Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes.

Stroke has multiple etiologies, but the underlying genes and pathways are largely unknown. The international research groups including Yoshinori Okada (IFReC & Graduate School of Medicine, Osaka University) conducted a multiancestry genome-wide-association meta-analysis in 521,612 individuals (67,162 cases and 454,450 controls) and discovered 22 new stroke risk loci, bringing the total to 32. The group further found shared genetic variation with related vascular traits, including blood pressure, cardiac traits, and venous thromboembolism, at individual loci (n = 18), and using genetic risk scores and linkage-disequilibrium-score regression. Several loci exhibited distinct association and pleiotropy patterns for etiological stroke subtypes. Eleven new susceptibility loci indicate mechanisms not previously implicated in stroke pathophysiology, with prioritization of risk variants and genes accomplished through bioinformatics analyses using extensive functional datasets. Stroke risk loci were significantly enriched in drug targets for antithrombotic therapy.

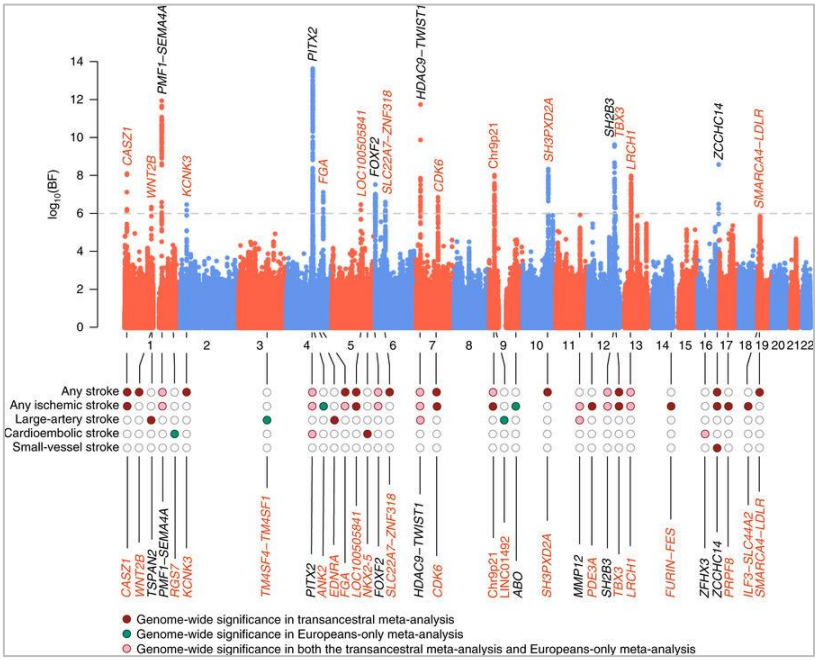

Fig.1. Genetic loci identified by the trans-ethnic genome-wide meta-analysis of stroke.

(Osaka University)

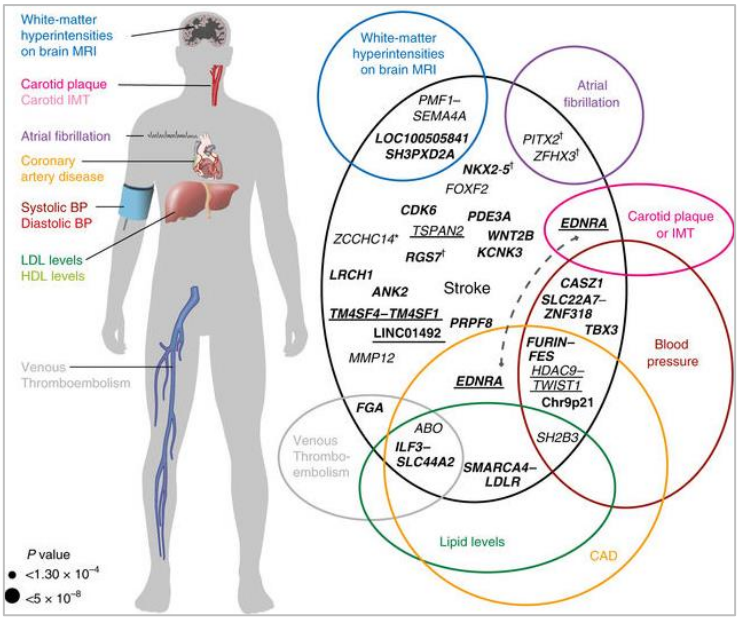

Fig.2. Overlap of the stroke-associated genes among the clinical subtypes of stroke.

(Osaka University)

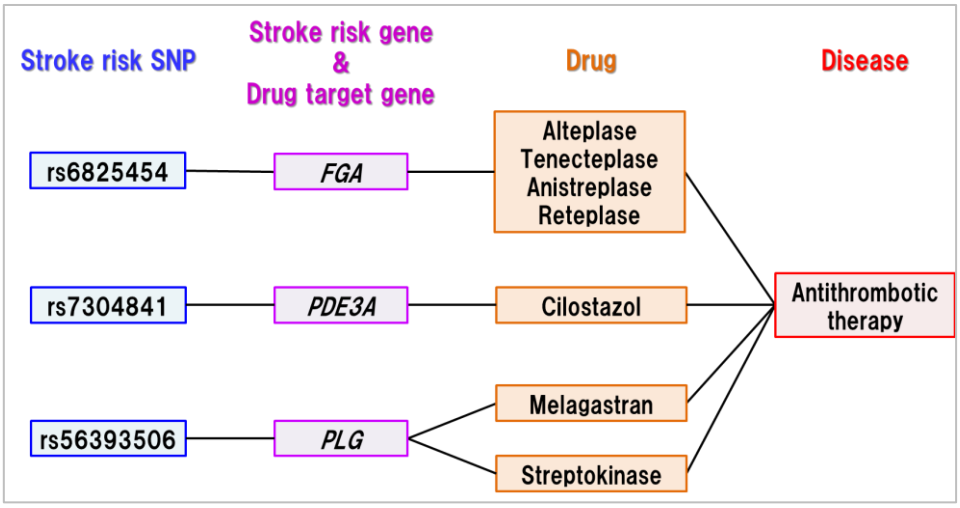

Fig.3. Connection from the stroke risk SNPs to clinical indication of antithrombotic therapy.

(Osaka University)

Article

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