

Overview: A component of precision medicine is aimed at providing individualized medical treatments for patients. However, over-utilization of tests, treatments, and procedures is common.

Aims: The purpose of this study was to assess how critical care clinicians were individualizing patient care and implementing *Choosing Wisely*[®] recommendations in clinical practice.

Methods: A descriptive survey methodology was used with Research Electronic Data Capture (REDCap). The survey, consisted of 6 questions assessing if the respondent was familiar with the *Choosing Wisely*[®] initiative and if so, what recommendations had been implemented in clinical practice.

Results: A total of 2,520 responses were received from nurses (61%, n = 1538), physicians (25.9%, n = 647), advanced practice providers (10.5%, n = 263), and pharmacists (2.1%, n = 52). Overall, 1,273 (50.6%) respondents were familiar with the *Choosing Wisely*[®] campaign. Respondents reported that *Choosing Wisely*[®] recommendations had been integrated in a number of ways including being implemented in clinical care (N = 817, 72.9%), through development of a specific clinical protocol or institutional guideline (n = 736, 65.7%), through development of electronic medical record orders (n = 626, 55.8%), or with integration of longitudinal tracking using an electronic dashboard (n = 213, 19.0%).

Conclusions: Conclusions: The results of this national survey identify the application of the *Choosing Wisely*[®] recommendations to clinical practice for critical care clinicians. As only half of the respondents report implementation, additional strategies are needed to promote the *Choosing Wisely*[®] recommendations to make impactful change to improve care in critical care settings.

Family Management of Down Syndrome: Cross-Cultural Perspectives

Marcia L. Van Riper, PhD, RN, FAAN, University of North Carolina at Chapel Hill; George Knafel, PhD, University of North Carolina at Chapel Hill; Kathleen Knafel, PhD, FAAN, University of North Carolina at Chapel Hill

Aims: With a worldwide incidence of one in every 1000 – 1100 live births, Down Syndrome (DS) is the most common genetic cause of intellectual disability. How families incorporate the child's special needs into everyday family life (family management) influences both child and family adaptation. The purpose of this analysis was to assess the internal consistency reliability of seven translations of the Family Management Measure (FaMM) and to examine cross-cultural differences in family management of DS.

Methods: 2740 parents of individuals with DS (2387 mothers and 353 fathers) from 11 countries completed the 53-item FaMM as part of a cross-cultural study of adaptation in families of individuals with DS. Selected

descriptive statistics were computed. Reliability was assessed using Cronbach's alpha. Cross-cultural comparison of family management was addressed by rank ordering FaMM subscale means with a higher rank indicating greater ease in family management.

Results: Parents from Portugal, Spain and the US had mean scores reflecting greater ease in family management across all FaMM subscales; parents from Ireland, Italy, Korea, and Thailand had mean scores across all FaMM subscales indicating more problematic family management. The rankings for Brazil, Netherlands, and United Kingdom reflected areas of both management ease and difficulty.

Conclusions: Findings from this study suggest there are cross-cultural differences in family management of DS. More research is needed to fully understand if these differences are related to social determinants of health such as culture, societal attitudes towards DS and national approaches to integrating non-invasive prenatal testing into clinical practice.

Genetic Variations Hasten Decline in Young Onset Dementia

Lauren Massimo, PhD, CRNP, University of Pennsylvania; Lior Rennert, University of Pennsylvania; Sharon Xie, PhD, University of Pennsylvania; David Irwin, MD, University of Pennsylvania; Murray Grossman, MD, University of Pennsylvania; Corey McMillan, PhD, University of Pennsylvania

Aims: There is increasing interest in the influence of single nucleotide polymorphisms (SNPs) on the trajectory of cognitive decline in dementia. We evaluated the hypothesis that rs1768208 risk allele copies are associated with cognitive decline in behavioral variant frontotemporal degeneration (bvFTD), a common form of young-onset dementia.

Methods: Forty-three individuals diagnosed with bvFTD (mean baseline age = 60.1 years \pm 7.7, mean disease duration at baseline 3.6 years \pm 2.2, mean baseline MMSE 26.2 years \pm 7.1) were studied. All subjects had at least 2 verbal fluency observations to assess executive function. Patients were genotyped for rs1768208 using a custom pan-neurodegenerative disease SNP genotyping panel and were coded according to the number of risk (T) alleles (0,1,2). Linear mixed-effects models assessed the effect of genotype on performance changes over time. To evaluate the neuroanatomic basis for longitudinal decline, regression analyses related performance change in executive function to grey matter (GM) and white matter (WM).

Results: There was a significant dose-dependent genotype by time interaction ($F[2, 29] = 8.42$; $p = 0.001$) for declining performance on verbal fluency (B values refer to words per month): 2 risk alleles (B = 0.48; $p < .0001$), 1 risk allele (B = 0.23; $p = 0.0036$), and no risk alleles (B = 0.05; $p = 0.4822$). Furthermore, longitudinal