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| **eMERGE Network: Manuscript Concept Sheet** |
| **Reference Number** *(to be assigned by CC)* | NT349 |
| **Submission Date** | 06/12/2019 |
| **Project Title** | Family communication following return of positive results |
| **Tentative Lead Investigator** *(first author)* | Hila Milo Rasouly and Julia Wynn |
| **Tentative Senior Author** *(last author)* | TBD |
| **All Other Authors**  | Members of the ROR-ELSI Participant Survey subgroup |
| **Sites Participating** | All eMERGE III clinical sites |
| **Background / Significance** | Sequential genetic testing in families (i.e. cascade screening) is recommended to patients with dominant genetic disorders to identify at risk and affected relatives and guide screening and treatment. However, there are barriers that may prevent successful transmission of accurate information across family members, including low or inaccurate understanding of genetics and inheritance and subsequently need for cascade screening ,maladaption to genetic test results and family dynamics. Though healthcare providers may be better equipt to facilitate cascade testing there are legal limitations on their ability to contact at-risk relatives. There is limited knowledge about the familial implications of genomic screening of the population, as the one offered by the eMERGE III consortium. In order for genetic screening to reach its full potential, cascade screening is imperative. This study aims at learning about the sharing of genetic results by a diverse population with limited prior genetic experience who received positive results. |
| **Outline of Project** | Analyses will be conducted to address the question whether Family communication of postitive results is associated with the following factors:* + Gender
	+ Family size (number of siblings and children)
	+ Age
	+ Integrated healthcare system compared to university/tertiary care system
	+ the condition or gene
* Diagnostic result related to the indication for sequencing, compared to a finding unrelated to any known condition they have
* format of the return of result (in-person, over the phone, by mail,…)
* who returned the result (genetic counselor, geneticist, PCP,…)
* letter content (explicitely recommended to communicate the result with family members or not)
* recruitment format (biobank, clinics, flyers,…)
* psychological adaptation to results as measured by the FaCTOR
* decisional regret comprehension of the result
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| **Desired Data - Common Variables\*** *(Available from the CC)* | [ ] Demographics [ ] ICD9/10 codes[ ] CPT codes[ ] Phecodes[ ] BMI | [ ] Common Variable Labs[ ] Common Variable Meds[ ] Other: Case/Control status on Phase I and Phase II phenotypes |
| **Other Desired Data *(Available from participating sites)*** | *Please specifically list out any data elements that participating sites would collect or extract from clinical or other sources for this project (i.e. not common variables above)*  |
| **Desired Genetic Data** | [ ] eMERGE I-III Merged set (HRC imputed, GWAS)[ ] eMERGE PGx/PGRNseq data set [ ] eMERGEseq data set (Phase III)[ ] eMERGE Whole Genome sequencing data set[ ] eMERGE Exome chip data set[ ] eMERGE Whole Exome sequencing data set[ ] Other (not listed above): |
| **Does project pertain to an existing eMERGE Phenotype?** | [ ] Yes, if so please list [ ] No |
| **Planned Statistical Analyses** | Descriptive analysis, and logistic regression comparing the impact of different factors on the likelihood of communicating the result to family members. |
| **Ethical Considerations** | This survey assesses the risks and benefits of return of uncertain genomic information to participants. |
| **Target Journal** | TBD |
| **Milestones***(This section should include the key dates for completion of project, including approval, project duration, draft completion, and submission.)* | 1. Data collection completed at all sites – 8/2019
2. Formulate data analysis plan – 9/2019
3. Data analysis – 12/2019
4. Draft manuscript- 1/2020
5. Finalize manuscript 3/2020
6. Submission to journal – 4/2020
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**\*Common Variables available across all datasets:**

* Demographics: sex, year of birth, decade of birth, race, ethnicity
* Codes: (repeated values & age at event): ICD, CPT, Phecodes
* BMI: (repeated value & age at event) height, weight, BMI
* Labs: (lab name, repeated lab value & age at event) Serum total cholesterol, LDL, HDL, Triglycerides, Glucose fasting/non-fasting/unknown, & White Blood Cell count
* Medications: (medication name, repeated, & age at event) Cerivastatin sodium, Rosuvastatin, Simvastatin, Fluvastatin, Pravastatin, Lovastatin, Atorvastatin, & Pitavastatin
* Other: Case/Control status on Phase I and Phase II phenotype: only on GWAS dataset participants