Atypical sulcal patterns in pre-readers and beginning readers with a familial risk for developmental dyslexia

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Purpose: Developmental dyslexia (DD) is one of the most prominent specific learning disabilities, affecting 5-17% of children. DD is characterized by difficulties with accurate and/or fluent word recognition, poor spelling, and poor decoding performance. Substantial evidence suggests that cortical abnormalities and atypical brain function underlie DD in children and adults (*1*). To date, DD can only be diagnosed reliably at the end of second grade/third grade but psychological and clinical implications start long before this. Functional and structural neuroimaging studies of our group have demonstrated that characteristic neuroanatomical and functional alterations in DD can already be detected in pre-literate children with a familial risk for DD (*2, 3*). Recently, we presented a sulcal pattern comparison method using graph structure and showed that sulcal patterns have the potential to be a new important neuroimaging biomarker of brain function and development (*4, 5*). The goal of this study was to investigate possible structural pre-markers of DD in pre-readers as well as beginning readers using sulcal pattern analysis.

Methods: Whole brain T1-weighted MPRAGE structural scans were collected in 30 age and IQ matched children [15 with (FHD+) and 15 without familial risk for DD (FHD-, typical); mean age: 5.8 yrs, range: 4.9 – 7.0 yrs]. FHD+ children had at least one first degree relative with a clinical diagnosis of DD, and FHD- children have no family member with DD or reading difficulties. All children were examined using a standardized behavioral language battery. The images were processed to extract cortical surfaces using the FreeSurfer pipeline. Sulcal pattern topography was represented with a graph structure using sulcal pits as the nodes. Sulcal pits are defined as the deepest local regions of sulci, and show relatively invariant spatial distribution, which may be closely related to functional areas under tight genetic control (*6*). Sulcal pits and their corresponding sulcal catchment basins were automatically identified on the white matter surface using a watershed algorithm based on sulcal depth map. Each sulcal pit corresponds to a node in the graph representation. If sulcal basins met, sulcal pits in those basins were connected with an undirected edge. In order to quantitatively compare different sulcal graph sets, we used the geometric features of nodes (3D position (x, y, z), depth (d) and area of sulcal basin (s)) and their relationship. We also exploited the features of graph topology (the number of edges and the paths between nodes) (c) to reflect the interrelated sulcal arrangement and patterning. These features were weighted to give their relative importance, $F = (w_x x, w_y y, w_z z, w_d d, w_s s, w_c c)$. We determined the optimal match between two sulcal graphs and then computed their similarity, which ranged from 0 to 1, by using a spectral matching technique (*7*) (Fig. 1 reproduced from (*4*)). Furthermore, this method also allows variable weighting of geometric and topological features. First, all features are weighted in the sulcal pattern matching and similarity measure. In addition, only 1 feature is weighted and the other features are set to 0 to examine the effect of each individual feature on the sulcal pattern similarity. Sulcal pattern similarities of all possible pairs were automatically computed and a similarity matrix (30×30, 15 FHD- and 15 FHD+ children) was constructed for left and right hemispheres and lobes with various sets of weights. We tested whether the similarity within FHD- was significantly different when compared to the similarity between FHD- and FHD+ groups. For each FHD- child, the mean similarity with the other 14 FHD- children was calculated. Each FHD+ child had the mean similarity with all 15 FHD- children. The differences between the FHD- and FHD+ in the mean similarity were examined with an independent 2 sample t-test.

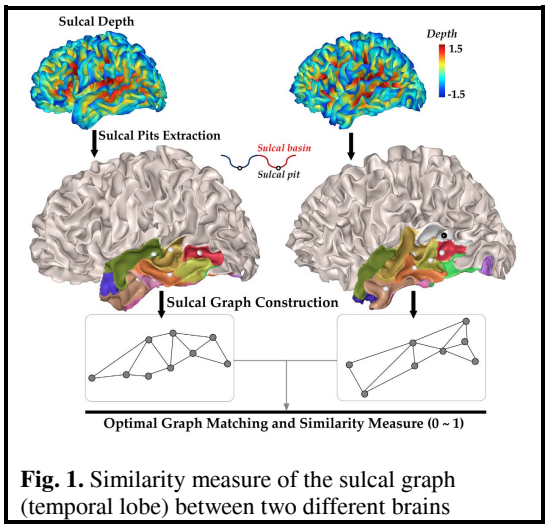

Fig. 1. Similarity measure of the sulcal graph (temporal lobe) between two different brains

Results: FHD+ children significantly differed from FHD- children during behavioral tasks of letter identification ($P = 0.007$), but not in age, gender or IQ ($P > 0.05$). FHD+ children scored lower on tasks measuring receptive and expressive language skills, phonological processing and rapid automatized naming; however significance was not reached. Sulcal pattern analysis revealed that the similarities between FHD- and FHD+ groups were significantly lower than the similarities measured within the FHD- group in the left parietal lobe in sulcal graph topology ($P = 0.0004$). In the whole right hemisphere, significantly lower mean similarities between the FHD- group and the FHD+ group were observed in the sulcal basin area ($P = 0.0099$). Only in the right parietal lobe the FHD+ group showed significantly lower mean similarity with the FHD- group for the whole feature set ($P = 0.0019$), including 3D position of sulcal pits ($P = 0.0300$), area of sulcal basin ($P = 0.0073$) and sulcal graph topology ($P = 0.0331$).

Discussion and Conclusion: We detected atypical sulcal patterns in FHD+ children compared to FHD- children primarily within bilateral parietal lobes. Sulcal pits have been hypothesized to be closely related to genetic control (*5*) and our finding supports the hypothesis that functional and structural alterations within developmental dyslexia are not due to experience-dependent brain changes after reading onset but may be present at birth or develop in early childhood prior to reading onset. Further studies using longitudinal designs have to determine whether sulcal patterns within the parietal lobe can be utilized as biomarkers for the early identification of children at risk for DD.

References

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