - Cellular radiosensitivity
  - Tumor hypoxia
  - Cell proliferation rate
- Studies suggesting the potential of all three as prognostic factors for radiotherapy

Cellular Radiobiology Assays

- Not only tumors, but also normal tissues of individuals, differ in their intrinsic radiosensitivity
- Correlation between cellular radiosensitivity of skin fibroblasts and severe reaction to radiotherapy in an individual with the genetic disorder ataxia telangiectasia (A-T) was initially discovered in 1975
- Several independent studies shown a correlation between the in vitro radiosensitivity of skin fibroblasts and the severity of late complications
- A promising predictive assay?

Cellular Radiobiology Assays



- In the early 1990s, 1 study per year was published (black bars), all of them showing a significant relationship between *in vitro* radiosensitivity of fibroblasts and late effects of radiotherapy
- Two large confirmatory studies (white bars) published in 1998 and 2000 showed no significant predictive value of this assay for late effects

Early predictive assays

- Inherent radiosensitivity for normal tissue side effects is predictive in only small subset of tumors
- Proliferation rate (doubling time) looked promising in many small studies but turned out not to be a significant predictor of radiotherapy outcome in a larger multi-center analysis of 476 patients with head and neck squamous-cell carcinoma (HNSCC)
- Only the Eppendorf microelectrode measurement of partial oxygen tension has consistently shown to have prognostic value, recently confirmed in a joint analysis of outcome after radiotherapy in 397 patients with HNSCC from 7 centers

New era of predictive assays

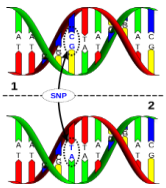
- The cellular-based assays lacked the sensitivity and specificity
- New opportunity emerged through the Human Genome Project (2001 – 2003)
- Accompanying development of new high-throughput techniques provide extensive capabilities for the analysis of a large number of genes

New era of predictive assays

- Molecular (biomarker) tests have the potential to be more robust, comprehensive, and capable of better standardization between centers
- These assays can be carried out in various clinical samples at the DNA (genome), RNA (transcriptome) or protein (proteome) level

DNA assays for normal tissue radiosensitivity

- It is now recognized that DNA mutations in a single or even a few genes are unlikely to be responsible for the patient-to-patient variability in sensitivity to radiation



- Single nucleotide polymorphisms (SNP) accounts for ~90% of the naturally occurring sequence variation within a population

Image from: http://en.wikipedia.org/wiki/Single-nucleotide_polymorphism

DNA assays for tissue response

- Work carried out to date exploring genotyping to predict normal tissue and tumor response to radiotherapy has involved a candidate gene approach
  - uses a priori knowledge of SNP and gene functions
- Such approaches require smaller sample sizes and benefit from reduced complexity by targeting relevant genes

RNA microarrays

- Gene expression microarrays provide the ability to monitor, rapidly and simultaneously, the RNA expression levels of thousands of genes or the whole genome
- Allows investigation of gene expression profiles associated with the radioresponse of tumors and normal tissues for the derivation of biomarkers to predict local control and toxicity after radiotherapy

RNA microarrays

Table 4 – Transcriptional response to irradiation

Reference	Cell/tissue	Gy	Time	Up-regulated genes*	Down-regulated genes*
[58]	Human lymphoblastoid	0.5	4 h	***STAT3***, *CAMKK2, SIRT1, CREM, MAPK13/7IP2, GPR56, CHD6, CRSP3, SNURF, CTR9, MZF*	*WASF2, LCP1, MSN, NIPSNAP1, KIF2C, MCM2, MCM3, MCM7, XRCC4*
[59]	Mouse bone marrow	6.5†	6 h	Jun, Bax, Apaf1, Ccng1, p21, Stat3	Rb1, Skt1, Ccne1, Cdk9, Cdk4, Cdk2, Mcm5, Mcm6, Rad1, Top2A, Top2B, Rad541, Pold2
[60]	Human fibroblasts	2	2 h	***GADD45A***, *BTG2, PCNA, IER5, CDKN1A, PPM1D, SERTAD1, PLK2, PLK3, BBC3, TP53INP1, SH2D2A, SLC1, GDF15, THSD1*	*CYR61, AMOTL2*
[61]	Rat hepatocytes	8	6 h	*Mif, Mdr1, Grb2, Prt1, Cabp2, Eif2a*	None detected
[62]	Human fibroblasts	3.5/3 × 3.5	2, 24 h	***TP53INP1, CDKN1A, DDB2,*** *SOD2, SOD3, CYP1B1, COL15A1*	*H2AX, TOP2A, CCNA2, EGR1, MMP3*
[63]	Mouse kidney	16	1–30 weeks	*Gulo, Klf5, Jag1, Ggps1, Pcm1, Xpo4, CyclinG, Tjc22d1*	*Slc22a7, Hba-a1, Syn1, Akp2*
[64]	Mouse rectum	16	1–30 weeks	*Klf5, Jag1, Xpo4,* ***RhoB***	*Hba-a1, Syn1, Akp2*
[65]	Bowel tissue	45–60	1–75 months	***RHOB,*** *CD47, MMP1, MMP3, MMP14, TIMP1, TINP2, IGFBP2, ERF1, POLA, CD27*	*TNF, ITGB4, EPHA1, DPP4, PTPRF*
[66]	Human lymphocytes	1.5–3†	6, 24 h	***CDKN1A, GADD45A, DDB2***	
[67]	Human lymphoblastoid	3, 10	1–24 h	***CDKN1A, GADD45A, DDB2,*** *TNFRSF10B, TNFRSF6, PIG3, FDXR, HSPCB, HSPE1, ATF3, PPM1D*	*CCNB1*
[68]	Human lymphoblastoid	5	4 h	***CDKN1A, GADD45A,*** *FAS, PCNA, CCNG1, MDM2*	*TNF, KIF23, MYC*
[69]	Human lymphoblastoid	1	4 h	*SRPK1, RENBP, TAN1, F2R, ETV3, MYB, MAPK1, CCNE1, MAPK3, HTR3A, TNK1*	*CSK, VEGFB, MT3, FLT3, DLK1, SFRP2, IGFHBP2, ICSBP1*

Genes highlighted in bold were up- or down-regulated in more than one study. *Selected genes — for full lists see reference. †Total body irradiation.

Proteomics and Tissue Microarrays

- The study of the function of all expressed proteins
- The promise of proteomics lies in the identification of biomarkers that could favorably affect disease diagnosis, as well as our ability to assess the response to treatment and, thereby, the prognosis
- Radioresistance-related proteins were identified in a proteomic study of pre-radiotherapy tumor biopsies from 17 patients with rectal cancer

Biomarker predictive assays

Table 3 – Large national/international genotyping studies

Study name	Full title	Planned recruitment	Primary	Based
Gene-PARE	Genetic Predictors of Adverse Radiotherapy Effects	>2000	Breast, prostate, head and neck	USA, Israel, France, Switzerland
GENEPI	GENEtic pathways for the Prediction of the effects of Irradiation	3000–4000	Breast, prostate, head and neck, rectal	Europe
RadGenomics	Japanese RadGenomics study	1071	Breast, cervix, prostate, head and neck	Japan
RAPPER	Radiogenomics: Assessment of Polymorphisms for Predicting the Effects of Radiotherapy	2200	Breast, prostate, gynaecological	UK

- Large studies are required with exploratory and validation cohorts of patients
- Tissue banks are being established with the aim of collecting tissue from cancer patients linked with high-quality outcome data—obtained generally within the context of clinical trials

Controversial observations

- Example: the tumor suppresser gene p53
  - Mutations of p53 generally lead to deregulation of cell cycle by eliminating the G1 checkpoint, and impairment of DNA repair process
- Reported to be associated with increased cellular resistance to irradiation and tumor relapse after therapy
- The loss of p53 also shown to either increase or not change radiosensitivity of cells
- Current trend: the p53 protein is analyzed in normal and tumor cells for its functional quality

Example: breast cancer

Table 1 Local and Regional Recurrence Rates by Breast Cancer Subtype

Study	n	Median Follow-up (mo)	Luminal A (%)	Luminal B (%)	HER2 (%)	Basal (%)
BCS + RT (Nguyen[19])						
5-year LR	793	70	0.8	1.5	8.4	7.1
BCS + RT (Millar[17])						
5-year LR	498	84	1.0	4.3	7.7	9.6
5-year LRR			2.0	4.3	15.3	14.8
BCS + RT (Voduc[18])						
10-year LR	1461	144	8	10	21	14
10-year RR			3	8	16	14
Mastectomy + RT (Kyndi[20])						
5-year LRR	489	204	2	3	13	21
Neoadjuvant chemotherapy + BCS + RT (Yu[16]) 5-year LRR						
0-3 LN	514	65	2	2	14	9
≥4 LN	77		7	0	34	44

Abbreviations: BCS, breast-conserving surgery; LR, local recurrence; LRR, local-regional recurrence; RR, regional recurrence; LN, lymph node.

- At least 4 biologically distinct molecular subtypes of breast cancer were identified, which correlated to different clinical outcomes: luminal A (ER+, and/or PR+, HER2-), luminal B (ER+, and/or PR+, HER2+), HER2+(ER-, PR-, HER2+), and basal-like (ER-, PR-, HER2-)
- Drugs developed for ER+/PR+, and HER2+ patients make these subtypes easier to manage (tamoxifen, and trastuzumab or Herceptin)

Example: breast cancer

- A study published by van't Veer et al. (2002) described a 70-gene signature derived from a DNA microarray analysis of 78 young patients with BC that was associated with a short interval to distant metastases
- The study was validated on a separate population of patients
- Later 76-gene classifier was developed in a similar group of patients by researchers from the Erasmus University in Rotterdam
- Unfortunately the 70- and the 76-gene signatures show relatively little overlap in terms of the genes selected: only 3 genes are common

Example: breast cancer

- Normal tissue complication studies
- Andreassen et al assessed 17 specific SNPs in TGFB1, SOD2, XRCC1, XRCC3, and APEX in 41patients receiving postoperative radiotherapy for breast cancer and found that 7 of these were associated with a significantly ($p<.05$) increased risk of developing severe subcutaneous fibrosis
- Later analysis showed that only a single one of these (XRCC3 codon 241 Thr/Met) remains significant

Example: HNSCC

- The EGF-signaling pathway is of potential importance in radiation oncology because of its involvement in orchestrating the proliferative response of epithelial tumors to fractionated radiotherapy
- EGFR (epidermal growth factor receptor) has been identified as oncogene
- A large randomized phase III trial has shown that cetuximab, a monoclonal antibody against EGFR, significantly improves radiation therapy outcome in HNSCC

Current (2002) status of various predictive assays

Assay	Brief description	Status (under study/clinical applicable)
Tumour clonogenic survival (SF_2)	♦ Proof of reproductive integrity, usually in semi-solid agar supplemented with growth factors ♦ Assay of fresh tumour biopsies	Clinical
Tumour growth assay (CAM)	♦ Assay of fresh tumour biopsies for fibronectin- coated plates, using crystal violet	Clinical
Chromosome aberrations (PCC & FISH)	♦ Target cells fused with mitotic cells ♦ Assessment of interphase chromosome malformations	Study
Micronucleus assay	♦ Acentric fragments or aborted whole chromosomes detected by Cytokinesis-block method	Clinical
Apoptotic assay	♦ Quantitative index of radiation injury: Apoptotic body or fragments	Study
Oncogene expression	♦ Alteration in either expression or function of cellular genes like c-erb B-2, p53 expression, ras gene, p21 product, c-myc oncogene	Study/Clinical
BUdR labelling index	♦ Fresh tumour biopsy incubated with BUdR and analysed by flow cytometry	Clinical
Growth Fraction	♦ Heat processed immunostaining with MIB1	Clinical
pMI	♦ Ratio of the Mitotic cells to Ki-67 positive cells	Study/Clinical
Mn-SOD	♦ Paraffin section, Immunostaining with anti-Mn-SOD antibody	Study

Current (2002) status of various predictive assays

Assay	Brief description	Status (under study/clinical applicable)
Serial Cytology	♦ Real time assay; evaluation of nuclear changes (micro- or multinucleation)	Clinical
Lymphocyte clonogenic survival	♦ Separation of peripheral blood sample and lymphocyte cultured in medium supplemented with PHA and IL2	Clinical
Microvessel density (MVD)	♦ Evaluation of tumour specimens using a variety of stains (CD31, factor VIII)	Clinical
DNA dsb rejoining assay by Pulsed Field Gel Electro-Phoresis (PFGE)	♦ Estimation of amount of residual DNA double strand breaks	Clinical
Biochemical	Determination of thiols (GSH, CySH) in tissue and plasma	Study/Clinical
Polarographic pO_2 Measurement	♦ Microelectrode sequentially moved through tissue	Clinical
Markers	♦ Nitroimidazole binding in hypoxic cells, detected by immunohistochemistry or physical method (eg PET)	Clinical
Comets	♦ DNA breaks are enhanced by O_2	Study/Clinical

Technical aspects and costs (2002)

Method	Technical difficulties	Grade of difficulties (high/low)	Time to obtain results (days)	Initial cost (US$)	Running cost per sample (US$)
Tumour clonogenic survival (SF_2)	Poor PE	high	28	32,000	200
CAM assay	Success rate 70%	high	21	32,000	400
Lymphocyte clonogenic survival	Success rate 95%	high	14	32,000	80
Chromosome aberrations (PCC & FISH)	Difficulty of fusion	high	15	36,000	1,000
Micronucleus assay	Not automated	low	7	27,000	20
Apoptotic assay		low	5	27,000	100
Oncogene expression	Reproducibility	low	1- 5	30,000	500
Growth Fraction (MIB1)		low	3	32,000	100
pMI		low	3	22,000	50
Mn-SOD		low	3	20,000	50
DNA dsb rejoining assay by PFGE	Requires a large tumour sample. Quantitation is complicated.	high	6–7	20,000 in a well equipped lab	50
MVD	no, success rate 100%	low	1 hour	16,000	16
Polarographic pO_2 measurement	Probe consistency, sterilisation, calibration	high	1 hour	80,000	200

Summary

- Very few prognostic markers and virtually no predictive assays have been established in routine clinical radiation oncology
- New approaches concentrating on biological markers as opposed to cellular assays are promising due to possibility of acquiring large datasets with controlled parameters
- It is still not possible to draw conclusions regarding the most appropriate biologic endpoints to use within clinical trials or provide a template for future studies

References

- Predictive assays and their role in selection of radiation as the therapeutic modality, IAEA, VIENNA, 2002
- C.M. L. West et al., Molecular markers predicting radiotherapy response: report and recommendations from an international atomic energy agency technical meeting, Int. J. Radiation Oncology Biol. Phys., Vol. 62, No. 5, pp. 1264–1273, 2005
- C.M. L. West , The Genomics Revolution and Radiotherapy, Clinical Oncology (2007) 19: 470-480
- S.N. Bentzen, From Cellular to High-Throughput Predictive Assays in Radiation Oncology: Challenges and Opportunities, Semin Radiat Oncol 18:75-88, 2008
- D.T. Miyamoto, J.R. Harris, Molecular Predictors of Local Tumor Control in Early-Stage Breast Cancer, Semin Radiat Oncol 21:35-42, 2011