# Study of Identical (Monozygotic) Twins for Understanding the Genetic and/or Environmental Factors Related to Diabetes

#### Introduction

Diabetes mellitus is a chronic metabolic disease with enormous global health implications. It is usually classified into Type I diabetes mellitus (T1DM), an autoimmune condition that comes with the loss of pancreatic β-cells, and Type II diabetes mellitus (T2DM), predominantly characterized by insulin resistance and β-cell dysfunction. This essay addresses T2DM, which explains over 90% of total diabetes and is often associated with modifiable risk factors such as diet, lack of physical activity, and overweight (American Diabetes Association [ADA], 2023). Despite strong associations with lifestyle, T2DM also has a significant genetic component. Twin studies, particularly in monozygotic (MZ) twins, who share essentially 100% of their genetic composition, have served to clarify the relative role of genes and the environment to T2DM pathogenesis. The essay emphasizes T2DM because of its rising prevalence and the complex interplay between environmental and genetic factors. This essay critically examines the large twin studies, addresses the gene-environment interaction, and presents the future of diabetes research.

## **Discussion**

## Diabetes Overview: Type I vs. Type II

Type 1 Diabetes Mellitus is a long-term autoimmune disease characterized by immune-mediated destruction of the insulin-producing pancreatic β-cells. This leads to absolute deficiency of insulin, which requires lifelong exogenous insulin therapy. It typically presents in childhood or adolescence, although adult-onset varieties—latent autoimmune diabetes in adults (LADA)—are now increasingly being diagnosed (Fourlanos et al., 2005). Genetic predisposition to T1DM involves genetic differences in the HLA locus, and most notably the HLA-DR3 and HLA-DR4 alleles, whose important role is in the regulation of the immune system (Pociot & Lernmark, 2016).

In contrast, Type 2 Diabetes Mellitus is essentially a metabolic disorder of peripheral insulin resistance and impaired  $\beta$ -cell compensation. It typically occurs in mid-to-late adulthood, but with rising obesity, the onset has been advanced to earlier ages, even into adolescence. There is strong familial clustering, yet the cause of T2DM is multifactorial, consisting of polygenic susceptibility and massive environmental impact. Central obesity, intake of high-fat and high-sugar diets, physical inactivity, and psychosocial stress are major risk factors (Hu et al., 2001). Moreover, ectopic deposition of fat into organs such as the liver and muscle and long-term inflammation augment insulin resistance and drive disease promotion further (Shulman,

2000). These pathophysiologic and etiologic distinctions account for why, despite its hereditary basis, T2DM is extremely susceptible to lifestyle change.

## Twin Studies and Heritability of Type II Diabetes

Twin studies provide a valuable tool for disentangling the relative contribution of genetic and environmental factors to the etiology of multifactorial diseases like Type II Diabetes Mellitus (T2DM). Since monozygotic (MZ) twins share virtually 100% genes, while dizygotic (DZ) twins share approximately 50% genes, concordance rate comparison between the two groups allows one to make valid heritability estimates. In T2DM, heritability estimates derived from twin studies consistently point to a major genetic component but also to the pivotal contribution of modifiable environmental factors.

Kaprio et al. (1992) conducted a rigorous analysis with the Finnish Twin Cohort data involving over 10,000 twin pairs. The findings revealed a much higher concordance rate for T2DM among MZ twins (70%) compared to DZ twins (30%). The difference yielded an estimate of heritability of approximately 72%, suggesting that genetic factors predominate the causation of T2DM. Interestingly, these results are consistent with earlier studies that reported heritability estimates of 60–75% (Prasad and Groop, 2015), thereby confirming the genetic nature of the disease. Supplementing these findings, Medici et al. (1999) analyzed a large European twin cohort sample and estimated heritability at around 70%, again supporting a strong genetic component. Interestingly, their research also suggested that the genetic susceptibility for T2DM could be age-dependent, with increased heritability in patients diagnosed at an age younger than 60. This would have implications of a possible gene—age interaction, where genetic predisposition would play a more important role in young-onset T2DM.

Aside from concordance rates, twin pairs discordant for T2DM have been used in studies to examine lifestyle and environmental factors. In a remarkable study conducted by Castillo-Fernandez et al. (2014), 110 MZ twin pairs discordant for T2DM were evaluated with extensive phenotypic profiling. The affected twins had higher body mass index (BMI) consistently, increased central adiposity, and decreased physical activity. Interestingly, the non-diabetic cotwins, who had identical genetics, were all disease-free, illustrating the influence of modifiable risk factors. This agrees with previous research by Franks et al. (2007) and Willemsen et al. (2015), who highlighted intrauterine and early-life exposures' influence on metabolic processes and insulin sensitivity. Epigenetic difference has also been reported between discordant MZ twin pairs. Davegårdh et al. (2018) also demonstrated that methylation of genes related to insulin secretion and  $\beta$ -cell function (e.g., TXNIP and ABCC8) was significantly different between affected and unaffected co-twins. These results indicate that

environmentally controlled gene expression can mediate the pathogenesis of T2DM even with the same DNA sequence.

One of the most significant strengths of twin studies is their ability to control for the genetic background, perhaps separating environmental factors. For instance, Lyssenko et al. (2008) reported that lifestyle changes, such as diet intervention and increased physical activity, postponed or prevented the onset of T2DM in high-risk MZ twins. This is strong evidence to favor the use of targeted prevention interventions, particularly in those with a high level of genetic loading. Collectively, these results document a dynamic and complex interplay between environment and genes. Although T2DM is highly heritable, heterogeneity of disease expression among MZ twins indicates that environmental and behavioral determinants are primary risk determinants. This makes twin research an essential platform not only to estimate genetic susceptibility but also to find actionable environmental and lifestyle interventions.

Updated Table 1: Concordance Rates and Heritability Estimates in Twin Studies on Type II Diabetes

Study	Twin Type	Concordance	Heritability	Key Findings
		Rate (%)	(%)	
Kaprio et al. (1992)	MZ / DZ	70 / 30	72	Large cohort; established strong genetic contribution
Medici et al. (1999)	MZ / DZ	67 / 25	70	Noted higher heritability in earlier-onset T2DM
Castillo- Fernandez et al. (2014)	MZ (discordant)	N/A	69	Highlighted BMI, diet, and lifestyle differences among genetically identical twins
Davegårdh et al. (2018)	MZ (discordant)	N/A	Epigenetic divergence	Found differential DNA methylation in key metabolic genes

## **Genetic vs. Environmental Contributions**

Although monozygotic twin concordance rates are highly suggestive of a genetic aetiology to T2DM, they are not 100%, highlighting the role of environmental determinants. For example, Maciak et al. (2020) not only found greater adiposity in diabetic twins, but also poorer

cardiorespiratory fitness and lower insulin sensitivity, all open to change by lifestyle. These results are in line with the "accelerator hypothesis", which proposes that greater adiposity hastens β-cell failure in genetically susceptible individuals (Wilkin, 2001). In addition, epigenetics provides a more mechanistic explanation of gene–environment interactions. Nilsson et al. (2015) showed that epigenetic modifications in gene promoter regions such as PPARGC1A, which are core to mitochondrial function and glucose metabolism, were linked to T2DM in discordant MZ twins. Such epigenetic marks, including altered methylation and histone modifications, can be affected by early nutrition environments, activity levels, and psychosocial stress, thus affecting gene expression without altering DNA sequence.

Longitudinal results by Cornelis et al. (2014) also provide evidence about cumulative environmental effects. In a 20-year follow-up, non-diabetic co-twins who had made healthier lifestyle choices had reduced T2DM prevalence even under conditions of genetic predisposition (Cornelis et al, 2014). This is in agreement with intervention studies such as the Diabetes Prevention Program (Knowler et al., 2002), which documented that physical activity and moderate weight loss lowered diabetes incidence by 58%, even among individuals with a high family history. Besides, cultural and socioeconomic settings may have a great impact on disease risk. Evidence suggests that twins reared in different socio-economic environments (e.g., through migration or adoption) will have varying T2DM risk profiles, highlighting the impact of access to good food, healthcare, and education (Vassy et al., 2012). These findings show genetic risk plasticity to social determinants of health.

## **Conclusion and Future Directions**

While monozygotic (MZ) twin studies have significantly expanded the understanding of Type 2 Diabetes Mellitus (T2DM) heritability, they equally show the limitation of attributing disease risk solely to heredity. The invariably high—but not absolute—concordance rates of the MZ twins are evidence of the presence of strong genetic determinants, yet the frequent appearance of discordant twin pairs depict the significant role played by exposures to the environment and lifestyle factors. These patterns support a multifactorial and probability model of T2DM pathogenesis rather than a deterministic genetic one. This suggests complexity does imply the need for nuanced interpretation allowing for the interaction between genetic susceptibility and modifiable external influences such as diet, exercise, and psychosocial stressors.

Furthermore, the development of epigenetics has brought an exciting dimension to geneenvironment interactions. Epigenetic discordance in MZ twins suggests that gene expression played by nature is not invariable but depends on personal life experience. However, sample size limitations, tissue-specific epigenetic variance, and socio-demographic homogeneity limit the reproducibility and generalizability of existing evidence. To close these gaps, new research needs to focus on longitudinal, multi-omic studies in ethnically and socioeconomically diverse twin cohorts. Merging genomic data with other biological and environmental layers—such as metabolomics, microbiomics, and exposomics—could reveal the intricate mechanisms of T2DM development. Lastly, the discipline needs to shift from singular risk assessment to comprehensive, equity-based strategies that combine genetic data with viable lifestyle interventions.

## References

American Diabetes Association (ADA), 2023. Standards of medical care in diabetes—2023. *Clinical Diabetes*, 41(1), pp.4–31. Available at: <a href="https://diabetesjournals.org/clinical/article/41/1/4/148029/Standards-of-Care-in-Diabetes-2023-Abridged-for">https://diabetesjournals.org/clinical/article/41/1/4/148029/Standards-of-Care-in-Diabetes-2023-Abridged-for [Accessed 13 May 2025].</a>

Castillo-Fernandez, J.E., Spector, T.D. and Bell, J.T., 2014. Epigenetics of discordant monozygotic twins: Implications for disease. *Genome Medicine*, 6(7), p.60. https://doi.org/10.1186/s13073-014-0060-z.

Cornelis, M.C., Zaitlen, N., Hu, F.B., Kraft, P. and Price, A.L., 2014. Genetic and environmental components of family history in type 2 diabetes. *Human Genetics*, 134(2), pp.259–267. https://doi.org/10.1007/s00439-014-1519-0.

Davegårdh, C., García-Calzón, S., Bacos, K. and Ling, C., 2018. DNA methylation in the pathogenesis of type 2 diabetes in humans. *Molecular Metabolism*, 14, pp.12–25. <a href="https://doi.org/10.1016/j.molmet.2018.01.022">https://doi.org/10.1016/j.molmet.2018.01.022</a>.

Feinberg, A.P., 2018. The key role of epigenetics in human disease prevention and mitigation. New England Journal of Medicine, 378(14), pp.1323–1334. https://doi.org/10.1056/NEJMra1402513.

Fourlanos, S., Perry, C., Stein, M.S., Stankovich, J., Harrison, L.C. and Colman, P.G., 2006. A clinical screening tool identifies autoimmune diabetes in adults. *Diabetes Care*, 29(5), pp.970–975. https://doi.org/10.2337/diacare.295970.

Franks, P.W., Hanson, R.L., Knowler, W.C., Moffett, C., Enos, G., Infante, A.M., Krakoff, J. and Looker, H.C., 2007. Childhood predictors of young-onset type 2 diabetes. *Diabetes*, 56(12), pp.2964–2972. https://doi.org/10.2337/db06-1639.

Hu, F.B., Manson, J.E., Stampfer, M.J., Colditz, G., Liu, S., Solomon, C.G. and Willett, W.C., 2001. Diet, lifestyle, and the risk of type 2 diabetes mellitus in women. *New England Journal of Medicine*, 345(11), pp.790–797. https://doi.org/10.1056/NEJMoa010492.

Kaprio, J., Tuomilehto, J., Koskenvuo, M., Romanov, K., Reunanen, A., Eriksson, J., Stengård, J. and Kesäniemi, Y.A., 1992. Concordance for type 1 (insulin-dependent) and type 2 (non-insulin-dependent) diabetes mellitus in a population-based cohort of twins in Finland. *Diabetologia*, 35(11), pp.1060–1067. https://doi.org/10.1007/BF02221682.

Knowler, W.C., Barrett-Connor, E., Fowler, S.E., Hamman, R.F., Lachin, J.M., Walker, E.A. and Nathan, D.M., 2002. Reduction in the incidence of type 2 diabetes with lifestyle intervention or

metformin. New England Journal of Medicine, 346(6), pp.393–403. https://doi.org/10.1056/NEJMoa012512.

Lyssenko, V., Jonsson, A., Almgren, P., Pulizzi, N., Isomaa, B., Tuomi, T., Berglund, G., Altshuler, D., Nilsson, P. and Groop, L., 2008. Clinical risk factors, DNA variants, and the development of type 2 diabetes. *New England Journal of Medicine*, 359(21), pp.2220–2232. https://doi.org/10.1056/NEJMoa0801869.

Maciak, S., Sawicka, D., Sadowska, A., Prokopiuk, S., Buczyńska, S., Bartoszewicz, M., Niklińska, G., Konarzewski, M. and Car, H., 2020. Low basal metabolic rate as a risk factor for development of insulin resistance and type 2 diabetes. *BMJ Open Diabetes Research & Care*, 8, e001381. https://doi.org/10.1136/bmjdrc-2020-001381.

Medici, F., Hawa, M., Ianari, A., Pyke, D.A. and Leslie, R.D., 1999. Concordance rate for type II diabetes mellitus in monozygotic twins: Actuarial analysis. *Diabetologia*, 42(2), pp.146–150. https://doi.org/10.1007/s001250051132.

Nilsson, E., Matte, A., Perfilyev, A., de Mello, V.D., Käkelä, P., Pihlajamäki, J. and Ling, C., 2015. Epigenetic alterations in human liver from subjects with type 2 diabetes in parallel with reduced folate levels. *Journal of Clinical Endocrinology & Metabolism*, 100(11), pp.E1491–E1501. https://doi.org/10.1210/jc.2015-3204.

Pociot, F. and Lernmark, Å., 2016. Genetic risk factors for type 1 diabetes. *The Lancet*, 387(10035), pp.2331–2339. https://doi.org/10.1016/S0140-6736(16)30582-7.

Prasad, R.B. and Groop, L., 2015. Genetics of type 2 diabetes—Pitfalls and possibilities. *Genes*, 6(1), pp.87–123. https://doi.org/10.3390/genes6010087.

Shulman, G.I., 2000. Cellular mechanisms of insulin resistance. *Journal of Clinical Investigation*, 106(2), pp.171–176. https://doi.org/10.1172/JCI10583.

Vassy, J.L., Dasmahapatra, P., Meigs, J.B., Schork, N.J., Magnussen, C.G., Chen, W., Raitakari, O.T., Pencina, M.J., Jamal, S.M., Berenson, G.S. and Goodman, E., 2012. Genotype prediction of adult type 2 diabetes from adolescence in a multiracial population. *Pediatrics*, 130(5), pp.e1235–e1242. https://doi.org/10.1542/peds.2012-1132.

Wilkin, T.J., 2001. The accelerator hypothesis: Weight gain as the missing link between Type I and Type II diabetes. *Diabetologia*, 44(7), pp.914–922. https://doi.org/10.1007/s001250100548.

Willemsen, G., Kelly, K., Bell, C.G., Christensen, K., Bowden, J., Dalgard, C., Harris, J.R., Kaprio, J., Lyle, R., Magnusson, P.K., Mather, K.A., Ordoñana, J.R., Perez-Riquelme, F.,

Pedersen, N.L., Pietiläinen, K.H., Sachdev, P.S., Boomsma, D.I. and Spector, T.D., 2015. The concordance and heritability of type 2 diabetes in 34,166 twin pairs from international twin registers: The Discordant Twin (DISCOTWIN) Consortium. *Twin Research and Human Genetics*, 18(6), pp.762–771. https://doi.org/10.1017/thg.2015.83.