**Appendix 1.**

**Transcranial magnetic stimulation**

We investigated reorganization (either ipsilateral or contralateral or both) of the corticospinal tract in two patients (patient I:1 and 3) using Transcranial Magnetic Stimulation (TMS). However, unlike previously published studies (e1-e3), we used navigated TMS (nTMS) (NBS, Nexstim, Finland), a method where subject specific structural MRI images are combined with conventional TMS for stereotactic navigation, allowing precise stimulation of motor eloquent cortex at millimeter level spatial resolution (e-4, e-5) ). MEP (Motor Evoked Potential) recorded, using surface EMG electrodes attached to muscles both contralateral and ipsilateral to the stimulated hemisphere. Initially the resting motor threshold (rMT) was estimated and used as a marker for cortical excitability, measured for respective hemispheres. Motor mapping were done at 110% of rMT.

In both cases (Patient I:1 in Family 1 and Patient 6), nTMS of the hand motor areas showed bilateral MEP from all the registered muscles, irrespective of the cortical side being stimulated. In contrast, focal stimulation of the leg motor area yielded MEP only contralaterally. Thus, TMS data clearly showed reorganized corticomotor projection patterns for the upper extremities but sparing not the lower extremities. Minor asymmetries in cortico-muscular latencies might be suggestive of mono-synaptic to poly-synaptic connections, although the discussion of the true nature of synaptic connectivity is beyond the scope of our two patient’s neurophysiological data. Our TMS findings are descriptive neurophysiogical information of CST reorganization, while for the reason that we have very small data set, we have not drawn any correlation between reorganization of CST pattern and MM.

Volumetric brain assessment in aforementioned patients was performed using FreeSurfer (e-6).

**Genetic analyses**

Genes associated with congenital mirror movements (*DCC*, *NTN1*, *RAD51* and *DNAL4*) and movement disorders (500 genes) were first analyzed. After Patient 6 was diagnosed with myelodysplastic syndrome (MDS), a re-assessment for variants involved in familial cancer was sought. For Patient 6 the search included genes associated with intellectual disability, seizures and agenesis of the corpus callosum. Genomic DNA from the patients was subjected to massive parallel sequencing with whole exome sequencing. Both sequencing and primary filtering of variants were performed at Clinical genomics, SciLife, Solna, Sweden. Sequence data was mapped to reference sequence [GRCh37/UCSChg19], and 95% of the target bases achieved at least 20x coverage (100% in the *DCC*, *RAD51* and *DNAL4* genes). Identified sequence variants were subsequently analyzed and filtered using designated software (SCOUT, Clinical Genomics, SciLife Solna). Sequences in exons and exon/intron boundaries, and variants with population frequencies <0.01 were interpreted. The variants c.1729delG and c.1466\_1476del in *DCC* have not been described before (gnomAD, ClinVar, HGMD). The first variant segregates with disease in Family 1. No other variants associated with intellectual disability, agenesis of the corpus callosum, familial malignancy, seizures or movement disorders were identified. In family 2, a novel variant in ADGRE2 was identified in the index case but it did not segregate with disease (Table 1), mutations in this gene are otherwise associated with familial vibration urticaria (e-7).

**Supplementary references**

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