CATCH - Cascade genetic testing of familial hypercholesterolemia: the CATCH multicenter randomized controlled trial

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To test in a multicenter open-label randomized controlled trial across Switzerland whether a cascade screening programme for FH, in comparison with usual care, will increase the detection rate of FH within families.

The primary outcome will be the difference in the yield of detection of familial hypercholesterolemia (FH) between arms. The yield of detection is the number of test performed/number of contactable relatives.

Secondary endpoints include the transmission rate of phenotype and genotype into families. After 6 months follow-up, the differences in the use of lipid-lowering drug and change in LDL-cholesterol will be the third endpoint.

keywords: familial hypercholesterolemia, genetic testing
project homepage: https://catch.unisante.ch/
type of project: clinical studies
status: scheduled
start of project: 2020
end of project: 2020

Multicenter open-label randomized controlled trial, with 2x2 arms. Index cases with clinical criteria for FH will be separated into two groups before randomization, based on the result of the genetic test, either positive or negative for a monogenic mutation in one of the three genes causing FH. In each of these two groups, a randomization procedure will allocate index cases and their family member into the intervention arm or the control arm to evaluate the best method to contact at-risk relatives and perform cascade screening. In the intervention arm, the index case will be actively supported by a web-based centralized service to initiate contact with their first-degree relatives. In the control arm or “usual care arm”, the index case will be encouraged to initiated contact with their
first-degree relatives, but without additional support. The presence or absence of a monogenic mutation in the index case will determine the screening test used for cascade screening of relatives, either genetic or lipid test.

**responsible person**

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