Variants of *GCKR* **Affect both Beta Cell and Kidney Function in Patients with Newly Diagnosed Type 2 Diabetes. The Verona Newly Diagnosed Type 2 Diabetes Study (VNDS). 2.**

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Experimental Design

The Verona Newly Diagnosed Type 2 Diabetes Study (VNDS) is an ongoing study aiming at building a biobank of patients with newly diagnosed type 2 diabetes. As of Jan 1 2002, all patients referred to the Division of Endocrinology and Metabolic Diseases of University of Verona School of Medicine, whose diabetes has been diagnosed in the last six months, are asked to participate in this research. The clinical evidence on which the diagnosis of type 2 diabetes has been made is reviewed and the diagnosis confirmed (1). Patients are drug-naïve or, if already treated with antidiabetic drugs, undergo a treatment washout of at least one week before metabolic tests are performed. Among the exclusion criteria are age>75 years, non-Italian ancestry, insulin treatment, presence of anti-GAD antibodies, malignancies, and any condition severely impairing liver and/or kidney function. In this study, we report the data collected in 509 patients, whose characteristics are summarized in Table 1.

All subjects consumed a weight-maintaining diet containing 200-250 g of carbohydrate/day for at least three days before studies. Body weight was stable in all subjects for at least 1 month before studies. No subject participated in any heavy exercise. Each subject gave informed written consent before participating in the research, which was approved by the Human Investigation Committee of the Verona City Hospital. Measurements of standard clinical phenotypes were collected in all patients. Metabolic tests were carried out on two separate days in random order. On both days, patients were admitted to the Metabolic Clinic Research Center at 07:30 after an overnight fast. All studies were carried out in a quiet, temperature controlled (22° C) room.

On one day an OGTT (75 g) was performed to assess beta cell function. For ethical reasons, the OGTT was not performed in patients presenting with FPG greater than 15 mmol/l. During the entire test patients were sitting in a comfortable cardiac chair. One teflon (21 g) venous catheter was inserted into an antecubital vein for blood sampling and kept patent with heparinized normal saline solution. After a 30' rest to establish baseline and after collecting a 20 cc blood sample for leukocyte DNA extraction, at time = 0' subjects ingested 75 g of glucose in 300 ml of water over 5 min. Blood samples to measure glucose, C-peptide and insulin concentrations were collected at times -10° , 0° , $+15^{\circ}$, $+30^{\circ}$, $+45^{\circ}$, $+60^{\circ}$, $+90'$, $+120'$, $+150'$, $+180'$, $+210'$ and $+240'$. In some patients further blood samples were collected at +270' and +300'. Urines were collected to measure glycosuria.

On a separate day, a euglycemic insulin clamp was performed to assess insulin sensitivity (2). During the entire test patients were lying in bed. One teflon catheter was introduced into an antecubital vein for the infusion of test substances. Another teflon catheter was placed retrogradely into a wrist vein for sampling arterialized venous blood, according to the "hot box" technique. After a 30' rest in bed to establish baseline, indirect calorimetry (at least 40') was performed as previously described, for a companion study (1). At the end of calorimetric measures, baseline blood samples were collected and a standard euglycemic insulin (intravenous prime: 4.8 nmol min⁻¹ m⁻² BSA; continuous infusion: 240 pmol $\min^{-1} m^{-2}$ BSA) clamp was performed (1). Plasma glucose was allowed to decline until it reached 5.5 mmol/l, after which glucose clamping started with a glucose concentration goal of 5 mmol/l. The duration of the glucose clamp was at least of 120', but it was prolonged, if and as needed, to ensure at least 60' of insulin clamp at euglycemia in each patient. Timed blood samples were collected to measure hormone and substrate levels. In the last 45' of the clamp indirect calorimetry was repeated to assess substrate oxidation and energy production rates for a companion study. Urines were collected to measure urea excretion rate.

In both metabolic tests, all blood samples were collected in pre-chilled tubes and readily spun at 1,500 g. Plasma and serum specimens were stored at –80° C.

Mathematical Modeling of Beta Cell Function

The analysis of the glucose and C-peptide curves during the OGTT follows the general strategy described in previous publications (3; 4) with some modifications and builds upon previous works from other laboratories (5; 6). The kinetics of C-peptide is described with a two-compartment model, in which the two pools (1 and 2) exchange with each other and the irreversible loss of the hormone is from pool 1, the same where C-peptide concentration is measured. C-peptide kinetic parameters are computed according to the equations by Van Cauter et al. (7).

Herein are the equations describing the model of glucose induced insulin secretion during an OGTT:

$$
dcp_1(t)/dt = ISR(t) + cp_2 \ k_{12} - (k_{01} + k_{21}) \ cp_1 \ (Eq.1)
$$

where ISR = insulin secretion rate, $cp_1 = C$ -peptide mass in the sampling (accessible) compartment, cp_2 $=$ C-peptide mass in the remote compartment, k_{12} and k_{21} = rate constants of the exchange between the two C-peptide compartments, and k_{01} = rate constant of the irreversible loss of C-peptide from the accessible compartment. Note that the values of the volume of distribution of C-peptide pool 1 (accessible compartment), k_{12} , k_{21} , and k_{01} are computed according to the equations by Van Cauter et al. (7).

$$
ISR(t) = BSR + DSR(t) + PSR(t) (Eq.2)
$$

where $BSR =$ basal insulin secretion rate. $DSR =$ insulin secretion rate due to the derivative (or dynamic) component, and PSR = insulin secretion rate due the proportional (or static) component.

$$
BSR = CP_{ss} \cdot V_1 \cdot k_{01} (Eq. 3)
$$

where CP_{ss} is basal C-peptide concentration and V_1 is the volume of the accessible compartment of Cpeptide.

From the modeling viewpoint, DSR(t) and PSR(t) are the components which in intravenous glucose tolerance tests or hyperglycemic clamps describe classical first phase insulin secretion and second phase insulin secretion, respectively. Furthermore, from a physiological viewpoint, the sum of BSR and PSR(t) describes the relationship linking glucose concentration and insulin secretion rate, in the absence of the derivative component (DSR).

DSR(t) and PSR(t) are mathematically defined as follows:

$$
\text{DSR (t) = X1 (t) \cdot \tau^{-1} \text{ (Eq. 4)}
$$
\n
$$
dX1 (t) / dt = \sigma I \left[dG(t)/dt \right] / \left[\log(1.1 + t) \right] - X1(t) \tau^{-1} \text{ if } dG(t)/dt > 0 \text{ (Eq. 5)}
$$
\n
$$
dX1(t) / dt = - X1(t) \tau^{-1} \text{ if } dG(t)/dt \le 0 \text{ (Eq. 6)}
$$

where σ = glucose sensitivity of derivative control of insulin secretion, $G =$ plasma glucose concentration, $X1 = C$ -peptide (insulin) mass made available for the derivative component of insulin secretion, τ = time constant of the derivative component of insulin secretion, and the term $log(1.1 + t)$ accomodates the time-associated decline of σ1 documented in humans during a hyperglycemic stimulus (8).

$$
PSR(t) = X2(t) \cdot \delta^{-1} \quad (Eq. 7)
$$

$$
dX2(t) / dt = \sigma 2 \quad [G(t) - \theta] - X2(t) \quad \delta^{-1} \quad (Eq. 8)
$$

where σ^2 = glucose sensitivity of the proportional component of insulin secretion, X^2 = C-peptide (insulin) mass made available for the proportional component of insulin secretion, δ = time constant of the proportional component of insulin secretion, θ = glucose threshold above which the beta-cell responds with the proportional component of insulin secretion to plasma glucose concentration.

This model was implemented in the SAAM 1.2 software (SAAM Institute, Seattle, WA) (9) to estimate its unknown parameters. Numerical values of the unknown parameters were estimated by using nonlinear least squares. Weights were chosen optimally, i.e., equal to the inverse of the variance of the measurement errors, which were assumed to be additive, uncorrelated, with zero mean, and a coefficient of variation (CV) of 6-8%. The unknown parameters of the model are: CP_{ss}, σl , τ , σz , δ , and θ. They were estimated with good precision, as shown by their CVs (online-only appendix table 1) A good fit of the model to data was obtained as shown by the table of the weighted residuals (onlineonly appendix table 2).

There are two main physiological outputs of the model:

- 1. derivative control (units: $[pmol·m⁻² BSA] \cdot [mmol·l⁻¹·min⁻¹]^{-1}$): it is the amount of insulin secreted in response to a rate of glucose increase of 1 mmol/l per min which lasts for 1 minute;
- 2. stimulus-response curve linking glucose concentration (x axis) to insulin secretion rate (y axis): as explained above, it is the sum of BSR and PSR. With the purpose of avoiding artifactual increases in the power of statistical analyses, we used the stimulus-response curve at the predetermined glucose concentrations of 5.5, 8.0, 11.0, 15.0 and 20.0 mmol/l.

References

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Supplementary Table 1. Coefficients of variation of the beta cell model parameters. CP_{ss}= basal C**peptide concentration;** σ**1 = parameter regulating glucose sensitivity of derivative control of insulin secretion,** τ **= time constant of derivative control of insulin secretion,** σ^2 **= glucose** sensitivity of proportional control of insulin secretion, δ = time constant of proportional control of **insulin secretion,** θ**: glycemic threshold of proportional control of insulin secretion.**

Supplementary Table 2. Weighted residuals of the model fit to the C-peptide data of the OGTT. Data are means±SD. The weighted residuals are a quantitative point-by-point assessment of the goodness-of-fit of the model to the data: a theorically perfect fit should generate weighted residuals with mean 0 and SD of 1.

Supplementary Table 3. Influence of rs6717980 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI.

*Variables were log-transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values. **rs6717980Additive model**

Supplementary Table 4. Influence of rs1049817 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI.

*Variables were log-transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values.

§ Analysis performed under recessive model.

Supplementary Table 5. Influence of rs65476256 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI. *Variables were log-transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values.

§ Analysis performed under recessive model.

Supplementary Table 6. Influence of rs780094 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. **Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI.**

*Variables were log- transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values.

 $\frac{8}{3}$ Analysis performed under recessive model

Supplementary Table 7. Influence of rs2384628 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI.

rs2384628 Additive model Phenotype N CC CA AA BETA SE *P* **Value** Minor allele (A) frequency, % 0.46 Number (M/F) 501 (338/163) 139 266 96 Age (yrs) 501 59 [50-66] 60 [62-65] 59 [52-66] 0.55 0.67 0.41 BMI* (kg/m²) 500 29.4 [26.1-33.3] 29.3 [26.6-32.9] 29.7 [26.9-33.6] $-0.003*$ 0.01* 0.81 Fasting P-glucose (mmol/l) 492 7.0 [6.3-7.8] 7.2 [6.2-8.3] 7.0 [3.0-7.8] -0.07 0.12 0.56 2hr P-glucose (mmol/l) 481 | 13.7 [11.1-16.2] | 13.8 [10.8-16.5] | 12.4 [10.0-15.7] | -0.29 | 0.27 | 0.29 Fasting insulin* (mU/l) 428 11.4 [6.8-17.2] 11.5 [7.8-16.1] 11.5 [7.7-16.8] 0.02* 0.04* 0.52 2hr insulin* (mU/l) 435 61.7 [45.6-106.8] 60.8 [33.3-89.1] 76.6 [44.9-136.5] 0.04* 0.05* 0.39 Insulinogenic Index (mU/mmol)* 394 3.8 [2.3-6.9] 3.6 [1.6-6.9] 3.9 [2.6-6.2] 0.01* 0.07* 0.89 CIR_{120} ^{*} $(mUxL/mmol²)$ 435 0.5 [0.3-1.1] 0.4 [0.2-1.1] 0.7 [0.3-1.4] 0.10* 0.08* 022 HbA1c 486 6.7 [6.2-7.4] 6.8 [6.2-7.6] 6.5 [6.1-7.1] -0.10 0.90 0.28 Triglycerides* (mmol/l) 492 1.5 [1.1-2.0] 1.4 [1.0-2.0] 1.5 [1.0-2.1] 0.003* 0.003* 0.93 HDL-cholesterol* (mmol/l) 489 1.1 [1.0-1.3] 1.1 [1.0-1.4] 1.1 [1.0-1.4] 0.007* 0.02* 0.69 Cholesterol (mmol/l) 491 4.7 [4.2-5.5] 5.0 [4.4-5.6] 5.1 [4.4-5.5] 0.12 0.07 0.08 SBP (mmHg) 488 136 [124-144] 140 [120-150] 130 [125-150] 0.20 1.17 0.87 DBP (mmHg) 488 85 [80-90] 84 [80-90] 80 [80-90] -0.48 0.62 0.44 Insulin Sensitivity* (μ mol/min/m² BSA) 490 563 [366-851] 556 [367.792] 565 [289-773] -0.04* 0.04* 0.37 eGFR (ml/min/1.73m²) 469 81.6 [71.6-93.1] 81.4 [72.0-96.1] 76.1 [66.9-92.1] -1.25 1.28 0.33 U-Alb/Creatinine* (mg/mmol) 431 0.8 [0.4-3.2] 0.7 [0.4-1.6] 1.1 [0.4-3] 0.04* 0.07* 0.52 Serum Creatinine (μmol/L) (1.34×10^{-10}) 469 (3.34×10^{-10}) 79 [68-87] (3.34×10^{-10}) 81 [69-93] (3.90×10^{-10}) (3.34×10^{-10})

*Variables were log-transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values.

Supplementary Table 8. Influence of rs8731 genotype on clinical and metabolic variables of patients with newly diagnosed type 2 diabetes in the VNDS. **Beta and SE are the multivariate model estimates of the change and its standard deviation, respectively, in the phenotypic trait associated to the presence of one minor allele. Reported p values were obtained after adjusting for age, gender and BMI.**

*Variables were log-transformed before statistical analysis to approximate a gaussian distribution; the coefficient beta and its S.E. refer to log-transformed values.

§ Analysis performed under recessive model.

Supplementary Table 9. Number of patients with newly diagnosed type 2 diabetes of the VNDS in each cell of the *GCKR* **score. The** *GCKR* **score was computed by counting 1 per each rs6717980 G allele and 1 per each rs2384682 C allele carried by each subject. The** *GCKR* **score could range from a minimum of 0 (a carrier of neither rs6717980 G alleles nor rs2384682 C alleles) to a maximum of 4 (a carrier of both GG in rs6717980 and CC in rs2384682).**

Supplementary Table 10. Statistically independent effects of *GCKR* **score (P = 0.012) on the stimulus (glucose)-response (insulin secretion rate) curve (proportional control) of beta cell in the VNDS patients. Data were analyzed by multivariate ANOVA for repeated measures; covariates of the multivariate model: body mass index (BMI; P = 0.014), glomerular filtration rate computed by** the MDRD formula (eGFR; $P = 0.0001$), age ($P = 0.17$) and gender (male=0, female=1) ($P = 0.06$).

