

**Genetics Plays a  
Limited Role in  
ESA-Hyporesponsiveness  
and Haemoglobin Outcomes  
in End-Stage Renal Disease  
Patients on Haemodialysis**

**Sivakumar Gowrisankar<sup>1</sup>, Audrey Y. Chu<sup>2</sup>,  
Jennifer L. Aponte<sup>2</sup>, Dana J. Fraser<sup>1</sup>,  
Gilbert Marlowe<sup>3</sup>, Jeffrey Connaire<sup>3</sup>,  
Lynn D. Condrey<sup>1</sup>, Margaret G. Ehm<sup>2</sup>,  
Rubeen K. Israni<sup>2</sup>**

*<sup>1</sup>Parexel International, Durham, North Carolina, United States;*

*<sup>2</sup>GlaxoSmithKline, Collegeville, Pennsylvania, United States;*

*<sup>3</sup>DaVita Clinical Research, Minneapolis, Minnesota, United States*

**Disclosures and Funding:**

- **SG** is an employee of Parexel International; **AYC, JLA, MGE and RKI** are employees of and shareholders in GlaxoSmithKline; **DJF and LDC** are employees of Parexel International and shareholders in GlaxoSmithKline; **GM** is an employee of and shareholder in DaVita; **JC** reports consultancy agreements and research funding with GlaxoSmithKline, ownership interest in DaVita Inc., and is a scientific advisor to GlaxoSmithKline
- This study was funded by GlaxoSmithKline
- Medical writing support (in the form of collating author comments and grammatical editing) was provided by Joanna Wilson, PhD, of Ashfield MedComms, Glasgow, UK, and was funded by GlaxoSmithKline

# Introduction and Methodology



## Study Population:

- ESRD patients on HD from DaVita Inc., a large dialysis organization in the US
- African Americans: 1380 patients;  
European Americans: 1410 patients



## Objective:

To determine if genetic variation, as measured by genetic risk score (GRS) is associated with anaemia outcomes in the ESRD population. GRS is calculated as a sum of the individual variant effects on hemoglobin concentration.



## Method:

- A logistic regression model was used to study association between exposure variables and ESA\* hyporesponsiveness<sup>†</sup> and iron replete status<sup>‡</sup> outcomes
- A linear regression model was used to study association between exposure variables and Hgb concentration<sup>§</sup> outcome

## Exposures

- Genetic instruments:
  - Hgb Trans-ethnic GRS
  - Hgb European GRS
  - Hgb *EGLN* 1,2,3 GRS
- Demographics
- Prior treatments
- Baseline labs



## Anaemia Outcomes of Interest

- ESA Hyporesponsiveness
- Time-weighted mean Hgb
- Iron replete status

## Results

- Ancestry-specific baseline differences
- GRS, clinical variables association with outcomes

# Population-Level Differences of Baseline Variables Between African and European Americans



# Clinical Variable Associations With Anaemia Outcomes

Variable	AA vs EA mean/proportion diff: mean (95% CI)	P-value
Age, years	-6.93 (5.87 – 7.99)	3.35 x 10 <sup>-36</sup>
Sex, % female	5.80 (1.74 – 9.86)	0.0062
Time on dialysis, years	1.92 (1.56 – 2.30)	5.07 x 10 <sup>-24</sup>
Baseline albumin, g/L	0.39 (0.11 – 0.67)	0.0066
Baseline ferritin, ng/mL	80.01 (49.38 – 110.64)	3.24 x 10 <sup>-7</sup>
Baseline creatinine, µmol/L	214.58 (194.85 – 234.31)	7.24 x 10 <sup>-92</sup>
Baseline sys BP status, mmHg		1.78 x 10 <sup>-4</sup>
High [≥160mmHg], %	7.70 (3.78 – 11.62)	NA
Low [<120mmHg], %	-2.8 (-5.12 to -0.48)	NA

## Summary of observed differences



1. At enrolment AAs were on an average 6.93 years younger than EAs
2. The % of females in AA were 5.8% higher than the % in EA
3. AAs were 1.92 years longer on dialysis than EAs
4. Baseline differences in labs were also observed (see table)
5. AAs had higher % of patients with high BP (7.70% higher) and lower % of patients with low BP (2.8% lower) compared to EAs
6. Results indicate that population-level baseline variable differences need to be accounted for when designing clinical trials or providing clinical care

Clinical characteristic	Outcome		
	ESA (HypoR vs responsive)* OR, p-value	Hgb concentration† estimate, p-value	Iron outcome (not replete vs replete) OR, p-value
Age, years	0.98, p<0.01‡	NS	1.01, p<0.05‡¶
Sex [ref=female]	1.21, p<0.01‡ 1.14, p<0.05‡¶	NS	NS
Time on dialysis, months	1.01, p<0.01‡	8.33x10 <sup>-4</sup> , p<0.01§	NS
ARB/ACEi status [ref=no baseline use]	0.79, p<0.01‡	-0.09, p<0.05‡¶ -0.11, p<0.01§	NS
BMI, kg/m <sup>2</sup>	0.93, p<0.0001	NS	1.03, p<0.01§
Hgb, g/L	0.93, p<0.0001‡ 0.95, p<0.0001§	0.03, p<0.0001	0.97, p<0.0001‡
TSAT, %	0.97, p<0.0001‡ 0.99, p<0.01§	NS	0.89, p<0.0001
Albumin, g/L	0.93, p<0.001§	NS	0.91, p<0.0001§

When a single OR/estimate and p-value are shown without designating a particular population, the result applies to both the AA and EA populations. \*ESA hypoR vs responsive status during 1-year period post-enrolment; †Time weighted mean Hb concentration per day measured during 1-year period post-enrolment; ‡In EA population; §In AA population; ¶Nominal association

# Genetic Risk Scores Were not Associated With Outcomes of Interest

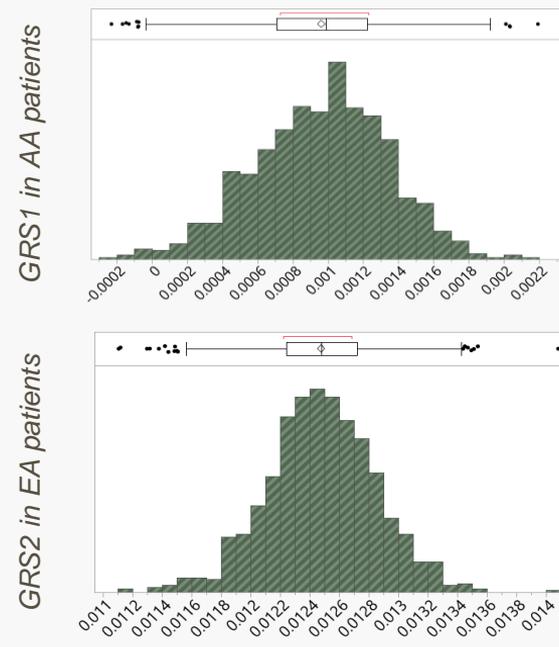


- 1 Hgb trans-ethnic GRS, constructed using variants from 5 ancestry-specific analyses with ~750K participants<sup>1</sup> (GRS1: only for AA patients)
- 2 Hgb European GRS, constructed using variants from UK biobank cohort with ~408K participants<sup>2</sup> (GRS2: only for EA patients)
- 3 Hgb GRS3 constructed from variants overlapping EGLN 1, 2, 3 and using beta/effect size from Vuckovic et al. 2020<sup>2</sup> (GRS3 used in both AA and EA patients)

GRS

	ESA (HypoR vs responsive) p-value		Hgb concentration p-value		Iron outcome (not replete vs replete) p-value	
	EA	AA	EA	AA	EA	AA
<b>GRS1</b>	NA	p>0.1	NA	p>0.1	NA	p>0.5
<b>GRS2</b>	p>0.1	NA	p>0.1	NA	p>0.1	NA
<b>GRS3</b>	p<0.05 <sup>‡</sup>	p>0.05	p>0.5	p<0.01 <sup>*</sup>	p>0.5	p>0.5

Distribution of GRS in cohort from this study



1. Chen M-H et al. Trans-ethnic and ancestry-specific blood-cell genetics in 746,667 individuals from 5 global populations. Cell. 2020; 182: 1198-1213;  
 2. Vuckovic et al. The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell. 2020 Sep 3;182(5):1214-1231.e11.

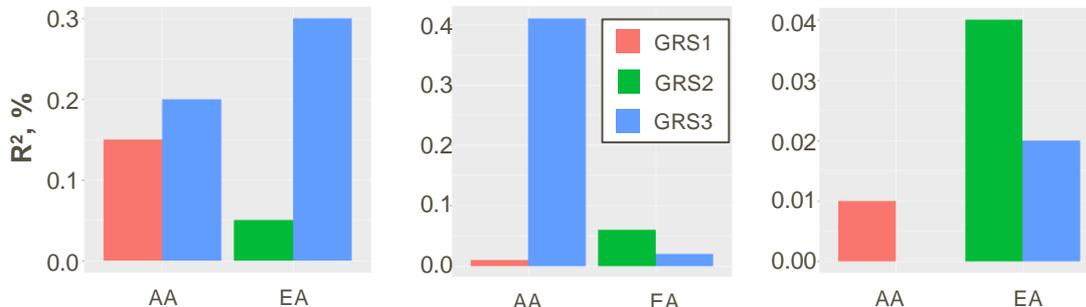
\*Low beta squared effect size =0.005; †High mean OR with high variability

AA, African American; EA, European American; ESA, erythropoiesis-stimulating agent; GRS, genetic risk score; Hgb, haemoglobin; HypoR, hyporesponsive; NA, not applicable; OR, odds ratio

# Genetic Risk Scores Have no Clinically Meaningful Associations With Outcomes



**R<sup>2</sup> coefficient of determination for GRS: A measure of variance captured. High R<sup>2</sup> means high ability to explain variation in outcomes**



a) ESA HypoR

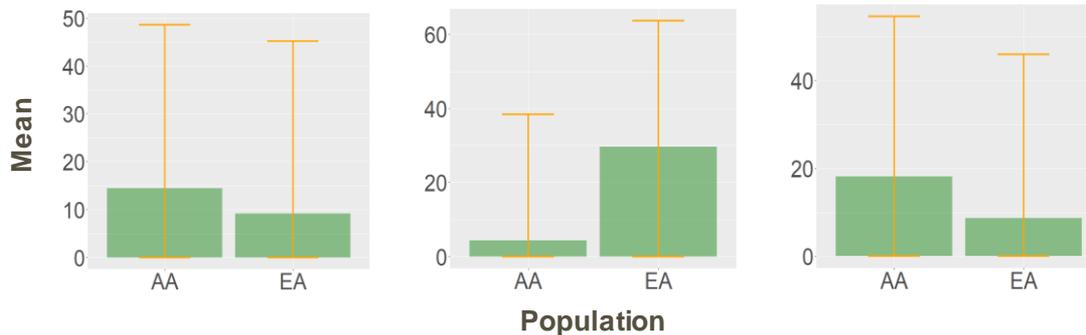
b) Hgb Conc

c) Iron outcomes

## Summary

For the statistically significant associations, the R<sup>2</sup> indicated that none of the GRSs evaluated explained clinically meaningful variation in outcomes of interest

**GCTA heritability estimates with SE**



## Summary

GCTA analysis showed moderate heritability with high SE, indicating inconclusive evidence for significant genetic component for outcomes

# Acknowledgements

---

- Sandra Stinnett (Parexel) for assistance with genetic sample genotyping
- Charles Cox (Pharmacogenetics, GlaxoSmithKline) for project support and insightful review and interpretation of results
- Alex Cobitz (Daprodustat team, GlaxoSmithKline) for input into protocol and data interpretation