Meta-Analysis of the INSI2G Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?


1 Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany, 2 Department of Epidemiology and Preventive Medicine, University Medical Center Regensburg, Regensburg, Germany, 3 Medical Research Council Epidemiology Unit, Institute of Metabolic Science, Cambridge, United Kingdom, 4 Division of Genetic Epidemiology, Department of Medical Genetics, Molecular and Clinical Pharmacology, Innsbruck Medical University, Innsbruck, Austria, 5 Institute for Clinical and Experimental Medicine, Prague, Czech Republic, 6 Department of Medicine and Clinical Epidemiology and Biostatistics, McMaster University, Hamilton, Ontario, Canada, 7 Broad Institute of Harvard and MIT, Cambridge, Massachusetts, United States of America, 8 Charité Campus Virchow Klinikum, Institut für Experimentelle Pädiatrische Endokrinologie, Berlin, Germany, 9 University of Southern Denmark, Copenhagen, Denmark, 10 Department of Epidemiology, German Institute of Human Nutrition Potsdam-Rehbrücke, Nuthetal, Germany, 11 Human Genomics Laboratory, Pennington Biomedical Research Center, Baton Rouge, Louisiana, United States of America, 12 Institute of Genetics and Biophysics ‘A.Buzzati-Traverso’, CNR, Naples, Italy, 13 Centre for Cardiovascular Genetics, Royal Free and University College Medical School, London, United Kingdom, 14 Preventive Medicine Department, University of Valencia, Valencia, Spain, 15 CIBER Fisiopatología de la Obesidad y Nutrición, Instituto de Salud Carlos III, Valencia, Spain, 16 Pasteur Institute, CNRS 8090–Institute of Biology, Lille, France, 17 Institut du Thorax, CNRS UMR1317, INSERM U 915, Nantes, France, 18 Departments of Medicine and Human Genetics, McGill University, Montréal, Québec, Canada, 19 Department of Child and Adolescent Psychiatry, University of Duisburg-Essen, Essen, Germany, 20 Robarts Research Institute, University of Western Ontario, London, Ontario, Canada, 21 Max Planck Institut für molekulare Genetik, Berlin, Germany, 22 Department of Medicine, Harvard School of Public Health, Boston, Massachusetts, United States of America, 23 Channing Laboratory, Brigham and Women’s Hospital and Harvard Medical School, Boston, Massachusetts, United States of America, 24 Cardiovascular Research Center, Prague, Czech Republic, 25 Cardiovascular Genetics Division, University of Utah School of Medicine, Salt Lake City, Utah, United States of America, 26 Department of Epidemiology and Public Health, Imperial College, London, United Kingdom, 27 National Public Health Institute, Department of Child and Adolescent Health, Oulu, Finland, 28 Institute of Health Sciences and Biocenter Oulu, University of Oulu, Oulu, Finland, 29 Institute of Genomics and Integrative Biology, Delhi, India, 30 Department of Genetics, University of North Carolina, Chapel Hill, North Carolina, United States of America, 31 Department of Internal Medicine II, University Medical Center Regensburg, Regensburg, Germany, 32 Children’s Hospital, Boston, Massachusetts, United States of America, 33 Genetics Division, Drug Discovery, GlaxoSmithKline, King of Prussia, Pennsylvania, United States of America, 34 Institute of Clinical Molecular Biology, Christian-Albrechts-Universität zu Kiel, Kiel, Germany, 35 Institut fuer Medizinische Biometrie und Epidemiologie, Philippus-Universitaet Marburg, Marburg, Germany, 36 First Department of Internal Medicine, St. Johann Spital, Paracelsus Private Medical University Salzburg, Salzburg, Austria, 37 Faculty of Medicine, Department of Social and Preventive Medicine, Université Laval, Québec, Quebec, Canada, 38 Department of Pharmacology, Emst Moritz Arndt University Greifswald, Greifswald, Germany, 39 deCODE genetics, Reykjavik, Iceland, 40 Faculty of Medicine, University of Iceland, Reykjavik, Iceland, 41 Department of Community Medicine, Emst Moritz Arndt University Greifswald, Greifswald, Germany, 42 Welcome Trust Center for Human Genetics, University of Oxford, Oxford, United Kingdom, 43 Oxford Center of Diabetes, Endocrinology and Metabolism, The Churchill Hospital, Headington, Oxford, United Kingdom, 44 Department of Biostatistics, Harvard School of Public Health, Boston, Massachusetts, United States of America, 45 Chair of Epidemiology, Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany, 46 Klinikum Großhadern, Munich, Germany
Abstract

The INSIG2 rs7566605 polymorphism was identified for obesity (BMI≥30 kg/m²) in one of the first genome-wide association studies, but replications were inconsistent. We collected statistics from 34 studies (n = 74,345), including general population (GP) studies, population-based studies with subjects selected for conditions related to a better health status (‘healthy population’, HP), and obesity studies (OB). We tested five hypotheses to explore potential sources of heterogeneity. The meta-analysis of 27 studies on Caucasian adults (n = 66,213) combining the different study designs did not support overall association of the CC-genotype with obesity, yielding an odds ratio (OR) of 1.05 (p-value = 0.27). The I² measure of 41% (p-value = 0.015) indicated between-study heterogeneity. Restricting to GP studies resulted in a declined I² measure of 11% (p-value = 0.33) and an OR of 1.10 (p-value = 0.015). Regarding the five hypotheses, our data showed (a) some difference between GP and HP studies (p-value = 0.012) and (b) an association in extreme comparisons (BMI≥32.5, 35.0, 37.5, 40.0 kg/m² versus BMI≤25 kg/m²) yielding ORs of 1.16, 1.18, 1.22, or 1.27 (p-values 0.001 to 0.003), which was also underscored by significantly increased CC-genotype frequencies across BMI categories (10.4% to 12.5%, p-value for trend = 0.0002). We did not find evidence for differential ORs (c) among studies with higher than average obesity prevalence compared to lower, (d) among studies with BMI assessment after the year 2000 compared to those before, or (e) among studies from older populations compared to younger. Analysis of non-Caucasian adults (n = 4889) or children (n = 3243) yielded ORs of 1.01 (p-value = 0.94) or 1.15 (p-value = 0.22), respectively. There was no evidence for overall association of the rs7566605 polymorphism with obesity. Our data suggested an association with extreme degrees of obesity, and consequently heterogeneous effects from different study designs may mask an underlying association when unaccounted for. The importance of study design might be under-recognized in gene discovery and association replication so far.

Introduction

One of the first genome-wide association (GWA) studies ever and the first on obesity identified the INSIG2 gene represented by the rs7566605 polymorphism as a novel gene for common obesity [1]. Functional evidence depicted the INSIG2 gene from the very start as an interesting candidate for obesity as being involved in the reversed cholesterol transport by an interaction with sterol regulatory element-binding proteins (SREBPs) [2], which are transcription factors that activate the synthesis of cholesterol and fatty acids in the liver and other organs [3].

The observed SNP-obesity-association was replicated in some, but not in all studies [4–11]. A letter to Science by the authors of the initial report in response to the emerging debate of the early inconsistent results [1] raised the question of whether the association might be more pronounced in studies that were not ascertained for reasons related to better health status, when comparing more severely obese subjects with normal controls, in populations with a higher prevalence of obesity or in populations with a higher mean age. The need for a meta-analysis was stated there for the first time and re-stated by Lyon and colleagues [12]. Furthermore, a secular trend for increasing prevalence of obesity was observed in two large population-based studies from the same geographical region using the same protocols but one recruited 1994/95 (KORA-S3) and the other 1999–2001 (KORA-S4) [13]. The later study showed a stronger INSIG2-obesity-association compared to the earlier study: This raised the additional question whether the changes in nutritional intake and physical activity [14,15] believed to contribute to the increase in the prevalence of obesity during the last decades were the reason for some of the between-study heterogeneity observed for this SNP’s association with obesity.

The inconsistent reported associations and the many resulting debates motivated us to undertake a systematic meta-analysis of all available data to investigate potential causes of heterogeneity and to look for consistent results among subgroups. It was thus the specific aim of this meta-analysis to explore five hypotheses for heterogeneity of the rs7566605 association with obesity: (Hypothesis I) The association depends on study design. Therefore, we classified studies as general population-based (GP) when they were neither selected for any disease nor for not having any disease, as any selection of this type was shown to potentially induce bias for outcomes associated with the disease [16]. We classified studies as ‘healthy population’ (HP) when they were selected for reasons related to a better health status (i.e. studies including subjects from working populations or studies excluding subjects for with diseases such as diagnosed type 2 diabetes), or obesity studies (OB) when they were specifically designed to investigate obesity, usually case-
Author Summary
A polymorphism of the INSIG2 gene was identified as being associated with obesity in one of the first genome-wide association studies. However, this association has since been highly debated upon inconsistent subsequent reports. We collected association information from 34 studies including a total of 74,000 participants. In a meta-analysis of the 27 studies including 66,000 Caucasian adults, we found no overall association of this polymorphism rs7566605 with obesity, comparing subjects with a body-mass-index (BMI) ≥30 kg/m² with normal BMI subjects (BMI < 30 kg/m²). Our data suggested an association of this polymorphism with extreme obesity (e.g., BMI ≈ 37.5 kg/m²) compared to normal controls. Such an association with extreme obesity might induce heterogeneous effects from different study designs depending on the proportion of extreme obesity included by the design. However, further studies would be required to substantiate this finding. The importance of study design might be under-recognized in gene discovery and association replication so far.

Table 1. Main meta-analysis results of the INSIG2 rs7566605 association with obesity.

|                  | # cases/controls (# studies) | OR (p-value) fixed effect | OR (p-value) random effect | I² (p-value) | P-value test for difference of fixed [random] effect ORs
|------------------|-----------------------------|--------------------------|----------------------------|--------------|----------------------------------------------------------
| All-CA           | 16,365/49,848 (27)          | 1.076 [0.023]            | 1.051 [0.268]              | 41.0 [0.015] |                                                          |
| All-CA*          | 10,761/30,168 (19)          | 1.077 [0.074]            | 1.054 [0.361]              | 36.4 [0.057] |                                                          |
| GP               | 9162/39,682 (16)            | 1.097 [0.015]            | 1.092 [0.035]              | 10.9 [0.329] | GP vs HP: 0.004 [0.005]                                   |
| HP               | 1307/6333 (5)               | 0.796 [0.028]            | 0.796 [0.028]              | 0.0 [0.415]  | HP vs OB: 0.038 [0.022]                                  |
| OB               | 5896/3833 (6)               | 0.821 [0.135]            | 0.772 [0.198]              | 46.2 [0.156] | HP vs OB: 0.038 [0.109]                                  |
| All-NC           | 553/4336 (4)                | 1.013 [0.936]            | 0.945 [0.818]              | 43.5 [0.150] |                                                          |
| All-CH           | 1802/1441 (3)               | 1.147 [0.216]            | 1.147 [0.216]              | 0.0 [0.830]  |                                                          |

Pooled association for all Caucasian adult studies combined (All-CA) as well as stratified by study type (GP = general population, HP = healthy population, OB = obesity study), for all non-Caucasian studies (All-NC), or the children studies (All-CH) indicating differential results among GP or HP studies (Hypothesis 1). Numbers stated are the number of obese (BMI ≥ 30 kg/m², ‘cases’) and non-obese (BMI < 30 kg/m², ‘controls’) subjects with the number of studies, the recessive model ORs (p-value) comparing the odds for obesity among the subjects with the CC genotype versus subjects with the CG or GG genotype using fixed or random effects models, the I² measure (p-value of the Q-statistics), and the P-value for pair-wise difference between GP, HP, and OB studies.

*Excluding studies published before the response letter in Science by Herbert et al., December 2006 [1], in which the hypothesis of potential heterogeneity due to study design and a first call for this meta-analysis were stated (i.e., excluding American, Polish, NHS, KORA_S4, EPIC_Norfolk, MRC_Ely, DESIR, SHIP, OB_adult).

**P-values corrected for pair-wise comparison of three subgroups need to be multiplied by three.

OR = Odds Ratios.

doi:10.1371/journal.pgen.1000694.001
Figure 1A–1C shows forest plots of the Caucasian adult studies with combined estimates by study type. The p-value testing for difference between the GP and the HP combined estimates was 0.004 [0.012 when corrected for pairwise testing of three subgroups] and 0.039 [0.089] when excluding the early published studies. Thus, there is some, but not completely conclusive evidence for Hypothesis 1 that study design might explain some of the between-study heterogeneity of this genetic association.

Studies in Non-Caucasian Adults or Children
In the pooled analysis of the four studies on non-Caucasian adults (n = 4689), we found no significant association of the CC genotype with obesity. The pooled analysis of the three pediatric studies (n = 3243) was also not significant (Table 1, Figure 1D and 1E).

Increasing Strength of Association in More Extreme Comparisons
Our data suggested an association with increased ORs among the Caucasian adults when more extremely obese subjects were compared to lean controls (Table S3; Hypothesis 2); combining over all studies, the ORs gradually increased from 1.156 to 1.183, 1.221, or 1.265 (p-values ranging from 0.001 to 0.003) when moving the BMI cut-off for the obese cases from 32.5 to 35.0, 37.5 or 40.0 kg/m², respectively, and comparing to controls with BMI<25 kg/m². A similar trend for increasing ORs was seen when comparing extremely obese subjects against controls with BMI<30 kg/m² or BMI<20.0 kg/m². Among the GP studies, the ORs increased from 1.198 to 1.257, 1.313, or 1.414 (p-values ranging from 0.001 to 0.003), respectively. The analogous comparison for HP studies revealed that the protective influence of the CC homozygous was reversed in the more extreme comparisons with ORs from 0.856 to 0.959, 1.139, or 1.604. For the OB studies, the ORs of the analogous comparisons were well above unity for all comparisons, but did not show a trend.

As summarized in Table 2, the accompanying trend analyses of the CC genotype frequencies across the various BMI categories indicated significantly increased CC genotype frequencies from 10.4% to 12.5% (p-value testing for trend = 0.0002), which persisted when excluding the early published studies (p-value = 0.0008). A similar trend was seen among GP studies.

In both types of analyses, the varying cut-point ORs as well as the trend in genotype frequencies by BMI categories, suggest an association of the rs7566605 with extreme obesity compared to normal controls (Hypothesis 2).

Further Hypotheses on Potential Sources of Heterogeneity
Table 3 summarizes the results of the further three hypotheses to explain heterogeneity, which were tested for the Caucasian adult studies. Hypothesis 3: there was some tendency towards higher ORs among 'more obese' study populations compared to the 'less obese' study populations (p-value = 0.052 [0.285] testing for difference of the fixed [random] effects ORs), but not statistically significant. Hypothesis 4: there was no evidence for any difference between studies from older populations (i.e. mean age of subjects above 50 years) as compared to studies from younger populations (i.e. mean age below 50 years). Hypothesis 5: there was a tendency towards more pronounced ORs for the studies with BMI assessed after the year 2000 as compared to studies with BMI assessed before 2000 (p-value = 0.007 [0.095]), but not statistically significant given the various tests performed and particularly not when excluding the early published studies (p-value = 0.086 [0.248]). Hypotheses 3–5 were not tested in the HP or OB stratified analyses as too few (3–6) studies were available.

Sensitivity Analyses
The sensitivity analyses (Table S4) indicated robustness of estimates towards selection of gender or age and no significant difference between published and unpublished studies. Excluding the two studies with self-reported BMI from the overall GP meta-analysis resulted in a slight increase of the OR estimate.

Genetic Model
We specifically examined the association under the recessive genetic model as suggested by the original paper [1]. Our data on the raw numbers of obese or non-obese subjects with one of the three genotypes underscored a recessive model in the Caucasian adult studies combined (OR_{CC\over GG} = 1.112 [1.029, 1.203], p-value = 0.007, and OR_{GG\over GG} = 0.983 [0.940, 1.037], p-value = 0.618) as well as among the GP studies (OR_{CC\over GG} = 1.076 [0.976, 1.183], p-value = 0.142, and OR_{GG\over GG} = 0.995 [0.936, 1.036], p-value = 0.813).

Secondary Analyses on BMI as a Quantitative Outcome
The secondary analyses on BMI as a quantitative outcome were only performed in GP and HP studies. These analyses generally showed results consistent with the obesity analyses, but less, if any, significance (Figure S1, Tables S3, S6, and S7).

Discussion
We conducted a systematic meta-analysis on published and unpublished studies by collecting summary statistics on the association of the rs7566605 SNP near the INSG2 gene using a recessive genetic model as proposed by Herbert and colleagues. This SNP was highly debated and the inconsistent findings were very much puzzling underscored by again inconclusive findings in two recent publications [21,22]. To solve this puzzle, we collected aggregated study-specific data from 34 studies with a total of 74,345 subjects analyzed according to a standardized model.

The main analysis did not support evidence for an overall association with obesity of the CC-genotype compared to the CG/GG (OR = 1.05, p-value = 0.268). Our data suggested an association for more extreme obese subjects (BMI≥32.5, 35.0, 37.5, 40.0 kg/m²) compared to normal controls (BMI<25 kg/m²) with ORs increasing to 1.16, 1.18, 1.22, 1.27 (p-values between 0.001 and 0.003) and significantly increased CC-genotype frequencies with increasingly high BMI categories (10.4% to 12.5%, p-value for trend = 0.0002).

The main analysis pointed towards significant between-study heterogeneity with an I² measure of 41%. When we restricted the analysis to GP studies, the I² declined to 11% and the OR increased to 1.10. This is in-line with a very recently published study, which found the OR to increase from 1.02 for a combined analysis of diverse types of studies including 15,781 subjects to an OR of 1.15 when restricting to the general population-based INTER99 cohort including 6,158 subjects [21]. This was the largest GP study on this SNP-association prior to this meta-analysis.

The Degree of Obesity and the Study Design as a Potential Source of Heterogeneity
The results of our analyses suggest an association of this SNP with extremely obese subjects compared to normal controls, but future research will need to confirm this finding. Study design can impact how many extremely obese subjects are included in the
Figure 1. Forest plot on Odds Ratio estimates of the *INSIG2* rs7566605 association with obesity. Association with obesity (BMI ≥ 30 kg/m²) for (A) the Caucasian adult general population-based (GP) studies, (B) the Caucasian adult studies ascertained for reasons related to health status (HP), (C) the Caucasian adult obesity case-control studies (OB), (D) the non-Caucasian adult studies, and (E) the pediatric studies. Shown are recessive model OR estimates comparing the CC genotype versus CG or GG for each study and pooled estimates. The fixed effect (FE) model OR is shown in case of no significant heterogeneity as tested by the Q-statistics; a random effect (RE) model is shown otherwise.

doi:10.1371/journal.pgen.1000694.g001
study. Study designs that sample more extremely obese subjects will have greater power to detect the association, while study designs that sample fewer of these subjects will have little power to detect the association. An association with extreme obesity might well be masked by study design, and meta-analyses which designs that sample fewer of these subjects will have little power to detect the association, while study designs that sample more recent BMI assessment might reflect this gene-environment interaction as well:

The tendency of higher OR estimates observed in the general population-based studies (GP) and the obesity case-control studies compared to ‘healthy population’ (HP) studies might possibly reflect the association for extreme obesity compared to normal controls. We have classified studies as ‘ascertained for criteria related to a better health status’ (HP) when patient groups were excluded or when the sample was ascertained based on working populations, which are known to be usually more healthy. We have performed this classification blinded for the study estimate to exclude bias from informative misclassification. It could be that the common rs7566605 directly or via tagging another possibly rare and quite penetrant variant does not so much alter BMI throughout the distribution, but really puts participants into the very obese category. Thus an effect is picked up in the GP samples, but not in the HP studies with fewer extremely obese persons. This would also be in-line with (i) our more pronounced findings in the studies with a more recent BMI assessment might reflect this gene-environment interaction as well:

The importance of ascertainment of the study sample might be under-recognized so far. Monses and colleagues [16] have illustrated that ascertaining for or against disease would induce a bias in genetic association estimates when the genetic marker as well as the phenotype under study (here obesity) are associated with the disease. As obesity is associated with many chronic diseases such as type 2 diabetes and cardiovascular disease, exclusion of such study participants opens up for bias, if association of the SNP with the disease cannot be precluded. We had specifically excluded studies ascertained for disease and had also planned on separating HP from GP studies ahead of the analyses. We would like to highlight that we have adopted a very strict definition of GP and that there might be special advantages

### Table 2. Comparing more extreme degrees of obesity.

<table>
<thead>
<tr>
<th>BMI (kg/m²)</th>
<th>&lt;20</th>
<th>20–25</th>
<th>25–30</th>
<th>30–32.5</th>
<th>32.5–35</th>
<th>35–37.5</th>
<th>37.5–40</th>
<th>&gt;40</th>
<th>P-value**</th>
</tr>
</thead>
<tbody>
<tr>
<td>All-CA</td>
<td>%CC</td>
<td>10.4</td>
<td>10.7</td>
<td>10.5</td>
<td>10.5</td>
<td>11.9</td>
<td>11.2</td>
<td>12.0</td>
<td>12.5</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>66,213</td>
<td>3314</td>
<td>22462</td>
<td>23072</td>
<td>5869</td>
<td>3578</td>
<td>2150</td>
<td>1404</td>
</tr>
<tr>
<td>All-CA*</td>
<td>%CC</td>
<td>9.9</td>
<td>10.8</td>
<td>10.9</td>
<td>10.8</td>
<td>11.6</td>
<td>12.0</td>
<td>12.1</td>
<td>12.7</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>39,414</td>
<td>2321</td>
<td>13671</td>
<td>3447</td>
<td>1962</td>
<td>1962</td>
<td>1162</td>
<td>829</td>
</tr>
<tr>
<td>GP</td>
<td>%CC</td>
<td>10.7</td>
<td>10.8</td>
<td>10.2</td>
<td>10.4</td>
<td>12.0</td>
<td>12.4</td>
<td>12.6</td>
<td>13.5</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>48,844</td>
<td>2490</td>
<td>18551</td>
<td>18641</td>
<td>4300</td>
<td>2299</td>
<td>1111</td>
<td>620</td>
</tr>
<tr>
<td>GP*</td>
<td>%CC</td>
<td>10.6</td>
<td>10.8</td>
<td>10.8</td>
<td>10.7</td>
<td>12.01</td>
<td>12.9</td>
<td>12.1</td>
<td>13.7</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>29,046</td>
<td>1684</td>
<td>10975</td>
<td>10584</td>
<td>2546</td>
<td>1432</td>
<td>727</td>
<td>421</td>
</tr>
<tr>
<td>HP</td>
<td>%CC</td>
<td>10.6</td>
<td>10.4</td>
<td>11.9</td>
<td>9.7</td>
<td>8.1</td>
<td>7.5</td>
<td>13.0</td>
<td>8.6</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>7640</td>
<td>273</td>
<td>2772</td>
<td>3288</td>
<td>679</td>
<td>323</td>
<td>147</td>
<td>77</td>
</tr>
<tr>
<td>HP*</td>
<td>%CC</td>
<td>8.3</td>
<td>10.1</td>
<td>11.8</td>
<td>10.1</td>
<td>7.0</td>
<td>9.6</td>
<td>17.6</td>
<td>2.9</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>4911</td>
<td>121</td>
<td>1716</td>
<td>2279</td>
<td>457</td>
<td>186</td>
<td>83</td>
<td>34</td>
</tr>
<tr>
<td>OB</td>
<td>%CC</td>
<td>8.5</td>
<td>10.3</td>
<td>10.8</td>
<td>11.8</td>
<td>13.1</td>
<td>10.3</td>
<td>11.3</td>
<td>12.4</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>9729</td>
<td>551</td>
<td>2139</td>
<td>1143</td>
<td>890</td>
<td>956</td>
<td>892</td>
<td>707</td>
</tr>
<tr>
<td>OB*</td>
<td>%CC</td>
<td>8.1</td>
<td>11.9</td>
<td>10.0</td>
<td>12.4</td>
<td>12.2</td>
<td>10.8</td>
<td>11.5</td>
<td>12.4</td>
</tr>
<tr>
<td></td>
<td>N</td>
<td>5457</td>
<td>516</td>
<td>980</td>
<td>842</td>
<td>444</td>
<td>344</td>
<td>352</td>
<td>374</td>
</tr>
</tbody>
</table>

The data suggest an association when comparing more extreme degrees of obesity with normal controls, which is a potential explanation for the heterogeneity of the INSIG2 rs7566605 association with obesity (Hypothesis 2). Numbers stated are frequencies of risk genotype CC (C being the minor allele) across BMI categories for the Caucasian adult studies combined (All-CA) as well as stratified by study type (GP = general population, HP = healthy population, OB = obesity study). Also given are the p-values from testing for a trend of genotype frequencies across categories. (Not for All-NC or All-CH due to the few subjects in each category.)

*Excluding studies published before the response letter by Herbert et al., December 2006 [1] in which the hypothesis of potential heterogeneity due to study design and a first call for this meta-analysis were stated (i.e., excluding American_Polish, NHS, KORA_S4, Essen_trios, EPIC_Norfolk, MRC_Ely, DESIR, SHIP, OB_adult, which are all Caucasian studies).

**P-value testing for a trend across the BMI categories.

doi:10.1371/journal.pgen.1000694.t002
in using either disease-ascertained studies [28] or particularly healthy samples in other instances [29].

Strengths and Limitations of This Study

This meta-analysis has several strengths: (1) We have conducted a systematic approach by collecting all studies published before January 1, 2008, including seven studies that were unpublished at that time. (2) The meta-analysis is large including a total of 74,365 subjects. (3) We separated working tasks, with one researcher designing the analysis plan, recruiting studies, classifying studies by study type, and deciding upon compliance to inclusion criteria, designing the analysis plan, recruiting studies, classifying studies by study type, and deciding upon compliance to inclusion criteria, which guarded against subtle post-hoc data-driven analysis decisions, study selection bias, and informative misclassification of study design. (4) We collected data according to a strict protocol including standardized analysis from each study partner, with strong quality control of study-specific results. (5) We performed only a limited number of pre-defined subgroup analyses with some amendment during the review process. (6) We had a strong focus on the diversity of study design, which is unique in genetic epidemiological research at the time being and an issue probably under-recognized so far.

It might be considered a disadvantage that we did not include studies with subjects selected for diseases, particularly those associated with type 2 diabetes and thus a higher prevalence of obesity, as the association might be stronger in such studies. This might have been one reason for the initial investigation by Herbert et al. [1], in which the hypothesis of potential heterogeneity due to study design and a first call for a meta-analysis were stated (i.e. excluding American_Polish, NHS, KORA-S4, Essen_trios, EPIC_Norfolk, MRC_Ely, DESIR, SHIP, OB_adult).

This meta-analysis has several strengths: (1) We have conducted a systematic approach by collecting all studies published before January 1, 2008, including seven studies that were unpublished at that time. (2) The meta-analysis is large including a total of 74,365 subjects. (3) We separated working tasks, with one researcher designing the analysis plan, recruiting studies, classifying studies by study type, and deciding upon compliance to inclusion criteria, which guarded against subtle post-hoc data-driven analysis decisions, study selection bias, and informative misclassification of study design. (4) We collected data according to a strict protocol including standardized analysis from each study partner, with strong quality control of study-specific results. (5) We performed only a limited number of pre-defined subgroup analyses with some amendment during the review process. (6) We had a strong focus on the diversity of study design, which is unique in genetic epidemiological research at the time being and an issue probably under-recognized so far.

It might be considered a disadvantage that we did not include studies with subjects selected for diseases, particularly those associated with type 2 diabetes and thus a higher prevalence of obesity, as the association might be stronger in such studies. This might have been one reason for the initial investigation by Herbert et al. [1], in which the hypothesis of potential heterogeneity due to study design and a first call for a meta-analysis were stated (i.e. excluding American_Polish, NHS, KORA-S4, Essen_trios, EPIC_Norfolk, MRC_Ely, DESIR, SHIP, OB_adult).
disadvantage that we were not able to recruit enough non-
Caucasian adult or children studies for a conclusive comparison
with the Caucasian adult studies.

Conclusions
This pooled analysis including all study designs does not provide
evidence for overall association of the INSIG2 rs7566605 CC
genotype with increased risk of obesity compared to the CG or
GG genotypes. Our data suggest an association with extreme
degrees of obesity and consequently heterogeneous effects from
different study designs may mask an underlying association when
unaccounted for. The importance of study design might be under-
recognized in gene discovery and association replication so far.

Materials and Methods

Meta-Analysis Concept
We designed our meta-analysis as a pooled analysis of study-
specific association estimates according to a standardized protocol
(see ‘data form’, Text S1B, and pre-defined analysis plan, Text
S1C) with an amendment added during the review process (Text
S1D).

Our eligibility criteria for studies were (i) data available on BMI,
the INSIG2 rs7566605 SNP genotypes, age and sex, (ii) sample size
of at least 200 subjects, (iii) ethical approval, and (iv) either general
population-based (GP), ascertained for reasons related to a better
health status such as studies including only subjects in the work-
force or studies excluding subjects with diseases (‘healthy
population’, HP), or designed specifically to study obesity such
as obesity case-control or obesity family studies (OB). We excluded
all studies selecting subjects for any disease. For more
information on the classification of studies by study type, see Text S1E. We did
not exclude on any age or ethnicity criteria to allow exploration of
potential heterogeneity. We controlled for study selection bias by
separating the two main tasks between the two first authors: IMH.
took care of study recruitment, compliance to inclusion criteria,
and classification of studies by study type, and CH performed
quality control and statistical analysis.

Study Recruitment, Collection of Aggregated Data, and
Quality Control
We identified all eligible studies published before January 1,
2008 by a systematic PubMed literature search using the search
terms ‘INSIG2’ OR ‘INSIG-2’ OR ‘rs7566605’. Additionally we
identified unpublished studies through contacting researchers in
the field by making a call for this meta-analysis in several consortia
(GIANT, KORA-500K, IL-6-consortium), in the letter to
Science by Herbert and colleagues [1], in the paper by Lyon and
colleagues [12], and in meeting presentations. We sent out and
collected standardized data forms, and verified all entries for
within-plausibility as well as consistency with publications, if
available. We made plausibility checks by use of double
analyses with exclusion of these hypotheses-generating studies.
All involved studies were conducted according to the principles
expressed in the Declaration of Helsinki. The studies were
approved by the local Review Boards. All study participants
provided written informed consent for the collection of samples
and subsequent analysis.

Statistical Analysis
For each study, OR estimates comparing the odds of obesity
(BMI≥30 kg/m²) for subjects with the minor-allele homozygous
genotype (CC) with subjects of the other genotypes combined (CG,
GG), thus assuming a recessive model, were calculated using
logistic regression adjusting for age and sex. We also collected OR
estimates with standard errors (SE) for the odds of more extreme
degrees of obesity (i.e. subjects with BMI≥32.5, 35.0, 37.5, or
40.0 kg/m²) compared to various degrees of leanness (i.e. subjects
with BMI<30, 25, or 20 kg/m²). Furthermore, we collected
summary statistics (mean and SE) on the difference in mean BMI
between subjects with the CC genotype compared to subjects with
the CG or GG genotypes using linear regression adjusted for age
and sex. For each study, analyses stratified for sex or age (with a
cut-off at 50 years) were performed as well. Among the six studies
from non-Caucasian populations, two studies had too few (<3)
subjects among the obese with the CC genotype to be included
into the dichotomous obesity analysis, while they were included for
the quantitative BMI analysis.

For the meta-analysis, we combined beta-estimates among
Caucasian adult studies (All-CA) followed by a stratified analysis
by study type (GP, HP, OB) and combined estimates among non-
Caucasian (All-NC) or children studies (All-CH), see ‘amendment
to analysis plan’, Text S1D.

The following was only performed on Caucasian adults as the
number of available non-Caucasians or children was too low. We
tested for differential association between the GP, HP, or OB
studies applying a t-test on the combined beta-estimates and
correcting p-values for testing three subgroups. We tested for a
trend in CC genotype frequencies across the different BMI
categories and tested for differential associations separating the
studies for higher or lower obesity prevalence, higher or lower
mean age of study subjects, or for a more or less recent BMI
assessment using a t-test on the combined beta-estimates. This was
complemented by sensitivity analyses stratifying on sex, age,
population status, and type of BMI assessment. As the hypotheses
were motivated by the early published studies mentioned in the
letter to Science by Herbert and colleagues [1], we repeated all
analyses with exclusion of these hypotheses-generating studies.

In all analyses, between-study heterogeneity was tested by the
χ²-based Q-statistic and quantified by I² as a measure of the
proportion of variance between the study-specific estimates that is
attributable to between-study difference rather than random
variation. We pooled study-specific estimates according to the
inverse-variance weighted fixed effect or the DerSimonian
and Laird random effects model [30]. Heterogeneity was considered to
be significant at the 10% level. All statistical analyses were
performed with SAS (statistical analysis software, SAS institute,
Inc.). Forest plots were prepared using Review Manager software
(Cochrane Collaboration, Copenhagen, DK).

Supporting Information

Figure S1  Forest plot on estimates of the INSIG2 rs7566605
association with BMI. Association of the INSIG2 SNP with BMI
for (A) the Caucasian adult general-population based studies (GP),
(B) the Caucasian adult studies selected for healthy population
(HP), (C) the Non-Caucasian adult studies, (D) the pediatric
studies. Shown are recessive model beta estimates comparing the
CC genotype versus CG or GG for each study and pooled
estimates. The fixed effect (FE) model beta is shown in case of no
difference between subjects with the CC genotype compared to subjects with
the CG or GG genotypes using linear regression adjusted for age
and sex. For each study, analyses stratified for sex or age (with a
cut-off at 50 years) were performed as well. Among the six studies
from non-Caucasian populations, two studies had too few (<3)
subjects among the obese with the CC genotype to be included
into the dichotomous obesity analysis, while they were included for
the quantitative BMI analysis.

Table S1  Characterization of eligible and recruited studies.
Found at: doi:10.1371/journal.pgen.1000694.s002 (0.12 MB DOC)
Meta-Analysis on the INSIG2 rs7566605 with Obesity

Table S2  More details on study characteristics. 
Found at: doi:10.1371/journal.pgen.1000694.s003 (0.20 MB DOC)

Table S3  Stronger genetic effects when comparing more extreme degrees of obesity as an explanation of the heterogeneity of the INSIG2 rs7566605 association (Hypothesis 2). Pooled association estimates for increasing degrees of obesity for all Caucasian adult studies combined (All-CA) as well as stratified by study type (GP = general population, HP = healthy population, OB = obesity study), for all Non-Caucasian studies (All-NC), but not for children studies due to non-comparability of BMI categories. Numbers stated are ORs comparing cases versus controls (p-values) from the pooled analysis (fixed and random effects), number of cases/controls (number of pooled studies), and the \( I^2 \) (p-value from Q-statistics).

Table S4  Sensitivity analyses for the association of the INSIG2 SNP with obesity regarding sex, age, published or unpublished status of studies, self-reported or measured BMI. Stated values are ORs (p-values) based on fixed or random effects models, the \( I^2 \) (p-value of Q test) for each group, and p-values testing for difference between the fixed effect [random effect] ORs of the two corresponding groups. (Not for HP, OB, All-NC, or All-CH due to low numbers of studies.)

Table S5  Main results of pooled association of the INSIG2 SNP with body-mass-index (BMI). The analyses for all Caucasian adult studies combined (All-CA) as well as stratified by study type (GP = general population, HP = healthy population, OB = obesity study), for all Non-Caucasian studies (All-NC), and for the children studies (All-CH) indicated some difference between GP and HP studies (Hypothesis 1). Numbers stated are recessive model beta-estimates (p-values), i.e., mean difference of BMI between subjects with the CC genotype compared to subjects with the CG or GG genotype, using fixed or random effects models, the \( I^2 \) (p-value of Q-statistics), and p-values testing for pair-wise difference between GP, HP, or OB studies.

Table S6  Exploring potential sources of heterogeneity of the INSIG2 rs7566605 association with BMI (Hypotheses 3–5). Stated values are pooled beta-estimates (p-values) based on fixed or random effects model, \( I^2 \) (p-values of Q-test) for each group, and p-values testing for difference between the beta-estimates of the two corresponding groups. (Not for HP, NC, or CH due to low numbers of studies.)

Table S7  Sensitivity analyses for the association of the INSIG2 SNP with BMI regarding sex, age, published status, or self-reported or measured BMI. Stated values are beta-estimates (p-values) based on fixed and random effects models, \( I^2 \) (p-value of Q test) for each group, and p-values testing for difference between the beta-estimates of the two groups. (Not for HP, All-NC, or All-CH due to low numbers of studies.)

Text S1  References of included published studies; data form sent to each study partner; predefined analysis plan; amendment to analysis plan; and classification of studies due by study type.

Acknowledgments

We thank all study participants in the many cohorts of this work for enabling this type of research by their participation. We would like to acknowledge the Indian Genome Variation Consortium and the KORA (Cooperative Health Research in the Region of Augsburg) group. We also would like to thank Julia Muller, Andrew J. P. Smith, Jeannine Sauber, Sabine Jyrch, Ron Do, Alexandre Belisle, Alexandre Monpetit, F. Horber, N. Potoczna, W. Terhalle, Eun-Kyung Suk, and the many people who contributed to the individual studies.

Author Contributions

Conceived and designed the experiments: IMH CH. Performed the experiments: IMH CH RJFL VA SAA KA HB PB HB CB MC JAC DC CD JCE EF FF PF JH RJA AH MRH FBH JAH SEH SCH TT MRJ MK BK HK JK LAL BL SL HNL DM KLM VM AN TTN BP LP IQ TR DR SS RS AS GT UT HV KSV NJW DMW SY CL MM CL JNH NL HEW. Contributed reagents/materials/analysis tools: IMH CH RJFL FK VA SSA KA HB PB HB CB MC JAC DC CD JCE EF FF PF JH RJA AH MRH FBH JAH SEH SCH TT MRJ MK BK HK JK LAL BL SL HNL DM KLM VM AN TTN BP LP IQ TR DR SS RS AS GT UT HV KSV NJW DMW SY CL MM CL JNH NL HEW. Wrote the paper: IMH CH AL NL. Advised with paper writing: RJFL Advised in design and paper writing: FK. Consulted in the revision: AL. Advised in study design: CL. Motivated the project and consulted in study design: HEW.

References


