available) were obtained at the time of surgical resection at Tokyo dental college Chiba Hospital after informed consent had been obtained from the patients according to a protocol that was approved by the institutional review board of Tokyo Dental College.
Result: Using quantitative real-time reverse transcription polymerase chain reaction, western blotting and immunofluorescence on seven OSCC-derived cell lines and NOKs, *Syk* mRNA and protein expression were commonly down-regulated in all cell lines compared with the NOKs. Although no sequence variation in the coding region of the *Syk* gene was identified in these cell lines, we found frequent hypermethylation in the CpG island region. Syk expression was restored by experimental demethylation. In addition, using a wound healing assay and in vitro invasion assay, we performed functional analysis using Syk transfected into the OSCC-derived cell lines, and they showed significant inhibition of motility and invasiveness. In clinical samples, high frequencies of Syk down-regulation were detected by immunohistochemistry (33 of 53 [62%]). Furthermore, the Syk expression status was correlated significantly ($P = 0.047$) with tumor metastasis to cervical lymph nodes.
Conclusion: These results suggest that the *Syk* gene is frequently inactivated during oral carcinogenesis and that an epigenetic mechanism may regulate loss of expression possibly leading to metastasis.

1335 POSTER

Vascular endothelial growth factor (VEGF) 936 C/T gene polymorphism is a risk factor for invasive ductal carcinoma of the breast in a sample of Croatian woman

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Cancer angiogenesis development mediatet thru vascular endothelial growth factor (VEGF) has important role in cancer metastasing and malignant growth. The aim of this study was to investigate potential relationship between VEGF gene 936 C/T polymorphism and coexistance of invasive ductal breast carcinoma in a sample of Croatian woman. In addition, there is no any data about described genetic polymorphism among Croatian feemale population. We enrolled two groups of feemale patients: 122 subjects with invasive breast carcinoma (mean age 54.1±4, range 36−81 years) and 156 healthy control subjects (mean age 57.4±6, range 32−75 years) without any history of malignancy in which the clinical evaluation including mammography and breast ultrasound did not reveal any breast pathology. Genomic DNA was isolated from peripheral venous blood, while single nucleotide polymorphism 936 C/T genotyping in the VEGF receptor was performed using PCR-RFLP methode. We have not detected any 936 T/T genotype of VEGF gene but significant association of breast cancer risk was shown in the group of woman with breast invasive ductal carcinoma compared to healthy group. Carriers of the 936 C/T genotype were more frequent among woman with invasive ductal carcinoma (46 of 122 examinies, 37.7%) than among control group (7 of 156 examinies, 4.5%). The difference was statisticaly significant ($p < 0.0001$). This study found significant evidence that examined gene polymorphism is a key factor associated with susceptibility to invasive ductal carcinoma of the breast in a sample of Croatian women.

1336 POSTER

The prognostic impact of serum angiogenic factors in renal cell carcinoma

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Background: To determine the selected serum angiogenic factors in patients with newly diagnosed renal tumor (RCC) and to correlate them with the clinical stage of the disease.
Patients: Nephrectomy or partial kidney resection was performed in 54 patients (34 men, 20 women) with newly diagnosed renal cell carcinoma (RCC). The mean age of patients was 64.4 years. The patients were divided into three groups based on the TNM classification: the 1st group – stages I + II, the 2nd group – stage III, the 3rd group – stage IV.
Method: The serum levels (collected before surgery) of GROα (CXCL1), IL-8 (CXCL8), IL-6, VEGF and bFGF were determined by the ELISA method. Clinical data (age, sex, tumor histopathology grading (HPG), disease progression and death during a-12-month follow-up period) were compared with serum levels of angiogenic factors. Kruskal-Wallis ANOVA, Mann-Whitney's test and Kolmogorov-Smirnov's test were used.
Results: In case of GROα, a significant difference was found between patients with and without progression period ($p = 0.006$), between surviving and dead patients ($p = 0.038$), between the1st and the 4th grade of HPG ($p = 0.05$), between the 2nd and the 4th grade of HPG ($p = 0.0043$) and between the 3rd and the 4th grade of HPG ($p = 0.044$). A statistically significant difference in serum concentration of IL-8 was found between patients with and without progression ($p = 0.007$), but no differences were found between the dead and surviving patients and between the various grades of HPG. A statistically significant differences in serum concentration of IL-6 were found between patients with and without progression ($p = 0.0006$) between dead and surviving patients ($p = 0.0042$), between the1st and the 4th grade of HPG ($p = 0.05$) and between the 2nd and the 4th grade of HPG ($p = 0.0041$). A statistically significant difference in serum levels of VEGF was found between patients with and without progression ($p = 0.0026$), between dead and surviving patients ($p = 0.021$). A statistically significant difference in serum levels of bFGF was found between dead and surviving patients ($p = 0.024$).
Conclusion: Out of the ten tested angiogenic factors, we found a correlation between serum levels and clinical findings for GROα, IL-8, IL-6, VEGF and bFGF. However, their use in clinical practice should be verified on a larger group of patients.
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1337 POSTER

Free light chains renal handling in patients with plasma cell dyscrasias

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Introduction: Serum immunoglobulin-free light chain (FLC) assay is a major marker in the evaluation and management of patients with plasma cell dyscrasias. In a number of these patients, anomalies in monoclonal FLC may induce tissue deposition and diseases, especially in kidney. We retrospectively analyzed the renal handling of FLC in different types of plasma cell dyscrasias.
Methods: K and L FLC concentrations were measured by nephelometry (Freelite ®, The binding site) in serum (s) and 24-h urine (u) from 85 patients. 11 patients had polyclonal hypergammaglobulinemia (H) but no monoclonal protein as detected by protein immunofixation electrophoresis (IFE) in serum and urine. 74 patients presented abnormal K/L FLC ratio (rFLC) in serum and/or urine. 22 of them had multiple myeloma (MM) with monoclonal intact immunoglobulin or FLC only, with K (MMK, n = 13) or L (MML, n = 9) light chain. 52 of them, without MM, had an increased (I) or a decreased (D) rFLC, and monoclonal protein detected by sIFE and/or uIFE.
Results: See the table.

	H	MMK	MML	I1	I2	D1	D2
CK ml/min	2.7 (0.6–6.6)	1.8 (0.9–12)	3.0 (1.9–12)	1.4 (0.4–7.3)	0.2 (0.1–0.4)$^{£}$	1.7 (0.4–4.9)	0.7 (0.2–3.9)
CL ml/min	0.6 (0.1–1.5)	1.2 (0.1–2.5)	0.8 (0.5–5.0)	0.2 (0.1–2.9)	0.1 (0.1–1.2)	0.8 (0.1–2.0)	0.02 (0.01–0.1)$^{\$}$
creatinine µmol/l	177 (112–461)	162 (63–559)	221 (72–799)	134 (60–730)	121 (61–278)	133 (64–474)	139 (60–220)

Values are median (ranges); Mann-Whitney test (significance: P < 0.05; *:MM vs H; $^{£}$: I1 vs I2; $^{\$}$:D1 vs D2).

In H, MMK and MML groups, comparable for glomerular filtration, renal clearance of K FLC (CK) and L FLC (CL) were similar indicating similar FLC renal handling in these patients with mono- or polyclonal diseases. I group was splited in 2 groups according to CK: in I2 (n = 11) as compared to I1 (n = 24) group, CK was decreased (P < 0.0001) and sFLC increased [343 (54–817) vs 47 (20–285)$^{£}$ mg/l]. D group also was splited in 2 groups according to CL: in D2 (n = 7) as compared to D1 (n = 10) group, CL was decreased (P < 0.002) and sFLC increased [213 (150–416) vs 90 (28–247)$^{\$}$ mg/l]. Low CK and CL values were also significantly decreased in I2 and D2 groups as compared to MMK, MML and H groups and as compared to patients without plasma cell dyscrasia, regardless of creatinine (not shown). Strikingly, in I2 group, 1 light chain deposition disease and, in D2 group, 2 AL-amyloidosis were diagnosed while 4 AL-amyloidosis were diagnosed in D1 group. Such low FLC renal clearance was also observed in 3 cases of MM (not included here).
Conclusions: Low FLC renal clearance might result from FLC renal tissue deposit or FLC aggregation reducing renal excretion. Whether FLC renal