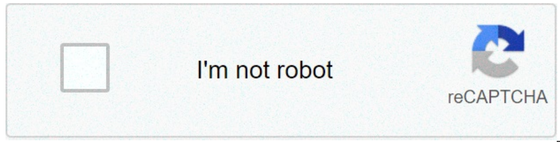

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Learn more about submitting to Asia-Pacific Journal of Clinical Oncology and submit today: The most cited articles published in the Last 2 Years , according to CrossRef.Xingchun Gao, Yajing Mi, Na Guo, Jing Luan, Hao Xu, Zhifang Hu, Ning Wang, Dian Zhang, Xingchun Gou, Lixian Xu, AbstractFull textPDFReferencesRequest permissionsYouchun Chen, Jiaxiong Tan, Shuxin Huang, Xin Huang, Jingying Huang, Jie Chen, Zhi Yu, Yuhong Lu, Jianyu Weng, Xin Du, Yangqiu Li, Xianfeng Zha, Shaohua Chen, AbstractFull textPDFReferencesRequest permissionsNazanin Rajai, Ali Ghanbari, Moein Yoosefi, Farnam Mohebi, Bahram Mohajer, Ali Sheidaei, Kimiya Gohari, Masoud Masinaei, Rosa Haghshenas, Farzad Kompani, Mohammad Vaezi, Farshad Farzadfar, AbstractFull textPDFReferencesRequest permissionsRana Muhammad Usman, Faryal Razzaq, Arshia Akbar, Arafat Ali Farooqui, Ahmad Iftikhar, Azka Latif, Hamza Hassan, Jianjun Zhao, Jennifer S. Carew, Steffan T. Nawrocki, Faiz Anwer, AbstractFull textPDFReferencesRequest permissions more > Research Article24 Aug 2021Ruhai Bai | Hui Huang | ... | Meng ChuPurpose. Skin malignant melanoma (SMM) is one of the fastest-growing cancers in China, with a poor prognosis, high invasiveness, and high mortality rate. The aim of this study was to determine the long-term trends in the incidence and mortality of SMM in China between 1990 and 2019. Patients and Methods. Incidence and mortality data were extracted from the Global Burden of Disease Study 2019 and were analyzed using an age-period-cohort framework. Results. The annual incidence net drifts were 3.523% (95% confidence interval (CI): 3.318% to 3.728%) and 3.779% (95% CI: 3.585% to 3.974%) for males and females, respectively, while the corresponding annual net drifts of mortality were −0.754% (95% CI: −1.073% to −0.435%) and –0.826% (95% CI: −1.164% to −0.487%). The local drift from 1990 to 2019 was highest in males aged from 25 to 29 years. After controlling for period deviations in a single birth cohort, the SMM incidence and mortality increased exponentially with age for both sexes. Similar increasing monotonic trends were found for period and cohort effects on the incidence, while a declining trend was found for mortality. Conclusion. While the age-standardized mortality rate of SMM in China has decreased in both sexes over the past 30 years, the crude incidence rate, age-standardized incidence rate, and crude mortality rate have all increased. SMM may greatly threaten the health of the elderly in China due to the aging population. Appropriate changes should be made to raise the awareness, reduce the exposure to risk factors, and promote the early detection of SMM.Research Article24 Aug 2021Dongdong Xiao | Jun Liu | ... | Pengfei YanBackground. There is a clinical demand for rapid estimation of meningioma volumes. Our objective was to assess the accuracy of three ABC-derived and three SH-derived formula methods on volume estimation of meningiomas. Methods. The study group comprised 678 patients treated at our department for histopathologically proven intracranial meningiomas. For each patient, tumor volumes were independently measured using six formula methods as well as planimetry. Maximum tumor diameter and ellipsoidity were also recorded. Volumes were compared using descriptive statistics, correlation analysis, and consistency analysis. Results. Among all methods assessed, 2/3SH and 1/2ABC outperformed the others. No significant differences were found between volumes obtained by the two methods and those of planimetry (). Spearman rank-correlation coefficients (rs) were 0.99 for both methods (), and ICC were 0.99 and 0.98, respectively. In Bland-Altman plot, most data points lay inside the limit of agreement. Overall, 2/3SH overestimated tumor volumes by 1.29%, and estimation errors in 93.66% cases were within 20%; 1/2ABC overestimated tumor volumes by 5.36%, and estimation errors in 93.51% cases were within 30%. The performance of 2/3SH and 1/2ABC in small-volume meningiomas was slightly worse, especially for 1/2ABC. Correlations between ellipsoidity and percentage errors of 2/3SH and 1/2ABC were weak ($rs = -0.06$ and -0.24, respectively). Despite a significant correlation between maximum tumor diameter and planimetric volume ($rs = -0.96$), volumes could vary significantly for a given diameter. Conclusions. Formula methods 2/3SH and 1/2ABC can estimate meningioma volumes with decent accuracy. Compared with the 1/2ABC method, the 2/3SH method showed slightly better performance, especially in small-volume meningiomas. Ellipsoidity is not a suitable parameter to predict estimation error, and maximum tumor diameter is not a reliable surrogate for actual meningioma volume.Research Article21 Aug 2021Weiqi Yao | Hongyun Gong | ... | Yu HuGlioblastoma multiforme (GBM), the most common malignant primary brain tumor, has a very poor prognosis. With increasing knowledge of tumor molecular biology, targeted therapies are becoming increasingly integral to comprehensive GBM treatment strategies. mTOR is a key downstream molecule of the PI3K/Akt signaling pathway, integrating input signals from growth factors, nutrients, and energy sources to regulate cell growth and cell proliferation through multiple cellular responses. mTOR/PI3K dual-targeted therapy has shown promise in managing various cancers. Here, we report that taxifolin, a flavanone commonly found in milk thistle, inhibited mTOR/PI3K, promoted autophagy, and suppressed lipid synthesis in GBM. In silico analysis showed that taxifolin can bind to the rapamycin binding site of mTOR and the catalytic site of PI3K (p110α). In in vitro experiments, taxifolin inhibited mTOR and PI3K activity in five different glioma cell lines. Lastly, we showed that taxifolin suppressed tumors in mice; stimulated expression of autophagy-related genes LC3B-II, Atg7, atg12, and Beclin-1; and inhibited expression of fatty acid synthesis-related genes C/EBPα, PPARγ, FABP4, and FAS. Our observations suggest that taxifolin is potentially a valuable drug for treating GBM.Research Article21 Aug 2021Dan Guo | Kang ZhengObjective. To explore the effect of prophylactic radiotherapy on patients with stage II-III esophageal cancer (EC) after esophageal cancer radical operation (ECRO) and influencing factors on EC recurrence. Methods. Totally, 65 patients with EC in our hospital were enrolled. Among them, 30 patients were treated by routine ECRO as a control group (Con group) and 35 patients by prophylactic radiotherapy as a research group (Res group). Then, the following measures were taken: record the efficacy on both groups, quantify their C-reactive protein (CRP) and white blood cell count (WBC) before and after therapy, evaluate their mental state through the revised piper fatigue scale (PFS-R) before and after therapy, determine their changes in Self-Rating Depression Scale (SDS) and Self-Rating Anxiety Scale (SAS) before and after therapy, compare them in terms of lymph-node metastatic rate (LNMR), hematogenous metastasis rate (HMR), anastomotic recurrence rate (ARR), and 3-year survival rate, compare them in terms of life quality after therapy via the Quality of Life-Core Questionnaire (QLQ-C30), and analyze influencing factors on their recurrence. Results. The Res group showed a notably higher total effective rate (TER) than the Con group (). After therapy, CRP and WBC in both groups increased, but their levels were not considerably different in both (). Additionally, after therapy, in contrast to the Con group, the Res group got notably lower PFS-R, SDS, and SAS scores, showed notably lower LNMR and ARR and notably higher 3-year survival rate, and experienced notably higher life quality (all), and the HMR results were not considerably different in both groups (). Moreover, carcinoembryonic antigen (CEA), carbohydrate antigen 125 (CA125), esophageal inflammation history, family medical history, postoperative complications, and lymphatic and vascular infiltration were risk factors for the disease recurrence, and treatment method was the protective factor for it. Conclusion. For patients with stage II-III EC after ECRO, prophylactic radiotherapy is highly effective and safe and can lower the recurrence rate, so it is worth popularizing in clinical practice.Research Article20 Aug 2021Yaping Deng | Kehua Li | ... | Hanbo LiuHead and neck squamous cell carcinoma (HNSCC) is a highly aggressive solid tumor. Because most studies have focused on the intrinsic carcinogenic pathways of tumors, we focused on the relationship between N6-methyladenosine (m6A) and the prognosis of HNSCC in the tumor immune microenvironment. We downloaded RNA-seq data from the TCGA dataset and used univariate Cox regression to screen m6A-related lncRNAs. The expression value of LASSO-screened genes was the sum of LASSO regression coefficients. We then evaluated relationships between the risk score and cellular components or cellular immune response. Differences in immune response under various algorithms were visualized with heat maps. The GSVA package in R was used to analyze GO, BP, KEGG, and hallmark gene sets of immune checkpoint clusters and immune checkpoint scores. The GSEA analysis was performed with the cluster profile package, yielding 21 m6A genes. Related lncRNAs were screened with Pearson's correlations, and the resulting 442 lncRNAs were screened using single-factor analysis. Eight lncRNAs closely related to prognosis were identified through survival random forest. Survival analysis showed that patients with a high risk score had a poor prognosis. Low- and high-risk-score groups differed significantly in m6A gene expression. Prognostic scores from different algorithms were significantly correlated with B cells, T cells, and memory cells in the immune microenvironment. Expression of immune checkpoints and signal pathways differed significantly across risk-score groups, suggesting that m6A could mediate lncRNA-induced immune system dysfunction and affect HNSCC development. A comprehensive study of tumor-cell immune characteristics should provide more insight into the complex immune microenvironment, thus contributing to the development of new immunotherapeutic agents.Research Article19 Aug 2021Hao Zhang | Renzheng Liu | ... | Xiao HuIn this study, we constructed the ferroptosis-related genes diagnostic and prognostic models. We analyzed the relationship between ferroptosis and tumor mutational burden in hepatocellular carcinoma (HCC). Eighty-four ferroptosis-related genes were analyzed by Cox regression and the least absolute shrinkage and selection operator method. Seven genes (SLC7A11, ACSL3, ACACA, SLC1A5, G6PD, ACSL6, and VDAC2) were used to construct models. The reliability of the model was verified by using the data from the ICGC database. Differential genes in high and low-risk groups revealed enrichment of many immune features by Gene Ontology and Kyoto Encyclopedia of Genes and Genomes. The degree of ferroptosis was negatively correlated with tumor mutational burden (i.e., the higher the degree of ferroptosis, the lower the tumor mutational burden). The tumor mutational burden was negatively correlated with survival. We also found that ALB, TP53, and DOCK2 may be a bridge between ferroptosis and tumor mutational burden. The reported models and the relationship with tumor mutational burden indicate new possibilities for individualized treatment of HCC patients.Page 2The minichromosome maintenance (MCM) protein family plays a key role in eukaryotic DNA replication and has been confirmed to be associated with the occurrence and progression of many tumors. However, the expression levels, functions, and prognostic values of MCMs in breast cancer (BC) have not been clearly and systematically explained. In this article, we studied the transcriptional levels of MCMs in BC based on the Oncomine database. Kaplan-Meier plotter was used to analyze prognostic value of MCMs in human BC patients. Furthermore, we constructed a MCM coexpression gene network and performed functional annotation analysis through DAVID to reveal the functions of MCMs and coexpressed genes. The data showed that the expression of MCM2–8 and MCM10 but not MCM1 and MCM9 was upregulated in BC. Kaplan-Meier plotter analysis revealed that high transcriptional levels of MCM2, MCM4–7, and MCM10 were significantly related to low relapse-free survival (RFS) in BC patients. In contrast, high levels of MCM1 and MCM9 predicted high RFS for BC patients. This study suggests that MCM2, MCM4–7, and MCM10 possess great potential to be valuable prognostic biomarkers for BC and that MCM1 and MCM9 may serve as potential treatment targets for BC patients.1. IntroductionSurveys show that breast cancer (BC) patients diagnosed worldwide are increasing, and BC is the most common carcinoma type in the female population [1, 2]. BC can be further divided into four subtypes, including luminal A, luminal B, basal-like, and human epidermal growth factor receptor-2 (HER2) overexpression [3]. Classic clinical prognostic markers, such as progesterone receptor (PR), HER2, and estrogen receptor (ER) have played positive roles in endocrine therapy or targeted therapy in BC patients [4]. Because of the heterogeneity of various tumors, the limitations of the current markers are sensitivity and specificity. Therefore, valuable biomarkers are needed as prognostic predictors to effectively upregulate prognosis and precisely individualized therapy effects.To date, the roles of minichromosome maintenance (MCM) protein family members identified in human cancers have been widely reported. The MCM family plays important roles in the cell cycle and genome replication, including ten members: serum response factor (SRF, also called MCM1) and MCM2–10 [5, 6]. The MCM2–7 complexes are involved in the formation of the prereplication complex and have helicase activity, which makes the DNA detach and leads to the recruitment of DNA polymerase and the activation of DNA replication [7, 8]. MCMs are also involved in the response of DNA damage [9, 10]. In addition, MCM interacts with cellular tumor antigen p53 binding protein 1 (53BP1) and Rad51, and the consumption of MCM leads to a reduction in 53BP1 and Rad51 foci formed after DNA damage [10, 11]. At present, the overexpression of MCM has been detected in various cancer tissues and cancer cell lines, including squamous cell lung carcinoma [12], kidney cancer [13], prostate carcinoma [14], BC [15], digestive system tumors [16–18], brain tumors [19], and lymphomas [20].The abnormal expression of MCMs and its relationship with clinicopathological characteristics and prognosis have been partially reported in human BC. However, bioinformatics analysis has not been performed to systematically explore the role of MCMs in BC. Based on online databases, we analyzed the expression patterns, clinicopathological characteristics, functions, and different prognostic values of MCMs in patients with BC. In addition, potential regulatory miRNA-regulating MCMs were screened, contributing to regulating the expression of MCMs in BC and identifying targets of precise treatment for BC patients. Our research helps to strengthen and acknowledge of the roles of the MCMs in BC.2. Materials and Methods2.1. Oncomine AnalysisOncomine [21, 22] (provides gene data that can be used to reveal the expression of target genes in various cancers. The mRNA expression level of MCMs in cancer samples was compared with normal samples. The threshold of value is 0.05, fold change is 2, and gene rank is top 5%.2.2. GEPIA AnalysisGEPIA [23] (can be used to analyze the RNA expression of various cancer and normal tissue samples based on TCGA and GTEx. GEPIA was used to perform the correlation analysis of MCMs in BC.2.3. Survival AnalysisKaplan-Meier plotter [24] (can be used to predict the impact of target genes on the survival rate of patients with different cancer types. We use it to analyze the prognostic value of MCMs and their regulatory miRNAs in BC.2.4. cBioPortal AnalysisThe Invasive Breast Carcinoma database (METABRIC, Nature 2012 and Nat Commun 2016, including 2509 samples) was selected to analyze and construct the cancer genome atlas of MCMs based on cBioPortal [25] ( ). Mutations, putative copy-number alterations from DNA copy, and mRNA expression (microarray) z-scores relative to diploid samples of the genomic profiles were chosen to be analyzed.2.5. STRING AnalysisWe used STRING [26] database ( ) to establish a protein-protein network that showed the coexpression relationships between MCMs and other nodes.2.6. Function Annotation AnalysisDAVID [27] (was used to analyze the MCMs and coexpressed genes to identify GO terms and to visualize genes on Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway maps.

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