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Original Article

EMR documentation of physician–patient communication following genomic counseling for actionable complex disease and pharmacogenomic results

Sweet K., Sturm A.C., Schmidlen T., Hovick S., Peng J., Manickam K., Salikhova A., McElroy J., Scheinfeldt L., Toland A.E., Roberts J.S., Christman M. EMR documentation of physician–patient communication following genomic counseling for actionable complex disease and pharmacogenomic results.
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Genomic risk information for potentially actionable complex diseases and pharmacogenomics communicated through genomic counseling (GC) may motivate physicians and patients to take preventive actions. The Ohio State University-Coriell Personalized Medicine Collaborative is a randomized trial to measure the effects of in-person GC on chronic disease patients provided with multiplex results. Nine personalized genomic risk reports were provided to patients through a web portal, and to physicians via electronic medical record (EMR). Active arm participants (98, 39% female) received GC within 1 month of report viewing; control arm subjects (101, 54% female) could access counseling 3-months post-report viewing. We examined whether GC affected documentation of physician–patient communication by reviewing the first clinical note following the patient's GC visit or report upload to the EMR. Multivariable logistic regression modeling estimated the independent effect of GC on physician–patient communication, as intention to treat (ITT) and per protocol (PP), adjusted for physician educational intervention. Counselees in the active arm had more physician–patient communications than control subjects [ITT, odds ratio (OR): 3.76 (95% confidence interval (CI): 1.38–10.22, $p < 0.0094$); PP, OR: 5.53 (95% CI: 2.20–13.90, $p = 0.0017$). In conclusion, GC appreciably affected physician–patient communication following receipt of potentially actionable genomic risk information.

Conflict of interest

The authors have no conflicts of interest to disclose.

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Genomic medicine is an emerging medical discipline that involves using a patient's family history, genetic, protein, metabolic and other biological marker profiles in the clinical setting. Knowledge of a patient's genomic profile could help identify and manage health risks, aid in the diagnosis of existing disease, determine what interventions (e.g. pharmacologic, surveillance) will have the greatest benefit, and improve patient-centered health outcomes. To reach this goal, a number of complex issues must be resolved, including optimizing patient genomic testing result delivery, preparation of the physician workforce, and evidence-based research to systematically evaluate the translation of genomics into clinical care (1–7).

To date, there have been relatively few studies examining the potential effects of delivery of actionable genomic risk information on physician–patient communication (8, 9), or how genomic counseling (GC) might affect this process. Physician–patient communication, including patient activation, is associated with greater adherence to health care provider recommendations and greater patient satisfaction (10, 11). However, even when actionable genomic risk information is available, participants often keep the results to themselves. Kaufman et al. surveying participants of direct to consumer genomic services, found that only 28% discussed actionable test results with a health care provider, most often a primary care physician, and seldom with a genetic counselor (12). Similar physician involvement was seen by Bloss et al. (13), and more recently, by van der Wouden et al. (14) (26.5 and 27%, respectively). Bloss et al. also found that (1) speaking with a physician or genetic counselor about results was not associated with a change in anxiety level, and (2) those who discussed results had a higher completion rate of recommended health screening tests (e.g. diabetes) at long-term follow-up (9).

We sought to determine whether in-person GC offered to patients receiving potentially actionable genomic risk information as part of a randomized trial affected patient communication with their physician team. Specifically, we examined whether GC affected documentation of physician–patient communication about genomic test results, determined by review of the first clinic note following test report upload to the electronic medical record (EMR), or after the patient met with a genomic counselor.

Methods

The Ohio State University-Coriell Personalized Medicine Collaborative (OSU-CPMC) parent study is a randomized clinical trial of in-person GC for patients with chronic disease (heart failure, hypertension) receiving potentially actionable results in an academic medical center setting (Fig. 1a). The primary study aim was to determine whether GC impacts risk perception and genomic test result comprehension (15). As part of the parent study, we recruited physicians taking care of OSU-CPMC patients into a pilot study to explore test result utilization and physician–patient communication regarding results (Fig. 1b) (15). The study was approved by the institutional review boards at Ohio State and the Coriell Institute for Medical Research.

Physician participants

Patients were enrolled with the assistance of Cardiovascular Medicine, Internal Medicine, and Family Medicine physicians. Physician leaders, one each from Cardiovascular Medicine and Internal Medicine, arranged informational group meetings among their physician colleagues. For these two groups, physician participation included attending a 1-h in-person educational module on the study randomization component, genetics/genomics/pharmacogenomics, single nucleotide polymorphisms and associated relative risks, test report composition, case examples and the process of GC. In all, we had 20 physicians (response rate, 57%; 12/27 Internal Medicine; 8/8 Cardiovascular Medicine) who consented to participate and worked with investigators to recruit patients. As study design required a sufficient number of physicians to be involved in order to accrue an adequate number of patients, leadership in the Department of Family Medicine were approached. However, this group was not interested in having their physician teams participate in the 1-h in-person educational module given work time constraints. Thus, a 1-h educational webinar accredited by Ohio State Wexner Medical Center for a maximum of 1.5 AMA PRA Category 1 Continuing Medical Education Credit(s)™ was made available. In total, 10 Family Medicine physicians participated in recruiting patients to study; however, none chose to view the webinar.

All study physicians were informed that each patient participant was provided access to nine personalized CPMC risk reports (coronary artery disease, type 2 diabetes, hemochromatosis, melanoma, prostate cancer, age-related macular degeneration, type 1 diabetes and lupus as well as impact of the *CYP2C19* gene on clopidogrel metabolism) through a private web portal. These eight conditions were chosen given the relative high frequency of the genetic variant used to assess risk; varied effect size of each variant on risk; and that each condition is potentially actionable via lifestyle modification or medical intervention (Table 1) (16). The reports present personalized risk information as relative risk for each of the eight health conditions, based on genetic variant, family history and health behavior risk factors individually, in both graphical and numeric format (Fig. S1, Supporting Information). To ensure readability, the report design was informed by multiple rounds of pilot testing conducted by allowing individuals with no scientific background to review report drafts and provide feedback.

Physicians were made aware that their patient's test reports would be made available following patient completion of required baseline surveys, genomic testing completion by the Coriell CLIA certified genotyping lab, report transfer from Coriell to Ohio State, and direct uploading to an EPIC® EMR. The CPMC reports were accessible by the study physician or any health care team member through hyperlinks to the report content via the

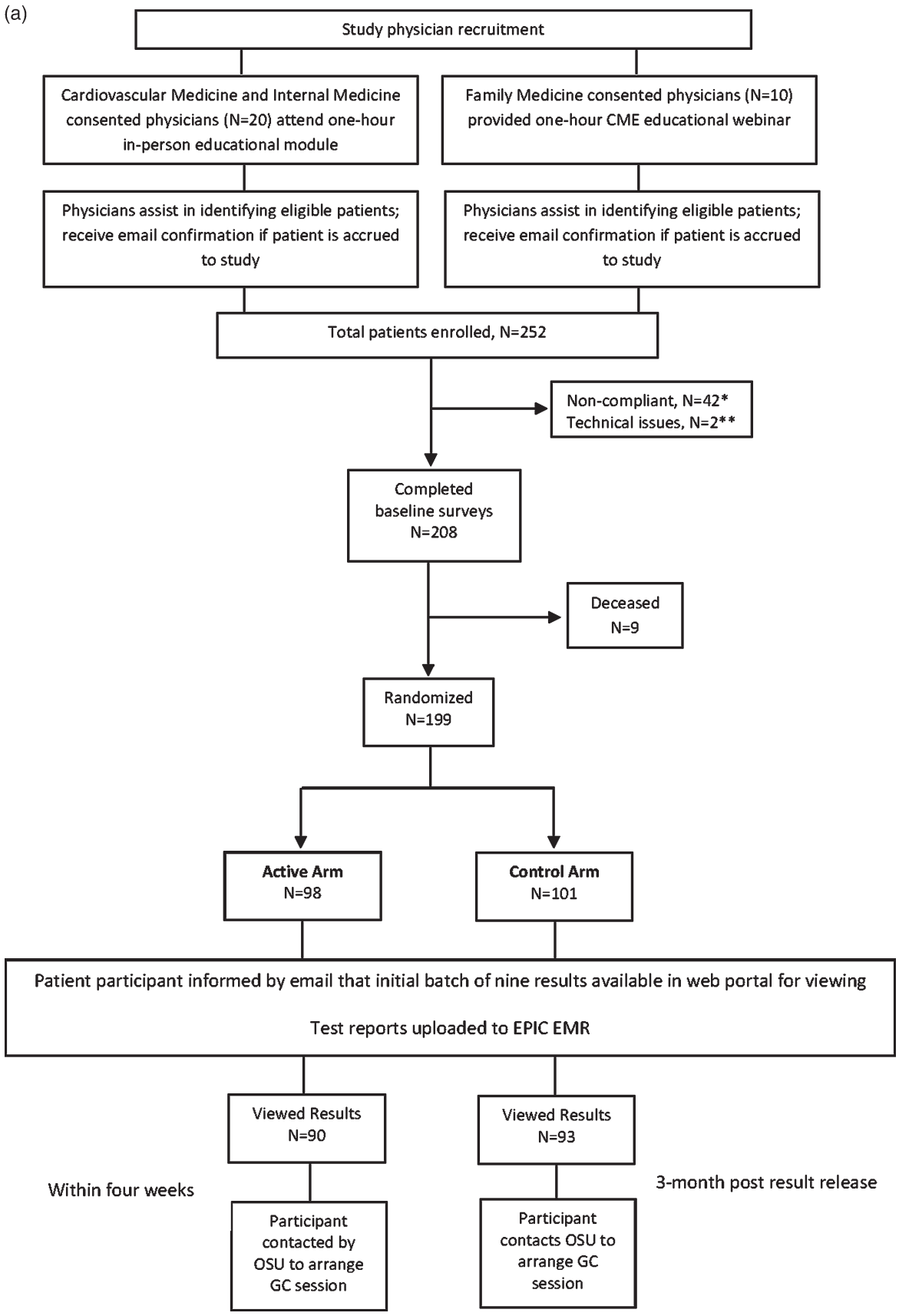

Fig. 1. (**a**) Parent study design. (**b**) EMR pilot to study physician-patient communication. *Non-compliance was when an individual had not completed the baseline surveys within a 45-day time limit. **Technical issues means the saliva DNA sample failed.

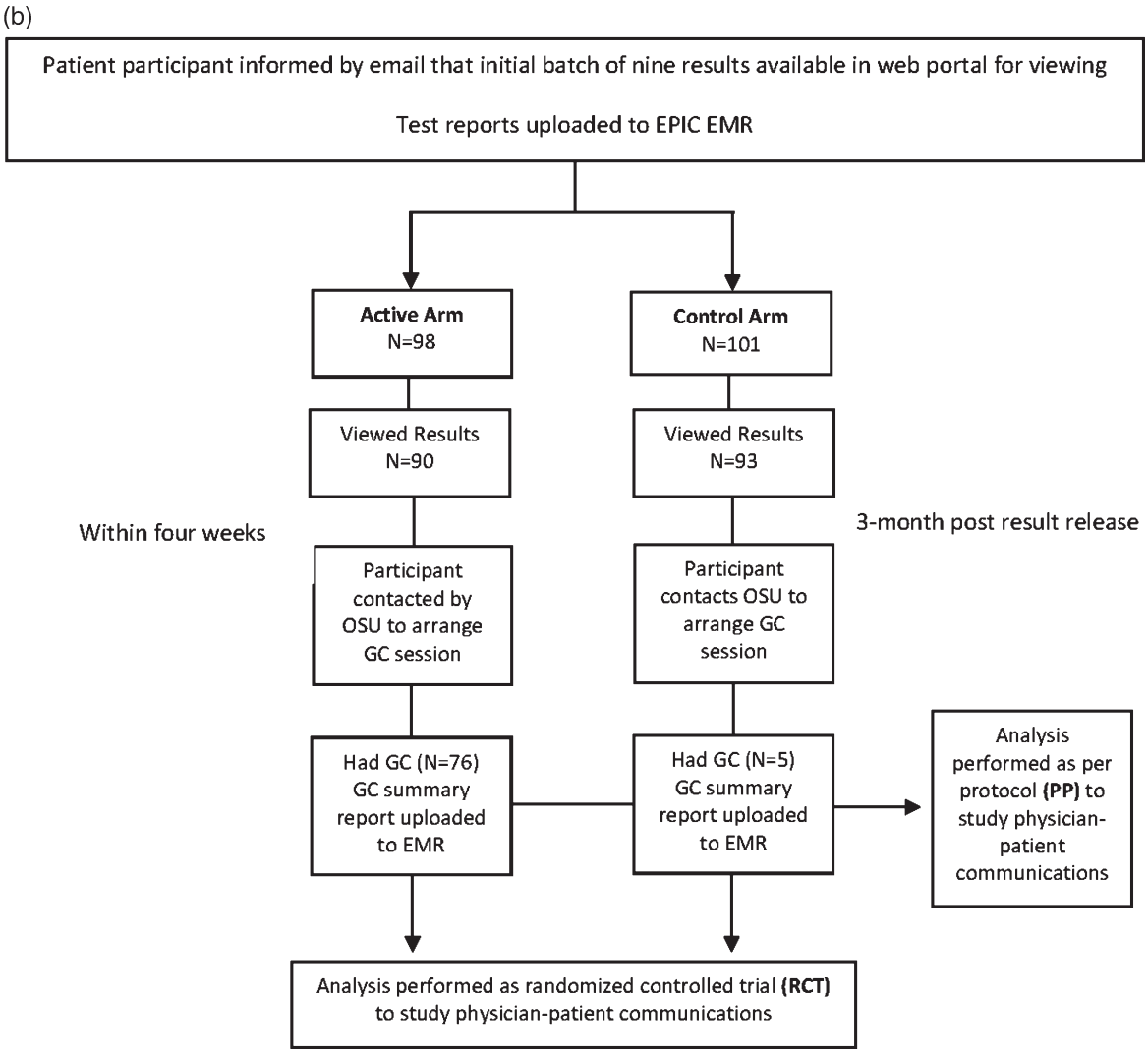

Fig. 1. Continued.

EPIC®/Labs tab. Similarly, physicians were made aware that if a patient participant was seen for GC, the summary letter would be made available in the EPIC® EMR as a research encounter. Per study design, there was no active notification of physicians for test report upload, or summary letter upload to the EMR.

Patient participants

A total of 252 patient participants were enrolled by study physicians with assistance of study recruiters over a 2-year period; four additional patients were recruited via Media/Research Match with physician involvement. Patient participants were administered a 1-h educational presentation including access to the CPMC web portal, background information on DNA, genes, and single nucleotide polymorphisms, CPMC test report composition, relative risk, the randomization component, and how they would be contacted regarding the availability of free GC. DNA samples and consent documentation were sent to Coriell, and unique CPMC web portal accounts were created for each patient participant. A total of 53 patients were subsequently removed from study (51 failed to complete all required parent study questionnaires; 2 due to unsuccessful genotyping). Thus, of the original 252 study participants, 199 patient participants comprised the study population. These individuals were randomized to either the active or control arm, with each arm receiving email notification of the availability of the initial batch of nine CPMC test reports. Active arm participants were called to schedule a GC appointment within 4 weeks of online viewing of at least one test report. Control arm participants were notified by email that they could request in-person GC after a 3-month randomization period, and after the viewing of at least one test report. Contact information to schedule the GC appointment for control arm participants was provided in the email. Study participants in both the active and control arms, who received GC, comprised the 'Received GC' group.

The in-person GC session, provided by one of two available licensed genomic counselors, focused on

Table 1. Reportable disease risk values for a Caucasian OSU-CPMC participant

Disease	Genetic Variant RR	Family history RR[a]	BMI RR	Smoking RR	Diabetes RR
AMD	2.4, 6.0	4.0	NA	1.4[b], 2.0[c]	NA
CAD	1.3, 1.7	1.2 F, 1.4 M	NA	2.1 M, 2.7 F	1.7 M, 2.4 F
DM1	0.08, 0.3	2.3; 6.6	NA	NA	NA
DM2	1.2, 1.3	1.9	2.3[d], 5.9[e]	NA	NA
HH	1.0 M, 27.0 M[f]	NA	NA	NA	NA
LUP	1.4, 2.0	4.1, 11.3	NA	1.0[b], 1.5[c]	NA
MEL	1.7, 3.0	2.2	NA	NA	NA
PRO	1.5 M, 1.5 M	1.9 M	NA	NA	NA

BMI, body mass index; F, female; M, male; NA, not applicable risk factor.

[a]Positive family history defined as follows: AMD (age-related macular degeneration), one or more first-degree relatives with age-related macular degeneration; CAD (coronary artery disease), one or both parents diagnosed with coronary artery disease; DM1 (type 1 diabetes), one (RR 2.3) or more (RR 6.6) first-degree relatives diagnosed with type 1 or type 2 diabetes; DM2 (type 2 diabetes), one or both parents with type 2 diabetes; LUP (systemic lupus erythematosus), one (RR 4.1) or two or more (RR 11.3) first-degree relatives with a history of any of the following autoimmune diseases: systemic lupus erythematosus (SLE/lupus), Sjogren's syndrome, rheumatoid arthritis, vitiligo, multiple sclerosis, celiac disease, type 1 diabetes, autoimmune hyperthyroidism-Grave's disease, autoimmune hypothyroidism, Crohn's disease, ulcerative colitis and psoriasis.; MEL (melanoma), one or more first-degree relatives with melanoma; PRO (prostate cancer), father and/or any brothers diagnosed with prostate cancer.

[b]Former smoker.

[c]Current smoker.

[d]BMI = 25.0–29.9 kg/m^2.

[e]BMI = ≥ 30 kg/m^2.

[f]RR (relative risk) only provided to males. Male heterozygotes and homozygote wild type received an RR of 1.0; females got absolute risk: homozygotes received 16% lifetime risk, heterozygotes and wild-type homozygotes received a lifetime risk of 1%.

individualized risk assessment for all nine personalized CPMC risk reports. During each session, the genomic counselor reviewed and expanded the patient's family history to obtain at least a three-generation pedigree, and reviewed the patient's medical and social history, environmental risk information, and current health promotion and screening practices (15). Sessions included active discussion of the major risk factors for a given disease, specific actions to prevent or lower disease risk, and recommendations for the patient participant to speak to their physician team regarding the recommended actions. A multi-page risk summary letter, developed by the investigation team, provided focused interpretation for each of the nine personalized CPMC risk reports, as well as recommendations based on the patient's medical and family histories. The GC summary letter was mailed to the patient, and also uploaded directly to the EMR.

Procedures

Each patient's EMR was reviewed from the date the genomic reports were uploaded (e.g. November 8, 2011 for the initial round of patients accrued to study), until the study was closed for analysis on August 22, 2014. Specifically, any documented interaction/note (e.g. office visit; phone call; Table 2(a)) that occurred between the patient participant, the study physician, or any member of the health care team was manually reviewed by KS for the following study-related search terms: Coriell, CPMC, genetic, genomic, GC, pharmacogenomic and variant. All relevant physician–patient communications (e.g. discussion of test results) related to these search terms, either by the study physician, or any medical provider were recorded. The number of times the patient participant was seen by the study physician during the time frame of chart review, with documentation of the first clinic interaction after upload of CPMC test reports, was recorded. If a patient participant was seen for GC, the number of times the patient was subsequently seen by the study physician, and date of the first clinic interaction post-GC was recorded. A second investigator, AS, subsequently performed manual review of the EMR with use of the seven study-related search terms for concordance. Both investigators (K. S., A. S.) agreed upon a subset of physician–patient communications. Following this initial round of manual chart review, investigators had opportunity to use a new EPIC informatics-based text search. As such, a second round of record review was performed by KS utilizing the same list of seven key search terms, and modifications were made to the original spreadsheet. Again, all recorded physician–patient communications were verified using the EPIC search function by a second investigator (A. S.). Both reviewers agreed on the final subset of physician–patient communications, as well as the placement of each communication into specific categories. Examples of physician–patient communications are found in Table 2(b). Review of the EMR took between 15 min and 3 h per patient participant to complete.

Outcome of interest

The primary study outcome of interest was defined as any physician–patient communication about the test results

Table 2. (a) Electronic medical record categories reviewed for documentation; (b) communication topics and examples of physician–patient result communication on the first interaction from the electronic medical record (EMR)

(a) Clinical support encounters
Documentation only (e.g. phone call; email correspondence)
Office visits
Patient letters
Problem list
Provider notes
Research encounters
Subspecialist referral

(b) Physician–patient communication	Frequency	Quoted examples from EMR
Discussion of complex disease test results	9	She had a number of questions about her genetic testing that was done during a recent study protocol. I have reviewed those test results and updated her records to indicate that she has a slight increased risk of melanoma. She also has a slight increased risk of macular degeneration and should be screened on a yearly basis
Specialty referral based on study findings	4	A clinical genetics research assessment (Coriell database) was performed in November of 2012 through a genetic counselor; this revealed genetics risk factors for the following: increased risk, coronary artery disease (CAD), type 2 diabetes: systemic lupus erythematous (SLE); age-related macular degeneration (AMD). Family history is relevant based on clinical genetics assessment for these diseases. FH was updated. Note, pt already receiving regular screening for CAD and DM2, and had elevated HgbA1c on a few occasions prior to consultation and afterward; then was diagnosed and treated for abdominal cancer. Referred to ophthalmology
Risk reduction conversation	3	Regarding macular degeneration prevention – speak with your eye doctor about EYE-caps or a similar vitamin with the 'AREDS' formula
Acknowledgement of study results in EMR	2	Documented CYP2C19 results from Coriell study: Ultra-rapid metabolizer
Blood testing/screening for lipids and glucose	1	Genetic risk assessment: he has been completed as a part of a project with Coriell Institute. He has genetic risk factors for type I and type II diabetes, as well as CAD. He is a rapid metabolizer for Plavix. To address risk factors, we are repeating fasting lipids and will obtain a fasting blood glucose
Patient sharing of study test results via EPIC MyChart	1	Dr. ____: Thought I had done this but doing some questionnaires on the CPMC study today. Attached is the letter that I think you need to be able to access my test result from the Study. Physician reply: Thanks.

CPMC, Coriell Personalized Medicine Collaborative.

on the patient's first interaction with their physician after EMR results were uploaded for control arm participants or after GC for active arm participants.

Statistical analyses

Descriptive statistics for socio-demographic and clinical variables were generated and compared between study arms. Both the 'Intention-To-Treat (ITT)' analysis and the 'Per-Protocol (PP)' analysis were performed for a robust interpretation of study results (17). As there were 30 subjects who did not return for a physician visit after the EMR report upload or after GC, comparison on age, gender, race, education, insurance, disease groups, and number of elevated genetic variant risks ($RR > 1.2$) between these 30 subjects with the rest of the sample population was performed to show no significant difference. Outcomes were analyzed on the assumption that physician communication could not be generated for those patients who did not come back for a clinical visit or have any documented physician encounter (null imputation). Multivariable logistic regression models were used to estimate the effects of GC and physician education intervention on any recorded physician–patient communication regarding genomic testing results. In order to capture the within-physician clustering arising from physicians who recruited more than one patient, these models were estimated using generalized estimating equations with an independent working correlation structure and robust standard errors. Possible confounder effects, including patient's age, gender, education, and disease group were also examined. Owing to the sample size limitation, these effects were examined in individual models. A two-sided significance level of $\alpha = 0.05$ was used for all tests. All analyses were carried out in SAS version 9.4 (SAS institute, Cary, NC).

Table 3. (a) Basic characteristics for each arm (ITT analysis); (b) basic characteristics for each arm as per protocol

(a) Variable	GC arm ($n = 98$)	Non-GC arm ($n = 101$)	Total
Age	57.8 ± 13.46	58.5 ± 12.6	58.1 ± 13.0
Gender[f]			
Male	60 (61.2%)	47 (46.5%)	107 (53.8%)
Female	38 (38.8%)	54 (53.5%)	92 (46.2%)
Race			
Caucasian	87 (88.8%)	93 (92.1%)	180 (90.5%)
Other	11 (11.2%)	8 (7.9%)	19 (9.6%)
Education			
≤High school	9 (9.2%)	10 (9.9%)	19 (9.5%)
Some college	17 (17.3%)	26 (25.7%)	33 (16.6%)
Associate degree	13 (13.3%)	12 (11.9%)	25 (12.6%)
Bachelor degree	22 (22.4%)	27 (26.7%)	49 (24.6%)
Graduate degree	37 (37.8%)	26 (25.7%)	63 (31.7%)
Income			
<$25 k	6 (6.1%)	12 (11.9%)	18 (9.1%)
$25–50 k	17 (17.4%)	20 (19.8%)	37 (18.6%)
$50–75 k	24 (24.5%)	14 (13.9%)	38 (19.1%)
$75–100 k	22 (22.5%)	17 (16.8%)	39 (19.6%)
>$100 k	26 (26.5%)	36 (35.6%)	62 (31.2%)
Did not want to answer	3 (3.1%)	2 (2.0%)	5 (2.5%)
Insurance			
Yes	90 (91.8%)	95 (94.1%)	185 (93.0%)
No	8 (8.2%)	5 (4.9%)	13 (6.5%)
Disease			
HF	45 (45.9%)	54 (53.5%)	99 (49.8%)
HTN	53 (54.1%)	47 (46.5%)	100 (50.2%)
Physician–patient result communication on first interaction			
Yes	13 (13.3%)	4 (4.0%)	17 (8.5%)
No	85 (86.7%)	97 (96.0%)	182 (91.5%)

(b) Variable	Had GC ($n = 91$)	Did not have GC ($n = 108$)	Total
Age	58.5 ± 12.8	57.9 ± 13.2	58.1 ± 13.0
Gender			
Male	47 (51.7%)	60 (55.6%)	107 (53.8%)
Female	44 (48.3%)	48 (44.4%)	92 (46.2%)
Race			
Caucasian	82 (90.1%)	98 (90.7%)	180 (90.5%)
Other	9 (9.9%)	10 (9.3%)	19 (9.6%)
Education			
≤High school	5 (5.5%)	14 (13.0%)	19 (9.5%)
Some college	18 (19.8%)	25 (23.2%)	33 (16.6%)
Associate degree	14 (15.4%)	11 (10.2%)	25 (12.6%)
Bachelor degree	26 (28.6%)	23 (21.3%)	49 (24.6%)
Graduate degree	28 (30.8%)	35 (32.4%)	63 (31.7%)
Income			
< $25 k	8 (8.8%)	10 (9.3%)	18 (9.1%)
$25–50 k	15 (16.5%)	22 (20.4%)	37 (18.6%)
$50–75 k	19 (20.9%)	19 (17.6%)	38 (19.1%)
$75–100 k	20 (22.0%)	19 (17.6%)	39 (19.6%)
>$100 k	26 (28.6%)	36 (33.3%)	62 (31.2%)
Did not want to answer	3 (3.3%)	2 (1.9%)	5 (2.5%)
Insurance			
Yes	82 (90.1%)	103 (95.4%)	185 (93.0%)
No	8 (8.8%)	5 (4.6%)	13 (6.5%)
Disease			
HF	39 (42.9%)	60 (55.6%)	99 (49.8%)
HTN	52 (57.1%)	48 (44.4%)	100 (50.2%)
Physician–patient result communication on first interaction			
Yes	16 (17.6%)	4 (3.7%)	20 (10.1%)
No	75 (82.4%)	104 (96.3%)	179 (89.9%)

GC, genomic counseling; ITT, intention to treat.

[a]p-value for comparison between the two arms = 0.04 (chi-square test).

Table 4. (a) Physician–patient result communication on first interaction (ITT analysis); (b) estimated OR of physician–patient result communication on first interaction adjusted for co-variants (ITT analysis)

(a)

Predictor	Levels	Physician–patient communication on first interaction: Yes ($n=17$)	Physician–patient communication on first interaction: No ($n=182$)	OR	95% CI	p-value
GC group as randomized	Active arm ($n=98$)	13 (13.3%)	85 (86.7%)	3.76	1.38–10.22	0.0094
	Control arm ($n=101$)	4 (4.0%)	97 (96.0%)	1.0		
Physician educational intervention	Yes ($n=122$)	10 (8.2%)	112 (91.8%)	0.82	0.24–2.80	0.76
	No ($n=77$)	7 (9.1%)	70 (90.9%)	1.0		

(b)

Effect	OR	95% CI	p-value
Adjusted on patient's age			
GC group as randomized	3.72	1.38–10.01	0.0095
Physician educational intervention	0.82	0.24–2.82	0.75
Adjusted on patient's gender			
GC group as randomized	3.47	1.24–9.70	0.020
Physician educational intervention	0.82	0.24–2.81	0.75
Adjusted on patient's education			
GC group as randomized	3.74	1.36–10.27	0.011
Physician educational intervention	0.81	0.25–2.68	0.74
Adjusted on patient's disease group			
GC group as randomized	3.67	1.36–9.90	0.011
Physician educational intervention	0.90	0.25–3.28	0.87
Adjusted on patient's number of elevated genetic variant risks			
GC group as randomized	3.70	1.34–10.22	0.011
Physician educational intervention	0.82	0.24–2.78	0.75
Adjusted on the number of days between EMR results uploaded and the first interaction			
GC group as randomized	6.16	2.07–18.37	0.003
Physician educational intervention	0.65	0.19–2.25	0.52

CI, confidence interval; GC, genomic counseling; ITT, intention to treat; EMR, electronic medical record; OR, odds ratio.

Results

Patient characteristics

Table 3(a) depicts basic characteristics and socio-demographic information for each arm (ITT analysis; 98 active; 101 control). Table 3(b) describes each arm per protocol (i.e. had GC *vs* did not have GC). There were no significant differences in demographics between the study groups based on randomization or receiving GC except more males were randomized into active arm. Of 199 study participants, 137 (68.8%) had an associate's degree or higher; 180 (90.4%) were white. There were more male participants, 107 (53.8%), than female; 25 (12.5%) worked in a health care-related occupation (e.g. nursing). Mean age was 58.1 years (range: 24–94). All 199 study participants received email notice of the availability of the initial batch of 9 test reports in their web portal, of which 183 participants viewed at least one CPMC report. There were 40 subjects with 1 elevated genetic variant risk variable; 68 subjects with 2 elevated genetic risk variables; and 87 subjects with 3+ elevated genetic risk variables. In all, 33 (16.6%) participants had intermediate and 3 poor metabolizer response to Clopidogrel. The average number of participants' visits to physician after initial results uploaded to EMR was 2.8 (median: 2; range 0–9). Of 80 active arm participants scheduled for in-person GC, 76 (95%) were seen. In the control arm, 15 of 101 contacted investigators after the randomization period and received in-person GC 3 or more months after viewing at least one result. Thus, the received GC group comprised 91 individuals. Comparisons on age, gender, race, insurance, education, disease groups, and number of elevated genetic risk variants did not show significant differences between the 22 subjects in the active arm who did not receive GC and the rest of the subjects in the active arm who did receive GC. No significant difference was found in the control arm between those who received GC and those did not. Participants in the GC arm were followed-up for an average of 222 days (median: 154; range: 36–1010), which was similar to an average of 175 days follow-up for participants in the control arm (median: 101; range: 30–739).

Physician–patient result communication on first clinic interaction (ITT analysis)

Using an ITT framework, there were a total of 17 physician–patient communications regarding genomic testing results (e.g. specialty referral; discussion of test results; Table 2(b)) on the patient's first clinic interaction (13, active arm; 4, control arm). Median time to first

clinic interaction was 198.5 days (range: 44–651) in the active arm and 78.5 days (range: 1–644) in the control arm. Active arm participants receiving GC as randomized was a significant predictor of physician–patient communication regarding testing results on the first clinic interaction (Table 4(a)). The odds of having this communication exchange on the patient's first interaction after EMR report upload or after GC for active arm participants was 3.76 times higher than for control subjects (95% CI: 1.38–10.22, $p < 0.0094$). Neither physician educational intervention nor its interaction with the GC arm was a significant predictor. The ORs were not significantly modified after adjusting for patient's age, gender, education, disease group, or number of elevated genetic variant risks in separate modeling (Table 4(b)). However, the odds of having communication exchange on the patient's first interaction for GC arm as randomized was greatly increased after adjusting for the number of days between the EMR results uploaded and the first clinic interaction (OR: 6.16, 95% CI: 2.07–18.37, $p = 0.003$). The association between physician–patient result communication with age, gender, education, disease number of elevated risks, or the number of days between the EMR results uploaded and the first clinic interaction was not significant in any of the separate models.

Physician–patient result communication on first clinic interaction (PP analysis)

Using a 'per protocol' framework, there were a total of 20 physician–patient communications regarding genomic testing results noted on the first clinic interaction after receiving GC (16 active arm; 4 control arm). Median time to first clinic interaction was 205 days (range: 44–833) for patients who received GC and 80 days (range: 1–534) for patients who did not receive GC. The distribution of physician–patient communications is shown in Fig. 1. The odds for participants that received GC to engage in physician–patient communication regarding genomic testing results at the patient's first clinic interaction after GC were 5.53 (95% CI: 2.20–13.90, $p = 0.0017$) times higher than for patients who did not receive GC (Table 5(a)). Neither physician educational intervention nor its interaction with actual GC group was a significant predictor. The ORs were not significantly modified after adjusting for patient's age, gender, education, disease group, the number of elevated genetic variant risks, or the number of days between EMR results uploaded and the first clinic interaction in separate models (Table 5(b)). The association between physician–patient result communication with age, gender, education, disease group, number of elevated risks, or the number of days between EMR results uploaded and the first clinic interaction was not significant in any of the separate models.

Physician–patient result communication for any interaction during the follow-up period

Secondary analyses were performed with any note documenting physician–patient communication about the study results throughout the follow-up period. Most of the physician–patient communication occurred on the first interaction, with only three additional communications (one participant in the active arm who actually received GC; two in the control arm who actually received GC) noted during the remainder of the follow-up period. The effect of actual GC on physician–patient communication throughout the follow-up period was 5.03 (95% CI: 2.19–11.71) times the odds for participants who did not receive GC in PP analysis. The effect of receiving GC as randomized was not a significant predictor of such communication throughout the follow-up period in ITT analysis (OR: 1.69, 95% CI: 0.88–3.23, $p = 0.12$). Neither ORs were significantly modified after adjusting for the total number of follow-up days.

Discussion

In our study, GC of patients with chronic disease receiving potentially actionable complex disease and pharmacogenomics results in an academic medical setting was associated with increased physician–patient communication regarding testing results. The effect on increasing physician–patient communication may rest on the ability of the genetic/genomic counselor to convey appropriate risks to the patient, and how their risk can be modified by individual actions (e.g. lifestyle modification) and through interaction with their physician team.

A number of studies have shown that genetic counseling can improve individual basic genetic knowledge (17), produce more accurate risk perceptions (18) and greater perceived personal control (19–23). We found that participants in our parent chronic disease study receiving GC had enhanced objective understanding of the genetic variant risk contribution to potentially actionable complex disease reports (24). Another study found that among women who received comprehensive *BRCA* testing ordered by their clinician, those receiving pre-test genetic counseling demonstrated improved knowledge and understanding of the information received, and greater satisfaction than non-counselees (21).

Although it is not clear in our study who initiated conversations (patients or physicians) regarding genomic testing results, having access to their personalized genomic data may help activate patients to take independent actions to manage their disease risks (25, 26) particularly when accompanied by GC. Patients who are more activated are more likely to self-manage and take a more proactive role in their health care than patients who are less activated (27). Given that counselees were provided specific actions to prevent or lower disease risk, both in the counseling session and in the GC summary letter, and advised to speak to their study physician team regarding these recommended actions, it is likely these recommendations would have been fresh in the patient's mind when they next saw or contacted their physician, which we found to be the case in our EMR review. Continued integration of genomic counselors to provide this necessary support and positive reinforcement can help patients discuss potentially actionable results with their

Table 5. (a) Physician–patient result communication on first interaction as per protocol; (b) estimated OR of physician–patient result communication on first interaction as per protocol adjusted for co-variants

(a)

Predictor	Levels	Physician–patient communication on first interaction: Yes ($n=20$)	Physician–patient communication on first interaction: No ($n=179$)	OR	95% CI	p-value
GC group as per protocol	Active arm ($n=91$)	16 (17.6%)	75 (82.4%)	5.53	2.20–13.90	0.0017
	Control arm ($n=108$)	4 (3.7%)	104 (96.3%)	1.0		
Physician educational intervention	Yes ($n=122$)	13 (10.7%)	109 (89.3%)	1.16	0.33–4.06	0.82
	No ($n=77$)	7 (9.1%)	70 (90.9%)	1.0		

(b)

Effect	OR	95% CI	p-value
Adjusted on patient's age			
GC group as per protocol	5.73	2.38–13.83	0.0014
Physician educational intervention	1.19	0.34–4.21	0.78
Adjusted on patient's gender			
GC group as per protocol	5.62	2.27–13.91	0.0016
Physician educational intervention	1.13	0.31–4.03	0.85
Adjusted on patient's education			
GC group as per protocol	5.51	2.19–13.91	0.0018
Physician educational intervention	1.14	0.32–4.03	0.84
Adjusted on patient's disease group			
GC group as per protocol	5.31	2.16–13.06	0.0019
Physician educational intervention	1.29	0.34–4.91	0.70
Adjusted on patient's number of elevated genetic variant risks			
GC group as per protocol	5.61	2.24–14.06	0.0016
Physician educational intervention	1.11	0.32–3.83	0.86
Adjusted on the number of days between EMR results uploaded and the first interaction			
GC group as per protocol	5.46	2.01–14.81	0.0028
Physician educational intervention	1.07	0.32–3.62	0.91

CPMC, Coriell Personalized Medicine Collaborative; CI, confidence interval; EMR, electronic medical record; GC, genomic counseling; OR, odds ratio.

physicians, who may not otherwise address them, and increase personal utility of the information.

We had a 21.9% rate of physician–patient communication in the setting of GC. This is somewhat low but not surprising, given the physician educational intervention occurred at the onset of patient recruitment, was a one-time event, and the test results were forthcoming for newly accrued patients over the course of more than 2 years. Moreover, we took a passive approach in uploading test reports and GC summary letters into the EMR without active notification of the physician team as per study protocol. It is possible that physicians may not have perceived much value or benefit in the results. Although concern remains that personal genome results could lead to unnecessary workup (28), significant post-test increases in the use of medical procedures (e.g. mammogram) are not well supported by the current literature (13, 21, 29), and were not found in our study (Table 2(b)). It is also likely that time was limited during visits with patients with at least one chronic disease, and therefore other medical concerns took precedence.

The low rate of physician–patient result communication does suggest an opportunity for more active alerting of the physician team regarding genomic consultations about potentially actionable results, and that we should be more active in EMR documentation and routing of potentially actionable results and their resulting preventive recommendations. Knowing that physicians may not raise the topic of genomic testing results during consultations with patients, even when they are available in the EMR, suggests an opportunity for intervention. Genomic counselors and other health care providers trained in patient activation can facilitate this intervention by building patient confidence and encouraging patients to talk to their physicians about their results.

The study has some limitations. First, the data were extracted from electronic chart notes. The content of undocumented oral communications between providers and patients, and the providers' unwritten thought processes, is unknown. It is possible that additional discussions about study results and/or the GC intervention did take place, was not recorded, or was recorded incorrectly by the physician. Second, due to sample size constraints, we were unable to adjust for all variables in a single logistic regression model. Moreover, these analyses are likely underpowered to allow comment about the possible effects on physician education. Lastly, these results may not generalize across practice settings, or more diverse populations.

Our data suggest that GC appreciably affected physician–patient communication post-receipt of genomic risk information for multiple complex disease risks. Results of a recent systematic review suggest that communicating DNA-based disease risk estimates has little or no effect on risk-reducing health behaviors (30); however, none of these prior studies facilitated participant behavior modification by providing GC for a range of multifactorial disease risks (relative risks 0.08–>6.0), and incorporating a summary plan with action steps provided to both the patient and provider team as was done in this study. Outcomes were primarily based on self-report of behavior change, and did not involve EMR review. Continued investigation of GC intervention in the genomic result delivery process, with the potential to motivate positive change in health-related measures is warranted (31).

Supporting Information

Additional supporting information may be found in the online version of this article at the publisher's web-site.

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