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# Data in Brief

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Data Article

# TH1 and TH2 cytokine data in insulin secretagogues users newly diagnosed with breast cancer



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#### article info

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#### abstract

Stimulation of insulin production by insulin secretagogue use may impact T helper cells' cytokine production. This dataset presents the relationship between baseline insulin secretagogues use in women diagnosed with breast cancer and type 2 diabetes mellitus, the T-helper 1 and 2 produced cytokine profiles at the time of breast cancer diagnosis, and subsequent cancer outcomes. A Pearson correlation analysis evaluating the relationship between T-helper cytokines stratified by of insulin secretagogues use and controls is also provided.

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#### Specifications Table

# Value of the data

- This dataset represents the observed relationship between insulin secretagogues use, circulating Thelper 1 and 2 produced cytokines at breast cancer diagnosis and cancer outcomes
- Presented data has the potential to guide future research exploring the potential use of insulin secretagogues in the modulation of type 1 and type 2 immunity
- Our observations can assist further research exploring the relationship between insulin secretagogues use and T-helper-driven signaling in the occurrence of breast cancer.

## 1. Data

Reported data represents the observed association between pre-existing use of injectable insulin before breast cancer diagnosis and the T-helper 1 and 2 produced cytokine profiles upon cancer diagnosis in women with both breast cancer and diabetes mellitus [\(Table 1](#page-2-0)). Data in [Table 2](#page-6-0) includes the observed correlations between T-helper 1 and 2 cytokines stratified by diabetes mellitus pharmacotherapy and controls.

#### 2. Experimental design, materials and methods

Evaluation of the association between profiles of T-helper 1 and 2 produced cytokines, injectable insulin use and BC outcomes was carried out under two protocols approved by both Roswell Park Cancer Institute (EDR154409 and NHR009010) and the State University of New York at Buffalo

# <span id="page-2-0"></span>Table 1

T-Helper 1 and 2 produced cytokines' associations with secretagogue use.







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<span id="page-5-0"></span>

\* Overall survival (OS)- and disease-free survival (DFS)-optimized biomarker ranges associated with poorer outcomes are represented in bold. ALQ=above limit of quantitation. MVP= p-value of the multivariate adjusted analysis. Interleukine-2, IL-2; soluble interleukine-2 receptor <sup>α</sup>, sIL-2Rα; interleukine-12 subunit p40, IL-12p40; interleukine-12 subunit p70, IL-12p70; interferon α 2, IFN-α2; interferon γ, IFN-γ; chemokine ligand 10, CXCL-10 (interferon gamma-induced protein 10, IP-10); chemokine ligand 9, CXCL-9 (monokine-induced by interferon γ, MIG); chemokine ligand 8, CXCL-8 (interleukine-8, IL-8); interleukine-5, IL-5; interleukine-10, IL-10; interleukine-13, IL-13.



<span id="page-6-0"></span>















Significant correlations are displayed in bolded text. The differences that are only significant in either adjusted or unadjusted correlations are further denoted by an outline. Interleukine-2, IL-2; soluble interleukine-2 receptor a, sIL-2Ra; interleukine-12 subunit p40, IL-12p40; interleukine-12 subunit p70, IL-12p70; interferon α 2, IFN-α2; interferon γ, IFN-γ; chemokine ligand 10, CXCL-10 (interferon gamma-induced protein 10, IP-10); chemokine ligand 9, CXCL-9 (monokine-induced by interferon y, MIG); chemokine ligand 8, CXCL-8 (interleukine-8, IL-8); interleukine-5, IL-5; interleukine-10, IL-10; interleukine-13, IL-13.

(PHP0840409E). Demographic and clinical patient information was linked with cancer outcomes and profiles of T-helper 1 and 2 produced cytokines of corresponding plasma specimen harvested at BC diagnosis and banked in the Roswell Park Cancer Institute Data Bank and Bio-Repository.

#### 2.1. Study population

All incident breast cancer cases diagnosed at Roswell Park Cancer Institute (01/01/2003-12/31/ 2009) were considered for inclusion ( $n=2194$ ). Medical and pharmacotherapy history were used to determine the baseline presence of diabetes.

#### 2.2. Inclusion and exclusion criteria

All adult women with pre-existing diabetes at breast cancer diagnosis having available banked treatment-naïve plasma specimens (blood collected prior to initiation of any cancer-related therapy surgery, radiation or pharmacotherapy) in the Institute's Data Bank and Bio-Repository were included.

Subjects were excluded if they had prior cancer history or unclear date of diagnosis, incomplete clinical records, type 1 or unclear diabetes status. For a specific breakdown of excluded subjects, please see the original research article by Wintrob et al. [\[1\]](#page-14-0).

A total of 97 female subjects with breast cancer and baseline diabetes mellitus were eligible for inclusion in this analysis.

#### 2.3. Control-matching approach

Each of the 97 adult female subjects with breast cancer and diabetes mellitus (defined as "cases") was matched with two other female subjects diagnosed with breast cancer, but without baseline diabetes mellitus (defined as "controls"). The following matching criteria were used: age at diagnosis, body mass index category, ethnicity, menopausal status and tumor stage (as per the American Joint Committee on Cancer). Some matching limitations applied [\[1\]](#page-14-0).

#### 2.4. Demographic and clinical data collection

Clinical and treatment history was documented as previously described [\[1\].](#page-14-0) Vital status was obtained from the Institute's Tumor Registry, a database updated biannually with data obtained from the National Comprehensive Cancer Networks' Oncology Outcomes Database. Outcomes of interest were breast cancer recurrence and/or death.

#### 2.5. Plasma specimen storage and retrieval

All the plasma specimens retrieved from long-term storage were individually aliquoted in color coded vials labeled with unique, subject specific barcodes. Overall duration of freezing time was accounted for all matched controls ensuring that the case and matched control specimens had similar overall storage conditions. Only two instances of freeze-thaw were allowed between biobank retrieval and biomarker analyses: aliquoting procedure step and actual assay.

# 2.6. Luminex $^{\circledR}$  assays

A total of 12 biomarkers - interleukine-2, soluble interleukine-2 receptor α, interleukine-12 subunit p40, interleukine-12 subunit p70, interferon α 2, interferon γ, chemokine ligand 10 (interferon gamma-induced protein 10), chemokine ligand 9 (monokine-induced by interferon γ), chemokine ligand 8 (interleukine-8), interleukine-5, interleukine-10, and interleukine-13 - were quantified according to the manufacturer protocol. The Luminex $\mathcal{B}$  HCYTOMAG-60K panel (Millipore Corporation, Billerica, MA) was used in this study.

#### 2.7. Biomarker-pharmacotherapy association analysis

Biomarker cut-point optimization was performed for each analyzed biomarker. Biomarker levels constituted the continuous independent variable that was subdivided into two groups that optimized the log rank test among all possible cut-point selections yielding a minimum of 10 patients in any resulting group. Quartiles were also constructed. The resultant biomarker categories were then tested for association with type 2 diabetes mellitus therapy and controls by Fisher's exact test. The continuous biomarker levels were also tested for association with diabetes therapy and controls across groups by the Kruskall-Wallis test and pairwise by the Wilcoxon rank sum. Multivariate adjustments were performed accounting for age, tumor stage, body mass index, estrogen receptor status, and cumulative comorbidity. The biomarker analysis was performed using R Version 2.15.3. Please see the original article for an illustration of the analysis workflow [\[1\]](#page-14-0).

Correlations between biomarkers stratified by type 2 diabetes mellitus pharmacotherapy and controls were assessed by the Pearson method. Correlation models were constructed both with and without adjustment for age, body mass index, and the combined comorbidity index. Correlation analyses were performed using SAS Version 9.4.

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### Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at [http://dx.doi.](http://dx.doi.org/10.1016/j.dib.2017.02.044) [org/10.1016/j.dib.2017.02.044.](http://dx.doi.org/10.1016/j.dib.2017.02.044)

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<sup>[1]</sup> Z. Wintrob, J.P. Hammel, T. Khoury, G.K. Nimako, H.-W. Fu, Z.S. Fayazi, D.P. Gaile, A. Forrest, A.C. Ceacareanu, Insulin use, adipokine profiles and breast cancer prognosis, Cytokine (2017) 45–61. <http://dx.doi.org/10.1016/j.cyto.2016.10.017>.