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Association between matrix metalloproteinase-3 gene polymorphism and risk of ischemic stroke: A meta-analysis

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Background & Purpose: Ischemic stroke (IS) is a complex and devastating vascular disease that has become one of the leading causes of disability and mortality worldwide. Various studies have shown the association between matrix metalloproteinase (*MMP*) family gene polymorphisms and IS. However, the results have been inconclusive.

Objective: The present meta-analysis aimed to provide a comprehensive account of the association between *MMP-3 5A/6A* gene polymorphism and susceptibility to IS.

Methods: A literature search for eligible genetic studies published before March 31, 2016 was conducted in the PubMed, Medline, EMBASE, OVID, and Google Scholar databases. The following combinations of main keywords were used: ('Matrix Mettaloproteinase-3 OR 'MMP-3') and ('genetic polymorphism' OR 'single nucleotide polymorphism') and ('ischemic stroke' OR 'cerebral infarction' OR 'IS'). Fixed or random effects models were used to estimate the Pooled Odds ratio (OR) and 95% confidence interval (CI). Statistical analysis was carried out by using STATA version 13.0 software.

Results: Total 11 studies were included in our meta-analysis. No significant association was observed between *MMP-3 5A/6A* gene polymorphism [OR=0.91, 95% CI: 0.65–1.16] and risk of IS.

Conclusion: Our meta-analysis shows that *MMP-3 5A/6A* gene polymorphism is not significantly associated with the risk of IS. Further prospective large epidemiological studies are needed to confirm these findings in different ethnicities.

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Fingerprinting heterogeneity of glioma using PET/MRI information

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This projects is proposing a novel machine learning algorithm based on Generative Method to characterize intra-tumor heterogeneity of glioma. The algorithm was applied on dynamic [18F] FET-PET, [18F] Fmiso PET, rOEF, MRI T1, T2, T1W, T2W, FLAIR, DCE MRI and so on. This probabilistic model allows for different tumor boundaries in each channel, reflecting difference in tumor appearance across modalities. Classification result shows partly distributed feature maps in order to be able to select relevant features amongst wide patient data. The identified parts with different malignancy were discussed and validated according to first, the manual segmentations by clinical experts to investigate the performance on the tumor borders and second, graph maps to investigate the performance on the intra tumor regions. The main aim of the project is focused on the extraction of the additive information from PET and combining it with the MRI images information for each patient and relating them to the grade of malignancy.

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