TELOMERE RESEARCH NETWORK

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In September 2019, NIA and NIEHS launched the Telomere Research Network (TRN) (trn.tulane.edu) to establish best practices for the measurement of telomere length in population-based studies. As a first step, this working document was drafted to reflect the current recommendations of the TRN. These recommendations are offered as initial guidelines for researchers, reviewers, and scientific research officers, and are considered *minimal* reporting guidelines for PCR-based measurement of telomere length. Over the next five years, the TRN expects to better define these parameters and integrate comments from our colleagues and experts around the world. To make comments and/or request clarification please contact Stacy Drury, M.D., PhD, Director of the TRN at telomerenetwork@gmail.com.

Minimum Reporting Recommendations for PCR-based Telomere Length Measurement

Sample type, storage, extraction and integrity:

- ☐ Sample type[1]
- ☐ Sample storage conditions, including temperature, duration, and buffer[2,3]
- ☐ DNA extraction method[4]
- ☐ DNA storage conditions, including freeze-thaw cycles[5,6,7]
- ☐ Method of documenting DNA quality and integrity[8]
- ☐ Percentage of samples specifically tested for DNA quality and integrity
- ☐ *For studies with repeated measures design, report the above for all time points*

qPCR assay:

- ☐ State whether qPCR, MMqPCR, aTL (absolute TL/PCR based) or other PCR based method
- ☐ PCR machine type[9]
- ☐ Source (manufacturer/home-made) of master mix and reagents, and final reaction volume[10]
- ☐ Telomere primer sequences and concentration[11]
- ☐ Single copy gene name, primer sequences, and concentration[11]
- ☐ Full PCR program description including temperature, times, and cycle numbers[11]
- ☐ PCR efficiency of single copy gene and telomere primers
- ☐ Source and concentration of control samples and standard curve[11]
- ☐ *For aTL PCR measurement only: sequence and concentration of oligo standards*

Data analysis:

- ☐ Mean and standard deviation or median and range of telomere lengths
- ☐ Number of sample replicates
- ☐ Level of independence of the replicates (plate vs day vs extraction)
- ☐ Analytic method, considering replicate measurements, to determine final telomere length[12]
- ☐ Method of accounting for variation between sample replicates
- ☐ Method for accounting for well position effects within plates[12]
- ☐ Method of accounting for between plate effects[12]
- ☐ % of samples repeated and % samples failing final QC and excluded from further analyses
- ☐ Acceptable range of PCR efficiency for the single copy gene and telomere primers
- ☐ ICCs of sample/study groups to address variability (not CV)[13,14]
- ☐ T/S ratio transformed to a z score prior before comparison across methods/studies[15]
- ☐ *For studies with family samples or repeated measure design: analytic method to account for this*[16,17]

Note: Currently, we do NOT recommend transformation of T/S measurement to base pairs for qPCR/MMPqPCR assays.

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