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Impact of rs699 and rs4762 AGT SNPs on functional networks in vascular dementia

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Vascular Dementia (VD) is the second cause of dementia in the world. Blood pressure (BP), which is regulated by the renin-angiotensin system (RAS), is associated with VD. The *AGT* gene belongs to RAS but little is known about its role in the occurrence and progression of VD. To clarify the physiopathological role of *AGT* in VD, we investigated the influence of two SNPs (rs699 and rs4762) associated with arterial hypertension and cerebrovascular pathology on brain activity in VD patients. We applied qEEG in 65 VD patients divided in three groups according to their vascular risk associated with *AGT* genotype: A group: 15 patients with high vascular risk (carriers of M allele in *AGT*174 and T allele in *AGT*235); B group: 38 patients with moderate vascular risk (carriers of M allele in *AGT*174 or T allele in *AGT*235); and C group: 12 patients with low vascular risk (no carriers of risk variants). Further analyses were performed using the eLORETA software. To visualize resting state synchronization across frequency bands in large scale functional networks, two lagged functional connectivity measures (lagged coherence and lagged phase synchrony), implemented in the eLORETA statistical package, have been proposed. We found that VD patients with higher genomic risk had higher connectivity in delta band between frontal, fronto-temporal and fronto-parietal regions. Our findings may indicate that high blood pressure disturbs the functional connectivity at the frontal level. The slow hyper connectivity observed may be a direct reflection of neural damage caused by arterial hypertension in susceptible individuals.

Biography

Juan C Carril is the Director of the Genomics and Pharmacogenomics Department at EuroEspes Biomedical Research Center, Institute of Medical Science and Genomic Medicine, Corunna, Spain. He has received his PhD from Santiago de Compostela University in 2000 with the thesis entitled Genetic structure and profile of the populations of the Iberian Peninsula by means of markers (STRs and SNPs) of the human Y-chromosome. He has published more than 40 scientific publications in the fields of population genetics, forensic genetics, genetic epidemiology and pharmacogenetics and over 40 papers at national and international conferences.

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