Results: To date:
- 14 patients have completed treatment in a frame, 6 in a shell (2 more now on treatment)
- 494 fractions delivered, 478 (97%) are adequate for inclusion, corresponding to 3136 kV images.

Data is available from 158 fractions in shell patients.
- Post correction pre-treatment, translational errors are ⩾2 mm in 0/158 fractions
- Post treatment, errors are ⩾2 mm in 9/158 fractions.

Table: Systematic & Random errors

	Systematic errors						Random errors					
	Translational (mm)			Rotational (°)			Translational (mm)			Rotational (°)		
	Vert	Long	Lat	Yaw	Roll	Pitch	Vert	Long	Lat	Yaw	Roll	Pitch
Shell												
Pre-correction	0.23	1.71	1.30	1.53	0.38	1.08	0.85	1.05	0.72	0.63	0.85	0.90
Post-correction	0.08	0.25	0.21	0.28	0.13	0.16	0.21	0.21	0.26	0.28	0.21	0.24
Post-treatment	0.29	0.39	0.28	0.23	0.23	0.34	0.43	0.45	0.35	0.43	0.27	0.32
Post floor twist (1st 5 fractions)	0.45	0.47	0.35	0.37	0.16	0.45	0.38	0.23	0.28	0.34	0.22	0.22
Frame												
Pre-correction	0.42	0.60	0.30	0.24	0.34	0.37	0.40	0.54	0.42	0.29	0.21	0.22
Post-correction	0.07	0.13	0.07	0.08	0.05	0.09	0.22	0.18	0.17	0.16	0.11	0.20
Post-treatment	0.19	0.26	0.24	0.16	0.09	0.16	0.42	0.29	0.35	0.19	0.16	0.24
Post floor twist (1st 5 fractions)	0.17	0.22	0.25	0.14	0.11	0.19	0.31	0.25	0.20	0.19	0.14	0.19

Conclusion: Data is awaited from the final 2 patients but margin reduction is likely to be safe in shell-immobilised patients when using ExacTrac for daily online correction.

Poster Presentations (Sun, 25 Sep, 09:30–12:00)
Head and Neck Cancer

8520 POSTER

Podoplanin Regulates the Proliferation of Oral Squamous Cell Carcinoma Cells via Its Binding to Extracellular Matrix

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Background: We have already reported that podoplanin (PDPN), one of the representative immunohistochemical markers for lymphatic endothelial cells, is enhancedly expressed in carcinoma in-situ and squamous cell carcinoma (SCC) of the oral mucosa, though its pathophysiological function remains largely unknown. Our aim was to determine its molecular role in oral SCC cells, based on a hypothesis that PDPN plays an important role in SCC cell activities such as cell proliferation and migration.
Material and Methods: Surgical specimens of oral SCC were used for immunohistochemistry for PDPN and Ki-67. ZK-1 and the other two SCC cell systems as well as three ACC cell systems of salivary adenoid cystic carcinoma origin were used for in-vitro experiments. PDPN expression levels were determined by quantitative real-time PCR, western blotting, and immunofluorescence. Transient PDPN knockdown was performed with siRNA. Cell growth curves were compared between ZK-1 cells with or without PDPN knockdown or in the absence or presence of anti-PDPN monoclonal antibodies capable of selectively recognizing its cell surface domain. The apoptotic effect of PDPN knockdown in ZK-1 was analyzed by flow cytometry. Their cell attachment, migration, and invasion assays were also conducted by conventional methods using microplates, scratch wounding, transwells, and matrigel.
Results: Immunohistochemically, PDPN was characteristically localized in the peripheral cells of SCC foci where Ki-67 positive cells were simultaneously localized. PDPN was specifically expressed in SCC cells, especially in ZK-1, but not in ACC cells at mRNA as well as protein levels. The cell growth was significantly suppressed in PDPN-knockdowned ZK-1 cells, which was not always due to apoptosis (less than 5%) but rather due to the inhibition of cellular attachment in initial stages after plating in plastic dishes. ZK-1 cell growth was also significantly repressed in the anti-PDPN antibodies in the culture medium. In contrast, migration and invasion activities were not affected at all in ZK-1 cells knockdowned by siRNA for PDPN.
Conclusion: The findings indicated that PDPN functions in cell proliferation but not in migration or invasion of oral squamous cell carcinoma cells by binding with extracellular matrix molecules via its extracellular domain.

8521 POSTER

Novel Candidate Genetic Polymorphisms Identified in Genome-wide Association Study for Base of Tongue Squamous Cell Carcinoma Susceptibility

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Background: In head and neck, we have traditionally combined squamous cell carcinomas (SCC) of the oral cavity, oropharynx, larynx and hypopharynx in clinical treatment. However, with the advances in our understanding of molecular biology of cancer, the tumours that where once considered to be relatively homogenous diseases are now being recognized as comprising distinct subtypes. Inherited genetic alterations, such as single nucleotide polymorphisms (SNPs), were described in association with oropharyngeal cancer risk in only few reports. Base of tongue (BT) SCC are common tumours of oropharynx; however, the association of SNPs and BTSCC risk is still not clarified and, therefore, this was the aim of the present study.
Methods: DNA of 49 BTSCC patients and 49 controls was extracted using the Qiagen QIamp kit (Qiagen®). Each sample was genotyped individually using DNA high-resolution microarrays containing 500.568 SNPs (SNP array 5.0, Affymetrix®). Further sample processing, including digestion, adaptor ligation, amplification, fragmentation, labelling, hybridization, washing and scanning was assayed according to the standard protocol. Genotype data were acquired by genotyping calling of samples using the corrected robust linear model with maximum likelihood classification algorithm provided by Bioconductor software, as per the recommended guidelines. The differences between groups were analysed by the logistic regression model.
Results: We observed 6.609 SNPs with distinct frequencies between BTSCC patients and controls. 52 SNPs (0.8%) were located in coding sequence (CDS) of amino acids, 51 (0.8%) in 3′ and 5′ untranslated regions (UTR), 3.461 (52.4%) in up or downstream regions and 3.045 (46.0%) in introns. The SNPs were clustered to their main function, evidencing those localized in CDS, 3′- and 5′-UTR, related to cell cycle (*CHFR*, *COSMC*, *ERP29*, *IQCE*, *IRS2*, *KANK4*, *MAU2* and *USP2*), apoptosis (*ARHGEF18*, *CTSB*, *GFRAL*, *JMJD6*, *PIHID1*, *RAB6C* and *SPATA4*), DNA repair (*CCDC6* and *GEN1*), transcriptional process (*GCN2*, *MLL3*, *RPAD1*, and *ZNF415*), cell adhesion (*COL6A3*, *COL22A1*, *IKAP* and *KIND1*) and metastasis (*GCNT1*, *LARS* and *SYNJ2*).
Conclusions: Our preliminary results suggest that SNPs in genes involved in tumour origin and development may predispose individuals to BTSCC. However, these results should be confirmed by functional studies of coded proteins and validated in larger epidemiological studies.
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8522 POSTER

Human Papilloma Virus in Head and Neck Squamous Cell Cancer

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Background: Epidemiologic and molecular evidence have established the strong link between high risk types of human Papilloma virus (HPV) and a subgroup of head and neck squamous cell carcinoma (HNSCC). We evaluated the frequency of HPV positivity in HNSCC and its relationship to demographic and some risk factor variables in an open case-control study.
Materials and Methods: Fourteen newly diagnosed patients of squamous cell cancer of oropharynx, hypopharynx and larynx aged between 18–50 years were examined from 2008–2010 in Tabriz/Iran. HPV DNA was extracted from paraffin-embedded block of each patient for evaluating by PCR. Saliva samples of 94 control cancer-free subjects were collected for DNA analysis. Multivariable logistic regression method was used to calculate odds ratio for case-control comparisons.
Results: High risk HPV was detected in 6 (42.8%) of patients and 6 (5.3%) of control subjects, which statistically was significant ($p < 0.0001$). HPV-18 was the most frequent type both in the case and control group. HPV-16