Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

eMethods. Additional information on statistical approach.

1. Model Selection and Fitting Process

The predictors in all models included time effect(s) and associated time-by-arm interaction terms. Our modelling approach assumes the study arms have equal baseline means, which is appropriate for a randomized control trial and is equivalent in efficiency to an ANCOVA model [1,2]. The process for selecting the best model for the primary outcome was a two-step process.

- In the first step we determined the "best" covariance structure by fitting a set of random coefficient models that included: 1) random intercept only; 2) random intercept and linear slope; and 3) random intercept, linear slope and quadratic slope. These models were fit using REML and AIC model selection criteria and assessed to determine the best fit model.
- In the second step, we used the random coefficient model identified in step 1 to determine the best mean structure. In this step, we fit separate models using linear time, quadratic time, and cubic time. These models were fit using ML and AIC model selection criteria were assessed to determine the best fit model.

Following this process, we ran the "best fit" model including stratification variables and estimated arm differences at 12 months from these models. All the final models were fit using REML. The final model for hemoglobin A1c as determined by this process was used for all subsequent sensitivity analyses. Final model code is available upon request.

2. Missing Data and Multiple Imputation Procedure.

Longitudinal models fit in our analysis used all available data, including data from

participants who had missing observations and/or were lost to attrition, with the estimation procedure implicitly accommodating missing values when related to prior outcome or to other baseline covariates in the model (i.e., missing at random (MAR)). We also conducted a sensitivity analysis using a multiple imputation (MI) approach that included additional baseline variables beyond those in our random effects models to strengthen the MAR assumption. As a first step, we used t-tests, Wilcoxon rank sum tests and chi-square tests as appropriate to assess each potential baseline variable's association with missingness at 12-months, and any variable with an association p-value of 0.3 or less was included in the imputation model. Baseline variables assessed included age, gender, race, ethnicity, marital status, education, employment, financial stability, distance to nearest VA, insulin use, number of diabetes medications, adherence to diabetes medications, weight, diagnosis of hypertension, diagnosis of hyperlipidemia, years since diabetes diagnosis, smoking status, housing status, number of people in the household, alcohol use, aspirin use, diabetes distress total and subscale scores, diabetes knowledge score, diabetes self-management total and subscale scores, PHQ-8 score, perceived competence score, PROMIS pain interference score, PROMIS self-efficacy score for managing medications and treatments, health-care climate score, and the newest vital sign score. Of these, the following were associated with missing status at week 48 and/or missing status at any time point and therefore included in the imputation model: age, gender, race, ethnicity, VA recruitment site, prior use of VHA home telehealth, pre-enrollment receipt of specialty diabetes care, smoking status, education, weight, distance to the nearest VA, diabetes distress interpersonal and physician-related distress subscores, perceived competence score, PHQ-8 score, and adherence to diabetes medications. The imputation model additionally included randomization arm, stratification

variables (VA recruitment site, prior use of VHA home telehealth, pre-enrollment receipt of specialty diabetes care - Endocrinology and/or Clinical Pharmacy) and all collected hemoglobin A1c measurements at the 5 possible time points. Missing hemoglobin A1c measurements at any of the 5 time points were imputed using a Markov chain Monte Carlo (MCMC) algorithm with 30 imputations. Results using imputed data were very similar to the main analysis results. Combining estimates from fit of primary model on each of the imputed datasets, the estimated mean difference at 12-months was -0.63%, 95%CI -0.95%, -0.35%; p-value=0.0298.

References

1. Liu GF, Lu K, Mogg R, Mallick M, Mehrotra DV. Should baseline be a covariate or dependent variable in analyses of change from baseline in clinical trials? Stat Med. 2009;28(20):2509-2530.
2. Fitzmaurice GM, Laird NM, Ware JH. Applied longitudinal analysis. Hoboken, NJ: Wiley-Interscience; 2004

eTable 1. Baseline characteristics of randomized and non-randomized patients.

Variable	Randomized (n=200)	Ineligible (n=510)[b]	Refused (n=293)	Unable to contact (n=123)[c]
Mean age (SD)	57.7 (8.2)	58.9 (7.9)	58.7 (7.3)	56.1 (8.2)
Male gender (%)	77.5	89.4	85.0	80.5
Prior diabetes specialty care (%)	65.0	31.2	62.1	61.8
Durham site (%)	57.5	55.3	62.1	50.4
Mean hemoglobin A1c (SD)[a]	10.2 (1.3)	9.8 (1.4)	10.2 (1.3)	10.5 (1.5)
Hypertension diagnosis (%)	86.0	51.8	89.8	82.9
Dyslipidemia diagnosis (%)	90.0	53.3	89.8	87.8

[a] Based on an average of available hemoglobin A1c data during the year prior to enrollment.
[b] 'Ineligible' includes 458 participants deemed ineligible prior to consent and 52 deemed ineligible after consent
[c] 'Unable to contact' includes 119 participants who could not be contacted prior to consent and 4 who could not be contacted after consent

eTable 2. Descriptive changes in medication use among participants randomized to each intervention arm from baseline to 12 months.

	Comprehensive Telehealth			Telemonitoring/Care Coordination		
Medication/class	**Baseline**	**12 months**	**Change**	**Baseline**	**12 months**	**Change**
Metformin	77%	75%	**-2%**	83%	74%	**-9%**
Sulfonylurea	35%	27%	**-8%**	49%	42%	**-7%**
Thiazolidinedione	7%	12%	**5%**	7%	12%	**5%**
DPP-4 inhibitor	0	5%	**5%**	4%	5%	**1%**
GLP-1 receptor agonist	11%	26%	**15%**	14%	22%	**8%**
SGLT-2 inhibitor	15%	25%	**10%**	7%	16%	**9%**
Insulin	77%	74%	**-3%**	65%	64%	**-1%**

Abbreviations: DPP-4 = dipeptidyl peptidase-4; GLP-1 = glucagon-like peptide-1; SGLT-2 = sodium-glucose cotransporter-2

eTable 3. Descriptive mean hemoglobin A1c (SD) by time point among comprehensive telehealth participants completing >20 and ≤20 encounters.

	Participants completing >20 encounters (n=68)	Participants completing ≤20 encounters (n=33)
Baseline	10.11 (1.27)	10.12 (1.20)
3 months	8.62 (0.87)	9.05 (1.09)
6 months	8.40 (1.04)	9.18 (1.31)
9 months	8.28 (1.04)	9.28 (1.63)
12 months	8.27 (1.17)	9.33 (1.27)