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RISK FACTORS AND BIOCHEMICAL CHARACTERIZATION OF DIABETES MELLITUS AMONG YOUNG ADULTS IN FAISALABAD, PAKISTAN

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ABSTRACT

Objective: The objective of this study was to determine risk factors and biochemical characteristics of diabetes mellitus among young adults in Faisalabad, Pakistan.

Methods: This cross-sectional study was conducted at Allied Hospital, Faisalabad, involving 100 young adults (14-40 years) with diabetes mellitus from families with diabetic history. Participants included 34 T1DM and 66 T2DM patients selected through convenient sampling. Detailed family pedigrees were constructed, and data on demographics, anthropometric measurements, and biochemical parameters were collected. Blood glucose levels were measured using a glucometer, and samples were analyzed at NIH-HRI Research Centre, Faisalabad Medical University. Familial aggregation was categorized based on the number and degree of affected relatives. Data were analyzed using SPSS, with Chi-square and independent t-tests applied where appropriate ($p<0.05$).

Results: Age at onset differed significantly, with 88.2% of T1DM cases diagnosed before age 25 compared to 95.5% of T2DM cases at or after 25 years ($p<0.001$). BMI >23 kg/m² was present in 84.8% of T2DM patients compared to 47.1% of T1DM patients ($p<0.001$). Family history of diabetes was present in 84% of participants, significantly higher in T2DM (90.9%) compared to T1DM (70.6%; $p=0.011$). Biochemical characterization revealed that glycemic indices (fasting blood glucose, HbA1c) and lipid parameters (total cholesterol, triglycerides) were comparable between T1DM and T2DM groups. However, serum creatinine was significantly higher in T2DM patients (0.96±0.25 mg/dl) compared to T1DM patients (0.82±0.23 mg/dl; $p=0.038$), suggesting early renal involvement in the T2DM group.

Conclusion: This study demonstrates that the high prevalence of family history (84%) and distinct familial aggregation patterns in Faisalabad reflect complex gene-environment interactions in young Pakistani adults with diabetes. Biochemically, most parameters were comparable across diabetes types; however, elevated serum creatinine in T2DM patients indicates early subclinical renal changes warranting monitoring.

KEYWORDS: Diabetes mellitus, familial aggregation, family history, Type 1 diabetes, Type 2 diabetes, Pakistan

INTRODUCTION

Diabetes mellitus (DM) is a chronic, non-contagious metabolic condition characterized by elevated blood glucose levels. This condition results from either an absolute or relative insulin deficiency or a combination of both[1]. It is a significant public health concern that particularly affects low-income countries, such as Pakistan[2]. According to the IDF, Pakistan has a high prevalence of diabetes with an estimated 31.4% of the adult population having diabetes in 2024[3]. An additional 11 million individuals are at increased risk of T2DM due to their reduced glucose tolerance [4].

This alarming trend is attributed to various factors, including rising rates of overweight and obesity, unhealthy diets, physical inactivity, and genetic and epigenetic predispositions[5]. These factors appear to significantly contribute to insulin resistance or dysfunction, which in turn exacerbates the disease[6]. Diabetes is a major cause of blindness, kidney failure, lower limbs amputation and other long-term effects that have a considerable influence on the quality of life [7].

Diabetes mellitus is primarily classified into two main types: Type 1 diabetes mellitus (T1DM) and Type 2 diabetes mellitus (T2DM). T1DM, accounting for approximately 5-10% of all diabetes cases, is an autoimmune condition characterized by the destruction of pancreatic beta cells, resulting in absolute insulin deficiency. It typically manifests in childhood or adolescence, though it can occur at any age[8]. T2DM, representing about 90% of the diabetes burden, is characterized by insulin resistance and progressive beta-cell dysfunction. About 90% of the population has T2DM, which is responsible for a significant portion of the diabetes prevalence[9]. While T2DM was traditionally considered

a disease of middle-aged and older adults, there has been an alarming increase in early-onset T2DM among younger populations, particularly in South Asian countries including Pakistan.

While lifestyle factors such as diet, physical activity, and obesity contribute significantly to T2DM development, both T1DM and T2DM demonstrate strong hereditary components with distinct familial aggregation patterns. First-degree relatives of T2DM patients face a two- to six-fold increased risk, while those with T1DM relatives have a 15-fold higher risk compared to the general population[10]. The genetic basis differs substantially between types, with T2DM involving complex polygenic variants related to insulin resistance, and T1DM primarily associated with human leukocyte antigen (HLA) genes and autoimmune susceptibility loci. Despite these established genetic contributions, comparative data on familial clustering patterns between T1DM and T2DM in young Pakistani adults remain limited, particularly regarding the influence of consanguinity and multi-generational involvement[11].

Despite the alarming prevalence of diabetes in Pakistan and established hereditary components, there is limited research examining familial aggregation patterns among young adults, particularly comparative data between T1DM and T2DM. Young adulthood represents a critical window for early detection and intervention, where preventive strategies can significantly alter disease trajectories. This study was conducted in Faisalabad to investigate familial clustering patterns including parental consanguinity, generational involvement, and number of affected relatives, alongside anthropometric measurements, biochemical profiles, and lifestyle factors. Understanding these patterns can inform risk stratification protocols, enable identification of high-risk individuals, and guide family-centered prevention strategies. This study therefore aims to assess familial aggregation of diabetes mellitus and identify associated risk factors among young adults with T1DM and T2DM in Faisalabad, Pakistan.

MATERIALS AND METHODS

Study Design and Participants

This cross-sectional study was conducted at Allied Hospital, Faisalabad, Pakistan. Ethical approval was obtained from the ERC of Faisalabad Medical University (FMU), Faisalabad and written informed consent was obtained from all participants. 100 young adults (aged 14-40 years) with diabetes mellitus were recruited using convenient sampling from families with a history of diabetes. Sociodemographic data, clinical history, and lifestyle information were collected through structured questionnaires. Detailed family pedigrees were constructed to document diabetes occurrence across generations. Parental consanguinity and the number of affected relatives were recorded to assess familial aggregation patterns.

Height and weight were measured using standardized equipment (SECA, Germany). BMI was calculated, and participants were classified as overweight or obese according to WHO criteria for Asian populations. Familial aggregation was categorized as high risk (two first-degree relatives or one first-degree plus two second-degree relatives with diabetes from the same lineage), moderate risk (one first-degree relative with or without one second-degree relative, or two second-degree relatives from the same lineage), or average risk (one second-degree relative or no family history). Venous blood samples (5 mL) were collected using aseptic techniques and processed at the NIH-HRI Research Centre, FMU, Faisalabad. Blood glucose was measured using a glucometer. Additional parameters included HbA1c, lipid profile (total cholesterol, triglycerides), renal function tests (serum creatinine, urea), and alanine aminotransferase (ALT). Data was analyzed using SPSS version 25. Categorical variables are expressed as frequencies and percentages, while continuous variables are presented as mean ± standard deviation. Chi-square test was used for categorical variables, and independent t-tests for continuous variables. Statistical significance was set at $p<0.05$.

RESULTS

The study included 100 young adults with diabetes mellitus from Faisalabad (34 T1DM, 66 T2DM). Age at onset showed a significant difference between groups ($p<0.001$), with 88.2% of T1DM patients diagnosed before age 25 compared to 95.5% of T2DM patients diagnosed at or after 25 years. BMI was significantly higher in T2DM patients, with 84.8% having BMI >23 kg/m² compared to 47.1% in T1DM patients ($p<0.001$). A strong family history of diabetes was observed in the study population, affecting 84% of participants and was significantly more common among patients with T2DM than those with T1DM. Sociodemographic and clinical characteristics of participants are presented in Table 1.

Table 1: Sociodemographic and Clinical Characteristics of Study Participants (n = 100)

Variable	Category	T1DM (n=34)	T2DM (n=66)	Total (n =100)	P value
Gender	Male	11 (32.4)	18 (27.3)	29 (29.0)	0.379
	Female	23 (67.6)	48 (72.7)	71 (71.0)	
Age at Onset (years)	<25	30 (88.2)	3 (4.5)	33 (33.0)	<0.001*
	≥25	4 (11.8)	63 (95.5)	67 (67.0)	
	15–20	21 (61.8)	0 (0.0)	21 (21.0)	<0.001*

Current Age Group (years)	21–25	3 (8.8)	1 (1.5)	4 (4.0)	
	26–30	3 (8.8)	8 (12.1)	11 (11.0)	
	31–35	2 (5.9)	18 (27.3)	20 (20.0)	
	36–40	5 (14.7)	39 (59.1)	44 (44.0)	
BMI (kg/m²)	≤23	18 (52.9)	10 (15.2)	28 (28.0)	<0.001*
	>23	16 (47.1)	56 (84.8)	72 (72.0)	
Marital Status	Unmarried	13 (38.2)	61 (92.4)	74 (74.0)	<0.001*
	Married	21 (61.8)	5 (7.6)	26 (26.0)	
Education Level	No formal schooling	6 (17.6)	23 (34.8)	29 (29.0)	0.249
	Primary	7 (20.6)	16 (24.2)	23 (23.0)	
	Secondary	14 (41.2)	21 (31.8)	35 (35.0)	
	Higher secondary	3 (8.8)	2 (3.0)	5 (5.0)	
	Graduation & above	4 (11.8)	4 (6.1)	8 (8.0)	
Occupation	Office job	3 (8.8)	10 (15.2)	13 (13.0)	<0.001*
	Business	1 (2.9)	5 (7.6)	6 (6.0)	
	Student	9 (26.5)	0 (0.0)	9 (9.0)	
	Housewife	2 (5.9)	21 (31.8)	23 (23.0)	
	Others	19 (55.9)	30 (45.5)	49 (49.0)	
Family History of Diabetes	Yes	24 (70.6)	60 (90.9)	84 (84.0)	0.011*
	No	10 (29.4)	6 (9.1)	16 (16.0)	

Glycemic control and most biochemical parameters were comparable between T1DM and T2DM patients, with no significant differences in fasting or random blood glucose, HbA1c, lipid profile, urea, or ALT levels. However, serum creatinine was significantly higher among T2DM patients. Detailed results are presented in Table 3.

Table 2: Biochemical Parameters of participants

Parameter	**T1DM (Mean ± SD)**	**T2D (Mean ± SD)**	**P value**
Fasting Blood Sugar (mg/dl)	174.91 ± 85.00	176.22 ± 79.69	0.948
Random Blood Sugar (mg/dl)	241.82 ± 118.93	207.98 ± 109.71	0.190
HbA1c (%)	7.59 ± 1.72	7.18 ± 1.58	0.339
Total Cholesterol (mg/dl)	186.77 ± 34.09	192.42 ± 39.03	0.583
Triglycerides (mg/dl)	147.09 ± 46.38	147.90 ± 49.94	0.949
Renal Function Tests			
Serum Creatinine (mg/dl)	0.82 ± 0.23	0.96 ± 0.25	0.038*
Urea (mg/dl)	24.08 ± 5.23	23.23 ± 4.40	0.512
Hepatic Enzyme			
Alanine Aminotransferase (U/L)	37.99 ± 12.38	37.69 ± 10.81	0.925

Dietary habits and physical activity patterns showed no significant differences between T1DM and T2DM groups. The majority of participants (54%) reported no cold drink consumption, while 75% avoided junk food. Regarding physical activity, half of the participants (50%) engaged in daily exercise, though 24% reported no physical activity. Cold drink consumption (p=0.381), junk food intake (p=0.208), and physical activity levels (p=0.193) were comparable across both diabetes types. Complete dietary and physical activity patterns are presented in Table 4.

Table 3: Dietary Habits and Physical Activity Patterns According to Type of DM (n = 100)

Variable	Category	T1DM (n=34)	T2DM (n=66)	Total (n =100)	P value
Cold Drinks Consumption	No	22 (64.7)	32 (48.5)	54 (54.0)	0.381
	Once per week	8 (23.5)	20 (30.3)	28 (28.0)	
	Twice per week	2 (5.9)	4 (6.1)	6 (6.0)	
	Once per month	2 (5.9)	10 (15.2)	12 (12.0)	
Junk Food Consumption	No	23 (67.6)	52 (78.8)	75 (75.0)	0.208
	Once per week	2 (5.9)	7 (10.6)	9 (9.0)	
	Twice per week	7 (20.6)	5 (7.6)	12 (12.0)	
	Rarely	2 (5.9)	2 (3.0)	4 (4.0)	
Physical Activity	No	5 (14.7)	19 (28.8)	24 (24.0)	0.193
	Daily	22 (64.7)	28 (42.4)	50 (50.0)	

	2–3 days/week	1 (2.9)	2 (3.0)	3 (3.0)	
	Rarely	6 (17.6)	17 (25.8)	23 (23.0)	
Total		34 (100.0)	66 (100.0)	100 (100.0)	

DISCUSSION

This cross-sectional study examined familial aggregation patterns and associated risk factors among 100 young adults with diabetes mellitus in Faisalabad, Pakistan. The findings show differences in familial clustering between T1DM and T2DM, with T2DM demonstrating significantly higher familial aggregation alongside elevated BMI and stronger family history.

The study demonstrated that 84% of participants had a family history of diabetes, with T2DM patients exhibiting significantly higher rates (90.9%) compared to T1DM patients (70.6%; p=0.011). This pattern substantiates existing evidence that T2DM demonstrates stronger familial clustering due to its polygenic inheritance involving multiple susceptibility loci[12]. This trend is aligns with studies from neighboring India and other South Asian populations, where genetic susceptibility appears amplified by shared environmental factors[13, 14].

BMI emerged as a significant discriminator between diabetes types, with 84.8% of T2DM patients demonstrating BMI >23 kg/m² compared to 47.1% of T1DM patients (p<0.001). This finding confirms the central role of obesity in T2DM pathogenesis and appropriately applies Asian-specific BMI cutoffs, recognizing that South Asian populations experience increased metabolic risk at lower BMI thresholds[15]. The intersection of high familial aggregation and elevated BMI in T2DM patients suggests gene-environment interactions. Conversely, the lower BMI in T1DM patients reflects the autoimmune pathophysiology independent of obesity[16].

The comparable glycemic and lipid parameters suggest similar diabetes management challenges regardless of type, though the mechanisms differ fundamentally between absolute insulin deficiency and insulin resistance[17]. Notably, serum creatinine was significantly higher in T2DM patients (0.96±0.25 mg/dl) compared to T1DM patients (0.82±0.23 mg/dl; p=0.038), despite both remaining within normal ranges. This difference may herald early nephropathy or reflect the higher prevalence of metabolic syndrome components in T2DM[18].

Interestingly, dietary habits and physical activity patterns showed no significant differences between groups. Most participants (54%) reported no cold drink consumption, 75% avoided junk food, and 50% engaged in daily physical activity. These findings suggest that in populations with high genetic susceptibility and strong familial clustering, diabetes may develop despite relatively healthy lifestyle practices, a phenomenon documented in South Asian populations where diabetes occurs at younger ages and lower BMI thresholds[19].

These findings have important implications for diabetes prevention and management in Pakistan. The positive family history particularly in T2DM, indicates that family-based screening programs could efficiently identify high-risk individuals before disease onset or during prediabetic stages when interventions are most effective[20].

This study has several limitations that should be acknowledged. The cross-sectional design limits causal inference regarding the relationships between familial aggregation, lifestyle factors, and diabetes development; longitudinal cohort studies would provide stronger evidence for disease progression patterns. The sample size of 100 participants, while adequate for detecting significant differences in primary outcomes, may have limited statistical power to identify subtle associations with lifestyle variables. The convenient sampling approach from families with known diabetes history was necessary to examine familial clustering patterns but may limit generalizability to the broader population. Despite these limitations, the study provides important data on familial diabetes patterns in young Pakistani adults and demonstrates the utility of systematic family history assessment for risk stratification.

CONCLUSION

This study demonstrates that family history (84%) and distinct familial aggregation patterns are prominent risk factors for diabetes mellitus among young adults in Faisalabad, reflecting complex gene-environment interactions characteristic of Pakistani families. T2DM patients showed significantly higher familial aggregation, elevated BMI, and later age at onset compared to T1DM patients. Biochemical characterization revealed broadly comparable glycemic and lipid profiles between the two diabetes types; however, significantly elevated serum creatinine in T2DM patients points to early subclinical renal involvement warranting longitudinal monitoring. These findings underscore the need for family-based screening programs utilizing systematic pedigree assessment to identify high-risk individuals during prediabetic stages, enabling timely preventive intervention in this population.

Disclaimer: None.

Conflict of Interest: None.

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