

The association between metabolic syndrome and elevated serum alanine transaminase levels in an indigenous population in Northern Taiwan: a community-based study

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Abstract

Background: Metabolic syndrome (MetS), a prevalent health condition in Taiwan, places individuals at higher risk of cardiovascular disease, diabetes, and stroke. Therefore, the identification of risk factors associated with MetS is crucial. Nevertheless, only limited studies about MetS have been conducted among indigenous peoples in Taiwan; these studies identified a high prevalence of MetS among an indigenous population, which encouraged us to investigate further. Thus, our study aims to determine the prevalence of MetS among the indigenous Taiwanese population and to explore the relationship between MetS and associated risk factors, especially serum alanine transaminase (ALT).

Methods: This is an observational, population-based, cross-sectional study that was conducted in remote villages of an indigenous community in northern Taiwan between 2010 and 2015. A total of 454 participants, 47.36% male and 52.64% female, were eligible for analysis. The participants underwent anthropometric assessment and measurements of blood pressure, serum triglyceride levels, fasting plasma glucose levels, serum HDL-C levels and serum ALT levels. MetS was defined based on the revised NCEP/ATPIII criteria from Taiwan Health Promotion Administration.

Results: A total of 454 participants were included in the analysis. There were 277 people with MetS and 177 people without. The prevalence of MetS was 61.01%. The average age was 49.50 years old. People with MetS had a significantly higher ALT level (average 31.21 ± 25.00 U/L vs. 23.29 ± 15.98 U/L, $p < 0.001$) than those without MetS. In addition, the chi-square comparison showed that participants with abnormal ALT levels (>36 U/L) had a tendency towards a higher prevalence of MetS (76.7% vs. 57.3%, $p = 0.001$) than those with normal ALT levels (≤ 36 U/L). The adjusted odds ratio (OR) of abnormal ALT levels for MetS was 2.58 (95% CI=1.23-5.44, $p = 0.01$). The area under the ROC curve (AUC) of the ALT level was 0.63 (95% CI=0.58-0.68, $p < 0.001$), which showed that the ALT level was positively associated with MetS.

Conclusions: The overall prevalence of MetS was 61.01% in the highland indigenous population in Taiwan, which suggests an unignorable health problem that should actively be addressed. Furthermore, these findings indicated that higher serum ALT levels (>36 U/L) were associated with an increased risk of MetS.

Background

Metabolic syndrome (MetS), a serious global health concern, is a constellation of different metabolic abnormalities in an individual, including central obesity, hyperglycemia, hypertension, elevated triglyceride levels, and low high-density lipoprotein cholesterol levels [1]. These abnormalities result in an increased risk of cardiovascular events, type II diabetes and chronic kidney disease [2, 3]. Therefore, the identification of risk factors associated with MetS is vital.

According to the Taiwan national survey, the Nutrition and Health Survey in Taiwan (NAHSIT), the prevalence of MetS increased from 13.6% (1993–1996) to 30% (2013–2016). Taking the regional and ethnic diversity in Taiwan into consideration, the NAHSIT 2005–2008 investigated the regional differences and showed that the indigenous area had the highest prevalence (52.1%) compared to the prevalence in the densely populated area, the offshore island and the Hakka area. Additionally, up to 71.6% of indigenous peoples were overweight or obese [4, 5]. Furthermore, two cross-sectional studies demonstrated a high prevalence of MetS among indigenous populations in Taiwan between 2010 and 2011 [6, 7]. Nevertheless, there are still limited studies on MetS among indigenous peoples in Taiwan. Thus, we intend to assess MetS status in an indigenous tribe, the Atayal tribe, which is widely distributed in the northern part of the Central Mountain Range of Taiwan.

Alanine transaminase (ALT) is an enzyme that mainly exists in hepatocytes, and when the liver is injured due to conditions such as viral hepatitis, ALT will be released, resulting in elevated serum ALT levels [8]. A large community study in Taiwan from 2003 to 2004 illustrated that the prevalence of elevated ALT in an adult population was 11.4%, and non-alcoholic fatty liver disease (NAFLD) seemed to be the most common cause of elevated ALT [9]. Moreover, there were 16.5% adults with abnormal ALT levels in an Atayal indigenous community [10]. Previous cross-sectional studies have reported a positive

association between serum ALT level and MetS [11, 12]. A systemic review and meta-analysis and a large cohort study both showed that the increase in serum ALT levels increased the risk of MetS [13, 14]. Therefore, our study aimed to determine the prevalence of MetS with abnormal serum ALT levels among the Taiwanese indigenous population.

Methods

Study design and study population

This is an observational, population-based, cross-sectional study. We collected data from three remote villages in an indigenous community in Northern Taiwan from 2010 through 2015. Subjects were residents who had lived in the community for more than 6 months, aged over 18 and were able to walk to the health station. Every subject completed a questionnaire containing questions regarding basic personal data and medical conditions, including race, age, sex, occupation, and history of hypertension, diabetes and hyperlipidemia. The questionnaires were completed after detailed explanations were provided by the trained interviewers in in-person interviews. Additionally, urine and blood samples were collected. Anthropometric measurements were performed by trained research assistants or nurses under the supervision of a medical doctor. After the exclusion of subjects who were pregnancy or who had incomplete, missing or repeated data, 454 participants were eligible for the analysis. The study was approved by the Chang Gung Medical Foundation Institutional Review Board (101-4156A3), and written informed consent was provided by all the subjects before enrollment.

Definition of metabolic syndrome and abnormal ALT level

MetS was defined by the revised NCEP/ATPIII criteria from Taiwan Health Promotion Administration [15]. In detail, a diagnosis of MetS requires the presence of three or more of the following factors: 1) waist circumference (WC) ≥ 90 cm in men or ≥ 80 cm in women, 2) systolic blood pressure (SBP) ≥ 130 mmHg and/or diastolic blood pressure (DBP) ≥ 85 mmHg, 3) serum HDL-C < 40 mg/dl in men or < 50 mg/dl in women, 4) serum triglycerides ≥ 150 mg/dl, and 5) fasting plasma glucose ≥ 100 mg/dl. An abnormal ALT level was defined as a level > 36 IU/L according to the laboratory method used in Chang Gung Memorial Hospital.

Anthropometric and laboratory measurements

Each subject's blood pressure (BP) was measured on the upper arm while they were in a seated position after at least 5 minutes of rest with a standardized electronic sphygmomanometer. WC was measured at the level midway between the iliac crests and the lowest rib margin with the subjects in a standing position. Height was determined by a height-measuring machine while subjects were barefoot and standing in an erect position with their arms by their side and their feet together. Weight measurements were performed with subjects standing at the center of the weighing scale in light clothing without shoes or socks. Body mass index (BMI) was defined as the weight in kilograms divided by the square of the height in meters (kg/m^2). Then, we classified the BMI values into 3 main categories according to the definition published by Taiwan Health Promotion Administration: 1) underweight (BMI < 18.5), 2) normal weight ($18.5 \leq \text{BMI} < 24$), and 3) overweight or obesity (BMI ≥ 24) [16].

Blood samples were obtained from the antecubital vein after a 12-h overnight fast. All blood analyses were carried out at the clinical laboratory department of the Linkuo Chang Gung Memorial Hospital, which is certified by the College of American Pathologists. Biochemical markers were analyzed on a Hitachi 7600-210 autoanalyzer (Hitachi, Tokyo, Japan); the biochemical markers included serum total cholesterol (TC), HDL-C, triglycerides (TGs), fasting plasma glucose (FPG), ALT, high-sensitivity C-reactive protein (HS-CRP), glycated hemoglobin (HbA1c), and uric acid.

Statistical analysis

Data are presented as the mean and standard deviation for continuous variables or numbers and percentages for categorical variables. In univariate analysis, independent sample t-tests and chi-square tests were used to compare MetS

and non-MetS subjects. The Chi-square test was also performed to determine the differences in two categorical variables and the prevalence of MetS in different serum ALT level groups. Correlations between different cardio-metabolic risk factors and serum ALT levels were assessed with Pearson's correlation coefficient. The odds ratios (ORs) and their 95% confidence intervals (CIs) were determined for the association between cardiometabolic risk factors and MetS with adjustment for potential confounders, such as age, sex, DM, HTN, and hyperlipidemia. The receiver operating characteristic (ROC) curve was produced to acquire the values of the area under the curve (AUC) with 95% CIs and sensitivity and specificity values for the serum ALT level as a predictor of MetS. The analyses mentioned above were performed with SPSS Statistics version 22 (IBM, SPSS Armonk, NY, IBM Corp). A p value of < 5% was considered to indicate a statistically significant result.

Results

The baseline characteristics of the study population according to MetS diagnosis are presented in Table 1. A total of 454 participants were enrolled in the analysis, including 215 (47.36%) men and 239 (52.64%) women. There were 277 people with MetS and 177 people without. The prevalence of MetS was 61.01%. The average age was 49.50 years old. People with MetS had a significantly higher ALT level (average 31.21 ± 25.00 U/L vs. 23.29 ± 15.98 U/L, $p < 0.001$) than those without MetS (Table 1).

Table 1
Study population characteristics according to the presence of MetS.

Variables	Total		Metabolic syndrome				p value
	(n = 454)		No (n = 177)		Yes (n = 277)		
Age (year)	49.50	± 16.01	43.83	± 16.97	53.12	± 14.26	< 0.001
SBP (mmHg)	133.03	± 21.26	123.45	± 18.21	139.15	± 20.84	< 0.001
DBP (mmHg)	83.80	± 13.85	78.82	± 12.53	86.97	± 13.74	< 0.001
WC (cm)	88.62	± 11.00	81.23	± 9.08	93.37	± 9.40	< 0.001
ALT (U/L)	28.13	± 22.25	23.29	± 15.98	31.21	± 25.00	< 0.001
FPG (mg/dL)	103.95	± 38.49	89.02	± 16.71	113.49	± 44.94	< 0.001
Hb-A1c (%)	6.19	± 1.22	5.74	± 0.63	6.48	± 1.41	< 0.001
HDL-C (mg/dL)	50.47	± 13.05	56.40	± 11.79	46.68	± 12.41	< 0.001
HS-CRP (mg/L)	2.84	± 4.86	2.41	± 5.90	3.12	± 4.05	0.13
TC (mg/dL)	194.28	± 39.79	184.14	± 33.21	200.75	± 42.27	< 0.001
Total Bilirubin (mg/dL)	0.56	± 0.24	0.58	± 0.25	0.55	± 0.24	0.26
TG (mg/dL)	153.97	± 134.08	105.76	± 97.14	184.78	± 145.07	< 0.001
Uric Acid (mg/dL)	6.36	± 1.88	5.91	± 1.78	6.65	± 1.88	< 0.001
Men, n(%)	215	47.36%	94	53.11%	121	43.68%	0.0498
ALT							0.001
Nnormal (≤ 36 U/L)	368	81.06%	157	88.70%	211	76.17%	
Abnormal (> 36 U/L)	86	18.94%	20	11.30%	66	23.83%	

Notes: Clinical characteristics are presented as mean ± SD for continuous variables and n (%) for categorical variables. P-value were derived from independent t-test for continuous variables and chi-square test for categorical variables.

Abbreviations: SBP, systolic blood pressure; DBP, diastolic blood pressure; WC, waist circumference; ALT, alanine aminotransferase; FPG, fasting plasma glucose; HbA1c, glycated hemoglobin; HDL-C, high-density lipoprotein cholesterol; HS-CRP, high-sensitivity C-reactive protein; TC, total cholesterol; TG, triglyceride; BMI, body mass index; HTN, hypertension; DM, diabetes mellitus.

	Total		Metabolic syndrome				
BMI							< 0.001
< 18.5	10	2.21%	8	4.55%	2	0.72%	
18.5–24	152	33.55%	103	58.52%	49	17.69%	
≥ 24	291	64.24%	65	36.93%	226	81.59%	
HTN, n(%)	172	38.05%	35	19.89%	137	49.64%	< 0.001
DM, n(%)	62	13.66%	1	0.56%	61	22.02%	< 0.001
Hyperlipidemia, n(%)	362	79.74%	96	54.24%	266	96.03%	< 0.001
Notes: Clinical characteristics are presented as mean ± SD for continuous variables and n (%) for categorical variables. P-value were derived from independent t-test for continuous variables and chi-square test for categorical variables.							
Abbreviations: SBP, systolic blood pressure; DBP, diastolic blood pressure; WC, waist circumference; ALT, alanine aminotransferase; FPG, fasting plasma glucose; HbA1c, glycated hemoglobin; HDL-C, high-density lipoprotein cholesterol; HS-CRP, high-sensitivity C-reactive protein; TC, total cholesterol; TG, triglyceride; BMI, body mass index; HTN, hypertension; DM, diabetes mellitus.							

Furthermore, people with MetS had significantly higher levels of SBP, DBP, WC, BMI, FPG, serum Hb-1Ac, TGs, and uric acid than those without MetS (Table 1). People with MetS were also older, more likely to be male and had a higher prevalence of hypertension, diabetes, and hyperlipidemia but lower serum HDL-C levels. However, there were no statistically significant differences in serum HS-CRP levels between the two groups.

The comparisons of the prevalence of MetS in groups with different ALT levels (> 36 U/L and ≤ 36 U/L) and the total study group are shown in Fig. 1. The chi-square comparison showed that participants with abnormal ALT levels (> 36 U/L) had a tendency towards a higher prevalence of MetS (76.7% vs. 57.3%, p = 0.001) compared with the prevalence of those with normal ALT levels (≤ 36 U/L) (Fig. 1). The bar chart illustrates that the abnormal ALT level (> 36 U/L) group had the highest MetS prevalence among the groups.

The correlations between serum ALT level and cardiometabolic risk factors are displayed in Table 2. The age-adjusted Pearson's coefficients of BMI, SBP, DBP, WC, FPG and HS-CRP were 0.21 (p < 0.001), 0.14 (p = 0.01), 0.18 (p < 0.001), 0.26 (p < 0.001), 0.11 (p = 0.03), and 0.14 (p = 0.01), respectively, which indicated positive linear relationships with serum ALT levels (Table 2). The age-adjusted Pearson's coefficient of HDL-C was - 0.12 (p = 0.02), which indicated a weak negative linear relationship with serum ALT levels. The serum Hb-1Ac, TC, TG and uric acid levels had no statistically significant correlations with the serum ALT level.

Table 2
The correlations between ALT and cardiometabolic risk factors.

ALT U/L (n = 454)				
Variables	Unadjusted		Adjusted for age	
	Pearson's coefficient	p value	Pearson's coefficient	p value
Age (year)	-0.07	0.147	NA	NA
BMI (kg/m ²)	0.24	< 0.001	0.21	< 0.001
SBP (mmHg)	0.11	0.02	0.14	0.01
DBP (mmHg)	0.16	< 0.001	0.18	< 0.001
WC (cm)	0.26	< 0.001	0.26	< 0.001
FPG (mg/dL)	0.09	0.04	0.11	0.03
Hb-A1c (%)	0.08	0.08	0.09	0.10
HDL-C (mg/dL)	-0.12	0.01	-0.12	0.02
HS-CRP (mg/L)	0.15	0.001	0.14	0.01
TC (mg/dL)	0.02	0.60	0.01	0.82
Total Bilirubin (mg/dL)	0.19	< 0.001	0.23	< 0.001
TG (mg/dL)	0.11	0.02	0.09	0.09
Uric Acid (mg/dL)	0.10	0.03	0.10	0.05

Abbreviations: ALT, alanine aminotransferase; BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; WC, waist circumference; FPG, fasting plasma glucose; HbA1c, glycated hemoglobin; HDL-C, high-density lipoprotein cholesterol; HS-CRP, high-sensitivity C-reactive protein; TC, total cholesterol; TG, triglyceride.

The ORs of cardiometabolic risk factors for MetS are shown in Table 3. In the univariate logistic regression model, the crude ORs of abnormal ALT levels, each additional year of age, sex (men versus women), hypertension, diabetes, hyperlipidemia, and BMI \geq 24 kg/m² for MetS were 2.46 (95% CI = 1.43–4.22, p = 0.001), 1.04 (95% CI = 1.03–1.05, p < 0.001), 1.46 (95% CI = 1.00–2.13, p = 0.05), 3.97 (95% CI = 2.56–6.16, p < 0.001), 49.70 (95% CI = 6.82–362, p < 0.001), 20.40 (95% CI = 10.42–39.94, p < 0.001), and 7.31 (95% CI = 4.72–11.32, p < 0.001), respectively. In the univariate logistic regression model, the adjusted ORs of abnormal ALT levels, each additional year of age, sex (men versus women), hypertension, diabetes, hyperlipidemia, and BMI \geq 24 kg/m² for MetS were 2.58 (95% CI = 1.23–5.44, p = 0.01), 1.03 (95% CI = 1.01–1.05, p = 0.002), 3.39 (95% CI = 1.89–6.08, p < 0.001), 3.11 (95% CI = 1.62–5.98, p = 0.001), 40.91 (95% CI = 2.96–566, p = 0.01), 21.79 (95% CI = 9.41–50.45, p < 0.001), and 9.57 (95% CI = 5.14–17.81, p < 0.001), respectively (Table 3). The adjusted ORs of BMI < 18.5 kg/m² for MetS were not statistically significant.

Variables	Crude Odds Ratio	(95% CI)	p value	Adjusted Odds Ratio	(95% CI)	p value
ALT (abnormal versus normal)	2.46	(1.43-4.22)	0.001	2.58	(1.23-5.44)	0.01
Age (year)	1.04	(1.03-1.05)	<0.001	1.03	(1.01-1.05)	0.002
Sex (men versus women)	1.46	(1.00-2.13)	0.05	3.39	(1.89-6.08)	<0.001
HTN (yes versus no)	3.97	(2.56-6.16)	<0.001	3.11	(1.62-5.98)	0.001
DM (yes versus no)	49.70	(6.82-362)	<0.001	40.91	(2.96-566)	0.01
Hyperlipidemia (yes versus no)	20.40	(10.42-39.94)	<0.001	21.79	(9.41-50.45)	<0.001
BMI (kg/m ²)						
<18.5	0.53	(0.11-2.57)	0.43	0.66	(0.09-4.82)	0.69
18.5-24	1.00	-	-	1.00	-	-
≥ 24	7.31	(4.72-11.32)	<0.001	9.57	(5.14-17.81)	<0.001

Abbreviations: ALT, alanine aminotransferase; HTN, hypertension; DM, diabetes mellitus; BMI, body mass index.

Table 3 Univariate and multivariate logistic regression on the cardiometabolic risk factors related to MetS among study population.

Finally, the AUC of the serum ALT level was 0.63 (95% CI = 0.58–0.68, $p < 0.001$), which showed that the serum ALT level was positively associated with MetS, and the cut-off point was 20.50 U/L (Table 4, Fig. 2).

Variables	AUC(95% CI)	p value	Cut-off point	Sensitivity	Specificity
ALT (U/L)	0.63 (0.58-0.68)	<0.001	20.500	0.643	0.559

Abbreviations: ALT, alanine aminotransferase; ROC curve, receiver operating characteristic curve; CI, confidence interval.

Table 4 The areas under ROC curve (AUC), sensitivity, specificity by the optimized cut-off points for ALT in predicting metabolic syndrome.

Discussion

The main finding of the present study is the high prevalence of MetS in a Taiwan indigenous population, and there was an association between serum ALT levels and MetS. Higher serum ALT levels, especially over 36 U/L, were associated with an increased risk of MetS.

The results were consistent with the findings of several previous studies. A hospital-based study showed that more than half of the indigenous adults in southeastern Taiwan had MetS [6], and two community-based studies revealed that the prevalence of MetS in indigenous populations in northern Taiwan was over 48% [7, 17]. In contrast, without regard to regional difference, the data from the Taiwan Health Promotion Administration revealed that the overall prevalence of MetS in Taiwanese adults above the age of 20 was 19.7% in 2007 [15]. According to a cross-sectional survey, the MetS prevalence in a Taiwan metropolitan area was 33.32% among adults aged over 40 years in 2007 [18]. Therefore, it seems that the prevalence of MetS is higher in the Atayal tribe than in the metropolitan or overall population in Taiwan. This

inference was in line with the results of the 2005–2008 NAHSIT, which revealed that the highest prevalence of MetS was found in the indigenous area (mountains) compared to the prevalence in other places in Taiwan [4]. Additionally, this idea was supported by a cross-sectional study illustrating that indigenous groups in Taiwan had a markedly higher prevalence of MetS than the Taiwanese and Hakka groups [19].

The reasons for the above phenomenon could be multifactorial. First, there were some health disparities between indigenous individuals and the general population in Taiwan [20]. For example, the lifetime prevalence of alcoholism according to ICD or DSM in four Taiwanese indigenous groups was 40–60% [21], and a large prospective cohort study revealed that heavy alcohol consumption is associated with an increased risk of the MetS [22]. In addition, a study suggested that 6% of inhabitants in Kaohsiung, the second-largest city of Taiwan, were current betel chewers, whereas 42% of the indigenous individuals aged over 15 years in southern Taiwan were current chewers [23]. Although areca nut chewing is deeply rooted in indigenous culture and symbolizes social belonging in Taiwan [24], chronic areca nut chewing is one of the independent risk factors for MetS and contributes to metabolic derangements via the involvement of tumor necrosis factor- α , leptin, and leukocyte count [25].

Second, there is a socioeconomic gap between the indigenous people and the general public in Taiwan. According to the economic status survey from the Council of Indigenous Peoples in Taiwan, the indigenous household income was approximately 61% of the average household income of Taiwan in 2014, and only 6.58% of primary income earners had a university education or above [26]. However, a study suggested that good socioeconomic status could protect against MetS [27], and a study with a large sample size also implied that a higher education level was related to a lower risk of MetS [28]. In other words, low socioeconomic status could negatively impact the health of indigenous people. Third, the indigenous population in our study was located in the mountains without adequate healthcare resources, and the lack of medical accessibility caused them to delay seeking care to improve their health outcomes. In summary, differences in health behaviors, low socioeconomic status and limited access to healthcare in remote areas all impacted the health inequality between the Atayal tribe and individuals from metropolitan areas.

In the present study, the second major finding was that baseline serum ALT level and MetS were positively associated with the cut-off point of 20.50 U/L based on the AUC, and the adjusted OR of abnormal ALT levels (> 36 U/L) for MetS was 2.58 after correction for age, sex, hypertension, diabetes, hyperlipidemia, and BMI. These results corroborate the findings from a large-population, community-based study conducted in China, which verified a positive correlation between normal serum ALT levels and the morbidity rate of MetS after age and BMI correction. The optimal ALT boundary value based on the ROC curve was 24.5 for men and 14.5 U/L for women [29]. In short, an elevated ALT level, even at a level still within the reference interval, may reflect early metabolic changes.

On the other hand, our study also implied that an abnormal ALT level (> 36 U/L) was associated with a tendency towards a higher prevalence of MetS compared to the prevalence associated with normal ALT levels (≤ 36 U/L). The finding was similar to the results of prior studies. A systematic review and meta-analysis revealed that the baseline circulating ALT level is associated with the risk of MetS and exhibits a linear dose-response relationship [14], which was identical to the results of a cross-sectional study including over 15000 adults and a longitudinal study with 7 years of follow-up from China [12] [13]. Taken together, these research studies have indicated that people with higher ALT levels have a higher risk of MetS.

In addition, a Korean study also confirmed that serum ALT levels were positively associated with MetS and its components (FPG, TGs, BP, and WC) [11], and we also found weak positive linear relationships between serum ALT levels and cardiometabolic risk factors (BMI, SBP, DBP, WC, FPG, HS-CRP) in our study. Although the present study only included adults aged over 18, a nationwide study conducted in Iran indicated that MetS and some cardiometabolic risk factors were significantly associated with ALT levels in children and adolescents aged 7–18 years [30].

Although the mechanisms underlying the association between serum ALT levels and MetS are not entirely understood, a study from the Netherlands shed light on a possible mechanism. Insulin resistance acts as a major mediator of the

association between the MetS and ALT level, while inflammatory adipokines, endothelial dysfunction, and nonesterified fatty acids also play minor roles but to a lesser extent [31]. ALT is a catalyzer that is involved in the transfer of the amino group of alanine to α -ketoglutarate [32], and a study from Argentina proposed that abnormal ALT levels are related to a dysregulation of normal amino acid metabolism in the liver, and aberrant liver metabolism could lead to MetS and insulin resistance [33]. Further studies are required to better clarify the pathophysiology.

Strengths and limitations

A key strength of this study is that it was a community-based study targeting the Taiwan indigenous population and demonstrating the positive association between baseline serum ALT levels and MetS in the Taiwan Atayal tribe. There were also three limitations in this study. First, the cross-sectional design resulted in the inability to effectively determine the causal relationship between MetS and serum ALT levels. Second, serum ALT is a sensitive marker for liver dysfunction and is affected by heavy alcohol consumption [34] and some medications [35]. However, there was a lack of information on drug history, such as nonsteroidal anti-inflammatory drugs (NSAIDs), antibiotics, and lipid-lowering drugs in this study. There was also no clear personal history for viral hepatitis, NAFLD, or alcohol consumption. Third, there were more female subjects than male subjects. The participants in the study were from three remote villages of Taoyuan County and had lived in these villages for over 6 months. The shift from rural low-wage labor to metropolitan higher-paying jobs reduced the available number of indigenous men in the mountain region. Therefore, more comprehensive and meticulous consideration should be used in future studies.

Conclusions

In the present study, the overall prevalence of MetS was high in an indigenous population in Taiwan, and higher serum ALT levels, especially those over 36 U/L, were associated with an increased risk of MetS. Further studies need to be performed in regard to this serious health problem in indigenous communities of Taiwan.

Abbreviations

MetS: metabolic syndrome; NCEP: National Cholesterol Education Program Expert Panel; ATP III: Adult Treatment Panel III; NAFLD: non-alcoholic fatty liver disease; SBP: systolic blood pressure; DBP: diastolic blood pressure; WC: waist circumference; ALT: alanine aminotransferase; FPG: fasting plasma glucose; HbA1c: glycated hemoglobin; HDL-C: high-density lipoprotein cholesterol; HS-CRP: high-sensitivity C-reactive protein; TC: total cholesterol; TG: triglyceride; BMI: body mass index; HTN: hypertension; DM: diabetes mellitus.

Declarations

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding authors upon reasonable request.

Authors' contributions

Yi-Fang Chen was involved in writing of the manuscript. Yen-An Lin, Wei-Chung Yeh, Yu-Chung Tsao, Wen-Cheng Li and I-Ju Chen provided opinions about the study designs and help collect data. Jau-Yuan Chen contributed conceived, designed and performed the experiments, collected and analyzed the data, revising it critically for important intellectual content and final approval of the version to be submitted.

Ethics approval and consent to participate

The study was approved by Chang-Gung Medical Foundation Institutional Review Board (99-0231B, 101-4156A3), and written informed consent was provided by all the participants before enrollment.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Figures

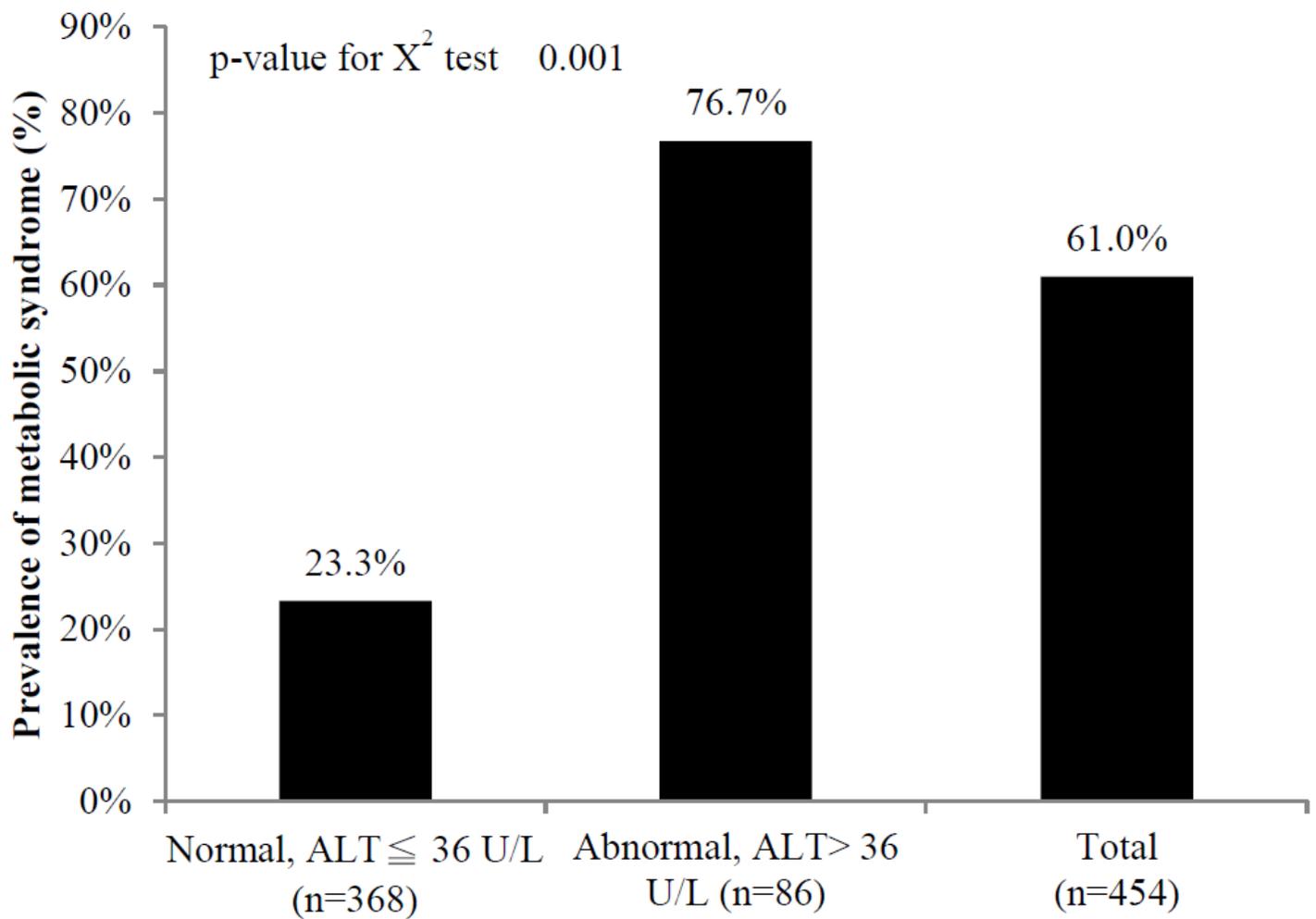


Figure 1

Prevalence of MetS in different serum ALT level groups. ROC curve and AUC for ALT as a predictor of MetS.

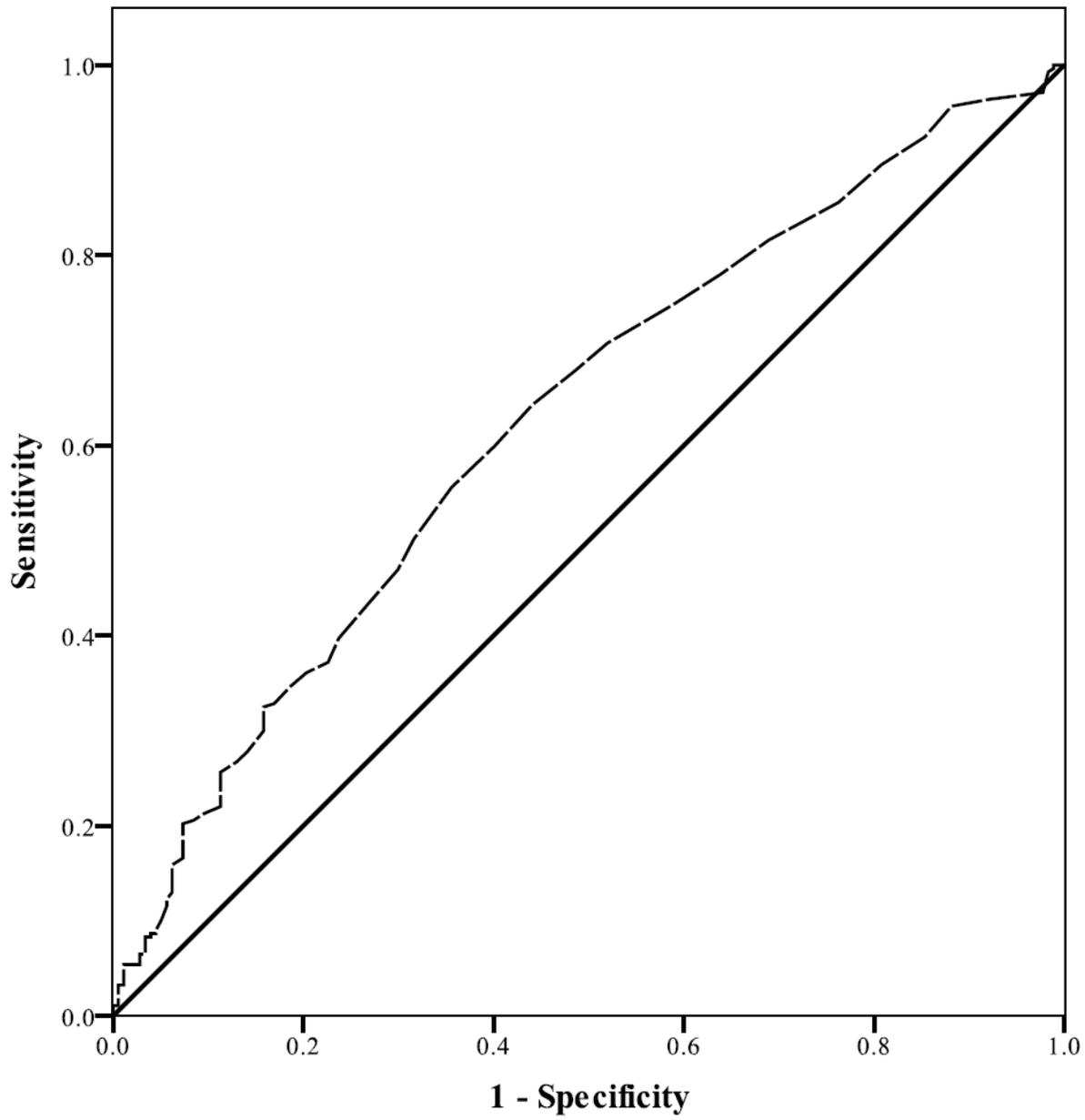


Figure 2

ROC curve and AUC for ALT as a predictor of MetS. Abbreviations: ALT, alanine aminotransferase.