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Full Length Research Paper

Incidence of pre-pregnancy and pregnancy-related illnesses in rural women accessing antenatal care services in Awka, south-east, Nigeria

**Ugoma Deborah Ezeani, Olaoluwa Samson Agbaje*, Chucks E. Ezedum, Prince Iheanachor
Christian Umoke, Cylia N. Iweama and Kiloh A. Nfor**

Department of Health and Physical Education, University of Nigeria, Nsukka, Enugu State, Nigeria.

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Nigeria accounts for a considerable proportion of maternal deaths that occur annually worldwide. The study investigated the incidence of pre-pregnancy and pregnancy-related illnesses in women accessing antenatal care services at health facilities in Awka South Local Government Area, Anambra State. The study adopted cross-sectional research design. The population comprised 3,207 registered pregnant women from January to September 2012. The sample for the study consisted of 650 pregnant women. A pre-tested questionnaire was administered by the interviewers to women who had attended antenatal care services within six months prior to the date of data collection. Malaria (66.6%), morning sickness (58.0%), hyperemesis gravidarum (39.7%), sexually transmitted infections (28.6%), gestational diabetes (23.8%), pre-eclampsia and eclampsia (23.0%) and anaemia (15.8%) were the common illnesses in women. There were statistically significant differences in the women's pre-pregnancy illnesses according to the level of education ($p = 0.032$) and pregnancy-related illnesses according to age ($p = 0.023$) and level of education ($p = 0.045$). It was concluded that the interplay of several factors is responsible for the incidence of pre-pregnancy and pregnancy-related illnesses in women. Identification of these factors is expedient while scaling up of maternal health interventions; improved access and uptake of facility-based care hopefully, will drastically reduce morbid conditions in women and improve maternal and newborn outcomes.

Key words: Prevalence, Pregnancy-related illnesses, antenatal care, maternal health.

INTRODUCTION

Illnesses during pregnancy portend severe threats to maternal and fetal health with adverse maternal, fetal and

newborn health outcomes. The status of maternal health in poor countries is often described in terms of maternal

*Corresponding author. E-mail: agbajesam@yahoo.com.

mortality alone, despite the evidence that far more women suffer from morbidities/disabilities relating to pregnancy and childbirth (Filippi et al., 2007). About 289,000 maternal deaths occur annually worldwide, and Nigeria accounts for about 14% of these preventable deaths (United Nations, 2010). About 20 million women suffer from acute severe obstetric complications, including haemorrhage, obstructed/prolonged labour, preeclampsia/ eclampsia, puerperal sepsis, and septic abortion (Glasier et al., 2006; Hogan et al., 2010). The burden of maternal ill-health extends beyond these complications and includes different short- and long-term morbid conditions that can result from acute obstetric complications or poor management at delivery (Gulmezoglu et al., 2004; Zwart et al., 2008; Lindquist et al., 2013). In Nigeria, the estimated maternal mortality ratio (MMR) of 576 deaths per 100 000 live births reported in 2013 was higher than the 545 deaths per 100,000 live births recorded in 2008 (National Population Commission-NPC and ICF International 2013) and fell far short of the Millennium Development Goal of 250 deaths per 100,000.

Hospital records according to Federal Ministry of Health (FMOH, 2013) and National AIDS and Reproductive Household Survey (NARHS) in 2012 have shown that for many years, illnesses are the major causes of maternal mortality with variations between women in urban and rural communities (Doctor et al., 2011; Ajayi and Osakinle, 2013). Vanderkruik et al. (2013) asserted that complications of pregnancy, childbirth, and the postpartum period may lead to death or cause a continuum of morbidities that affect a woman's health for short or long-term periods during and after pregnancy, and even throughout her life. Community-based studies conducted in various countries have reported that women suffer significant morbidity both during pregnancy and postnatal period (Wall, 1998; Zishiri et al., 1999; Walraven et al., 2001; Bang et al., Filippi, 2004).

Such morbidities are also associated with poor fetal and newborn outcomes. Defining maternal morbidity poses serious challenges because there are diverse definitions, identification and classifications of maternal morbidity in literature. Currently, there is a lack of an agreed-upon definition for maternal morbidity (Vanderkruik et al., 2013). Existing work on maternal morbidity includes an array of conditions, both short- and long-term in varying combinations (Waterstone et al., 2003; Chersich et al., 2009; Ukachukwu et al., 2009). Three major issues have limited valid, routine, and comparable measurements of maternal morbidity to date. These include lack of a common definition and identification criteria for maternal morbidity, lack of standardized assessment tools especially at community or primary health care level, and lack of common indicators to measure morbidity (Vanderkruik et al., 2013).

To guide this study, the authors used a well-defined term-illness.

Parsons (1951) viewed illness as a human response to the disease process or to the perception by an individual that he has some form of impairment. It is an abnormal process in which the person's level of functioning is changed. Illness is described as feelings experienced by an unwell person. A person may feel 'ill' without a disease being evident or diagnosed (Alpert et al., 1967). Illness has been conceptualized as the patient's experience of ill-health and comprises his/her impaired sense of well-being, the perception that something is wrong with the body and various symptoms of pain, distress, and disablement (Abanobi, 2003). Existing literature includes an array of methods for identifying and classifying maternal illness. Maternal morbidities or illnesses have been grouped under various categories such as direct obstetric morbidity, indirect obstetric morbidity and psychological obstetric morbidity (Reed et al., 2000) or obstetric complications, pre-existing medical conditions (Danel et al., 2003; Berg et al., 2009) or categories of obstetric morbidity that occur during pregnancy, during delivery, or after delivery (Zurayk et al., 1993). In addition to the wide range of how maternal morbidity conditions are categorized, the methodology for detecting a maternal morbidity varied across studies as well, including interview-based diagnosis and hospital records (for example birth/hospital discharge data) (Stewart et al., 1996; Roberts et al., 2009). This study explored a few typologies of maternal morbidity/illness. Two typologies of illnesses associated with pregnancy have been identified in the literature (Arkutu, 1995). These are illnesses caused by pregnancy such as ectopic pregnancy, hyperemesis gravidarum, miscarriage, pre-eclampsia, eclampsia, sepsis and haemorrhage and pre-existing illnesses or medical conditions which anybody can suffer but which are made worse in pregnancy. These include malaria, anaemia, diabetes, essential hypertension, backache and sexually transmitted infections (STIs). Another category of illnesses in pregnancy as identified in literature (Elaine, 2000; Nursing and Midwifery Council of Nigeria, 2006) include: malaria, anaemia, diabetes, essential hypertension, pulmonary tuberculosis, sickle cell disease, urinary tract infection, cardiac disease, asthma, sexually transmitted infections (STIs), renal problems as well as backache and headache. This study investigated typologies of illnesses in pregnancy based on literature, which include: illnesses that are caused by pregnancy such as backache, pre-eclampsia, hyperemesis gravidarum, gestational diabetes (GDM); hypertensive disorders (pre-eclampsia and eclampsia) and pre-pregnancy illnesses which are made worse in pregnancy such as malaria, anemia, diabetes, hypertension, STIs, tuberculosis and depression.

Studies have indicated associations between severe maternal morbidity and factors such as advanced maternal age, pre-existing medical conditions and obesity (Bouvier-Colle et al., 1997; Zhang et al., 2005). However, these factors are unable to explain entirely the differences in maternal morbidity found between different populations of women both within and between countries (Lindquist, 2013). Nevertheless, this study explored differences in pre-pregnancy and pregnancy-induced illnesses in women according to maternal factors (maternal age and education). Primary health centres (PHCs) in the study area offer ANC services amidst challenges such as shortage of vaccines and essential drugs, logistic problems, skilled health personnel, and unstable power supply, which hinder effective service delivery. The interplay of all or some of these variables may influence pregnant women's access to ANC services with attendant consequences for maternal and neonatal outcomes. This situation accentuates the need for the choice of the study area. In addition, studies have indicated that severe maternal morbidity may be a valid indicator of the quality and effectiveness of obstetric care than mortality alone (Mantel et al., 1998; Koeberle et al., 2000). There is paucity of data on incidence of pre-pregnancy and pregnancy-related illnesses among pregnant women accessing ANC at PHCs in Awka South LGA, Anambra State, Nigeria. In view of high maternal mortality rates in Nigeria, and potential complications inherent sub-standard care for pre- and pregnancy-related illnesses among women in Nigeria, this study was carried out.

MATERIALS AND METHODS

Study design, location and period

This cross-sectional study was undertaken from January to September, 2012 at the selected health facilities in Awka South LGA, Anambra State. Awka South, the area of the study is one of the 21 LGAs in Anambra State. It is located in the rainforest belt southeast, Nigeria. It shares boundaries with Awka North LGA to the North, Oji-River LGA, Enugu State to the East, Aniocha LGA to the south and Njikoka LGA to the west. Awka South comprises nine communities. The population for the study consisted of all pregnant women that registered and accessed antenatal care services in public, private and mission health facilities in Awka South LGA, Anambra State. Women in the area have limited access to quality maternal health services. Awka South LGA also has many rural communities. Thus, the study population consisted of rural pregnant women.

Study population and sample estimation

There were 3,207 registered pregnant women in Awka South LGA at the time of the study (Record and Statistics, General Hospital, Awka and Health Department, Awka South LGA, 2012). We used the following formula for sample size calculation:

$$n = \frac{Z^2 \cdot p(1-p)}{d^2},$$

Where, Z is a standard normal variant ($Z = 1.96$ when the confidence interval is 95%), p is the expected proportion of the outcome in population based or other studies, and d is the absolute accuracy or precision (Charan and Biswas, 2013). Since there was no previous study in the study area, we assumed that 50% of the population had suffered from at least one pre-pregnancy or pregnancy-related illness in the last 12 months. We calculated a minimal sample size of 384 that would be required to give a 95% probability of measuring the prevalence of pre-pregnancy and pregnancy-related illnesses with 5% accuracy. To minimize the effect of non-response rate and errors that may ensue due to small sample size, we increased the study sample to 650. Multi-stage sampling procedure was employed to select the pregnant women who attended health facility ANC services in the six months preceding the study. All the PHCs located in the study area were involved in the study. In each community, a health facility was randomly selected. In each of the selected health facilities, women were conveniently selected to make the sample for the study. The inclusion criteria were women aged 15-49 years and women who had attended antenatal clinics at least twice in the six months prior to the study.

Instruments for data collection

Two instruments were used for data collection—a checklist and structured questionnaire. The checklist was designed to collect data on reported pregnancy-related illnesses among pregnant women from hospital/health facility records three months (May, 2012) prior to the data collection period (data collection period began in August and ended in September, 2012). The most common pregnancy-induced illnesses were identified and integrated in the 19-item structured paper-based questionnaire titled Pre-Pregnancy and Pregnancy-Related Illnesses Questionnaire (PPRIQ), which was used for data collection. The PPRIQ was subdivided into five sections to elicit the following information:

- 1) Introduction: Contains information of what the study was all about;
- 2) Informed consent;
- 3) Respondent's sociodemographic data, which were made up of two items;
- 4) Pre-pregnancy illnesses in Pregnant women: this consists of nine items to obtain information on illnesses prior to pregnancy;
- 5) Pregnancy-related illnesses: This is a 10-item section to elicit information on illness induced by pregnancy.

The authors used a self-reported instrument to collect data from the participants. The PPRIQ was administered by trained interviewers (research assistants). After the women have responded to questionnaire items, researchers and research assistants retrieved copies of the questionnaire from the women. Nine pre-existing illnesses identified via literature (Zurayk et al., 1993; Danel et al., 2003; Zhang et al., 2005) were included in the questionnaire. The women were asked to indicate if they had suffered from any of the outlined illnesses six months prior to pregnancy. These included: malaria, anaemia, diabetes, hypertension, STIs, TB, sickle cell anaemia, urinary tract infections (UTIs) and asthma. The items were assigned dichotomous response of 'Yes' or 'No'. The participants were asked to tick (√) as many as applied to them. A "Yes" response implied "experience of illness" while a "No"

Table 1. Sociodemographic Characteristics of Pregnant Women ($n = 647$).

S/N	Variables	f	%
Age of pregnant women			
1	< 20 years	40	6.18
2	21-29 years	307	47.5
3	30-39 years	240	36.4
4	40 years ⁺	60	9.09
Level of education			
1	No Formal Education	66	10.2
2	Primary Education	83	12.8
3	Secondary Education	271	41.9
4	Tertiary Education	227	31.5

response implied “absence of illness”. Ten pregnancy-related illnesses of pregnant women were identified and included in the structured questionnaire based on the checklist. These included high blood pressure (pre-eclampsia and eclampsia), sexually transmitted infection (STIs), HIV/AIDS, severe vomiting (Hyperemesis gravidarum), diabetes due to pregnancy (gestational diabetes), anaemia, malaria, ectopic pregnancy, threatened abortion and morning sickness. The items were also assigned dichotomous response of ‘Yes’ or ‘No’. The participants were asked to tick (✓) as many as applied to them. A “Yes” response implied “experience of illness” while a “No” response implied “absence of illness”.

Ethical consideration

Permission to conduct the study was obtained from Primary Health Care coordinator of Awka South LGA, and Heads of health facilities. Informed consent was obtained from pregnant women who participated in the study after a detailed explanation of the purpose of the study and the required assistance. The pregnant women were free to withdraw at any time or to refuse to answer any question. Confidentiality was maintained during the course of the study by ensuring face to face interviews by each interviewer without a third party and information obtained during the study was kept confidential.

Data analysis

The SPSS version 18 (SPSS, Inc., Chicago) was used for data entry, cleaning, and analysis. We used descriptive statistics to describe the distribution of socio-demographic characteristics of participants accessing ANC at health facilities in Awka South LGA. The Kuder-Richardson-20 reliability test was used to determine the correlation coefficient index of sections B and C. This procedure yielded coefficient values of 0.88 and 0.75 respectively. The Chi-square test was used to examine differences in the pregnancy-related illnesses suffered by women. Educational level of women was treated as a categorical variable (no formal education, primary education, secondary education and tertiary education). The ages of the respondents were coded into four categories viz < 20, 20-29 years, 30-39 years, and > 40 years. Due to incomplete responses in

few copies of questionnaire administered, data from 647 properly completed questionnaire copies were used for analysis. All statistical tests were performed at $p < 0.05$.

RESULTS

Demographic variables

Among the participants, age ranged from 15 to 49 years, with a mean of 24.7 ($SD = 2.7$). About 6.18% were less than 20 years, 47.5% were within 21 to 29 years, 36.4% were within 30 to 39 years and 9.09% of women were above 40 years. In addition, about 10.2% of pregnant women had no formal education, 12.8% had primary education, 41.9% had secondary education and 35.1% had tertiary education (Table 1).

Reported pre-pregnancy illnesses by pregnant women

The findings are presented in three sections, which include: pre-pregnancy illnesses/medical conditions of pregnant women, reported pregnancy-related illnesses of pregnant women, and comparison of pregnancy-related illnesses based on maternal characteristics. Table 2 shows that the most common pre-pregnancy morbidity was malaria (66.6%). This was followed by STIs in 185 (28.6%) of the women. Anaemia occurred in 102 (15.8%) of pregnant women.

Reported pregnancy-related illnesses by pregnant women

Table 3 describes the occurrence of maternal illnesses

Table 2. Percentage of Reported Pre-pregnancy Illnesses in Pregnant women ($n = 647$).

S/N	Parameter	Yes		No	
		f	%	f	%
1	Malaria	431	66.6	216	33.4
2	Anaemia	102	15.8	545	84.2
3	Diabetes	62	9.6	585	90.4
4	Hypertension	89	13.8	558	86.2
5	Sexuality transmitted infections	185	28.6	462	71.4
6	Tuberculosis	54	8.3	593	91.7
7	Sickle cell anaemia	75	11.6	572	88.4
8	Urinary tract infection	76	11.7	571	88.3
9	Asthma	73	11.3	574	88.7

Table 3. Percentage of reported pregnancy-related illnesses by pregnant women ($n = 647$).

S/N	Items	Yes		No	
		f	%	f	%
1	High blood pressure (preeclampsia & eclampsia)	149	23.0	498	77.0
2	Sexuality transmitted infection (STIs)	100	15.5	547	84.5
3	HIV/AIDS	83	12.8	564	87.2
4	Severe vomiting/nausea	245	39.7	402	62.1
5	Anemia	224	34.6	423	65.4
6	Malaria	393	60.7	254	39.3
7	Ectopic pregnancy	47	7.3	600	92.7
8	Threatened abortion	143	22.1	504	77.9
9	Diabetes due to pregnancy	154	23.8	493	76.2
10	Morning sickness	375	58.0	272	42.0

diagnosed during pregnancy by health professionals among women. About 61.0% of pregnant women suffered from malaria. Other pregnancy-related illnesses suffered by women include morning sickness (58%), severe vomiting (39.7%), anaemia (34.6%), gestational diabetes (23.8%), preeclampsia and eclampsia (23%) and threatened abortion (22.1%).

Pre-pregnancy and pregnancy-related illnesses according to maternal characteristics

Data in Table 4 indicates that group-wise, about 22.5 and 34.79 % of women in age categories < 20 years and > 40 years respectively had suffered from at least one of the illnesses before pregnancy while 19.8 and 18.7% of women in age categories 30 to 39 years and 21-29 years respectively had suffered at least one illness before pregnancy. Table 5 indicates that group-wise, about 30.6 and 30% of women in age categories 31-39 years and >

40 years respectively had suffered from at least one of the pregnancy-related illnesses while 29.5% and 28.7% of women in age categories <20 years and 21-29 years respectively had suffered from at least one of the pregnancy-related morbidities/illnesses.

In reference to maternal level of education, Table 6 shows that 23.8 and 19.7% of women in categories NFE and PRE respectively had suffered from at least one of the illnesses before pregnancy while 19.8 and 18.5% of women in categories SEE and TEE respectively had suffered from at least one of the illnesses before pregnancy. Data in Table 7 show that about 36.1 and 32.8% of women in categories NFE and SEE respectively had suffered from at least one of the pregnancy-related morbidities as diagnosed by a physician while 31.5 and 22.9% of women in categories PRE and TEE respectively had suffered from at least one of the pregnancy-induced illnesses as diagnosed by a physician.

Data in Table 8 show that there was no significant difference in the reported pre-pregnancy illnesses in

Table 4. Reported pre-pregnancy illnesses in women according to age ($n = 647$).

S/N	Parameter	Age							
		< 20 years (n = 40)		20-29 years (n = 307)		30-39 years (n = 240)		40 years + (n = 60)	
		Yes %	No %	Yes %	No %	Yes %	No %	Yes %	No %
1	Malaria	80.0	20.0	69.1	30.9	60.4	39.6	70.0	30.0
2	Anemia	35.0	65.0	11.7	88.3	18.3	81.7	3.3	86.7
3	Diabetes	15.5	84.5	8.5	91.5	2.1	97.9	51.7	48.3
4	Hypertension	20.0	80.0	11.4	88.6	12.5	87.5	40.0	60.0
5	STIs	20.0	80.0	25.7	74.3	35.8	64.2	20.0	80.0
6	Tuberculosis	15.0	85.0	7.5	92.5	5.0	95.0	21.7	78.3
7	Sickle cell anaemia	0.0	100.0	15.6	84.4	11.2	88.8	0.0	100.0
8	UTIs	5.0	95.0	8.8	91.2	19.6	80.4	100.0	0.0
9	Asthma	12.5	87.5	10.1	89.9	13.8	86.3	6.7	93.3
	% Average	22.5	77.5	18.7	81.3	19.8	80.2	34.9	64.1

Table 5. Percentage of Reported Pregnancy-related Illnesses in women According to Age ($n = 647$).

S/N	Parameter	Age							
		< 20 years (n = 40)		20-29 years (n = 307)		30-39 years (n = 240)		40 years + (n = 60)	
		Yes (%)	No (%)	Yes (%)	No (%)	Yes (%)	No (%)	Yes (%)	No (%)
1	High blood pressure (preeclampsia and eclampsia)	32.5	67.5	15.0	85.0	23.3	76.7	56.7	43.3
2	STIs	30.0	70.0	14.7	85.3	12.5	87.5	21.7	78.3
3	HIV/AIDS	20.0	80.0	13.0	87.0	14.6	85.4	0.0	100.0
4	Severe vomiting (hyperemesis gravid rum)	15.0	85.0	40.7	59.3	44.2	55.8	13.3	86.7
5	Anaemia	60.0	40.0	32.2	67.8	29.2	70.8	51.1	48.9
6	Malaria	80.0	20.0	62.5	37.5	59.2	40.8	45.0	55.0
7	Development of foetus outside the womb	10.0	90.0	6.5	93.5	2.9	97.2	26.7	73.3
8	Threatened Abortion	15.0	85.0	20.5	79.5	20.8	79.2	40.0	60.0
9	Diabetes due to pregnancy	5.0	95.0	22.1	77.9	32.9	67.1	8.3	91.7
10	Morning sickness	27.5	72.5	59.3	40.7	66.7	33.3	36.7	63.3
	Average %	29.5	70.5	28.7	71.3	30.6	69.4	30.0	70.0

women according to age ($\chi^2 = 1.156 < 7.815$, $df = 3$, $p = 0.217$). This implies that women did not differ in their experience of pre-pregnancy illnesses according to age. However, there was a significant difference in the reported pre-pregnancy illnesses in women according to level of education ($\chi^2 = 44.99 > 7.815$, $df = 3$, $p = 0.032$). This implies that women did experience differences in illnesses according to level of education. Data in Table 9 show that there were significant differences in the reported pregnancy-related illnesses

based on maternal age ($\chi^2 = 35.36 > 7.815$, $df = 3$, $p = 0.045$) and level of education ($\chi^2 = 10.393 > 7.815$, $df = 3$, $p = 0.023$) respectively. This shows that incidence of pregnancy-related illnesses in women differed according to age and educational level.

DISCUSSION

Data on obstetric morbidity in developing countries are

Table 6. Reported Pre-Pregnancy Illnesses in Women according to Level of Education (*n* = 647).

S/N	Parameter Illnesses	Level of Education							
		*NFE (<i>n</i> = 66)		*PRE (<i>n</i> = 83)		*SEE (<i>n</i> = 271)		*TEE (<i>n</i> = 227)	
		Yes %	No %	Yes %	No %	Yes %	No %	Yes %	No %
1	Malaria	68.2	31.8	72.3	27.7	57.2	42.8	75.3	24.7
2	Anaemia	27.3	72.7	15.7	84.3	14.4	85.6	14.1	85.9
3	Diabetes	22.7	77.3	3.6	96.4	9.6	90.4	7.9	92.1
4	Hypertension	13.6	86.4	12.0	88.0	15.1	84.9	12.8	87.2
5	STIs	37.9	62.1	33.7	66.3	33.6	66.4	18.1	81.9
6	Tuberculosis	10.6	89.4	4.8	95.2	8.5	91.5	8.8	91.2
7	Sickle cell anaemia	10.6	89.4	12.0	88.0	16.2	83.8	6.2	93.8
8	UTIs	19.7	80.3	14.5	85.5	15.5	84.5	4.0	96.0
9	Asthma	4.0	96.0	8.4	91.6	8.5	91.5	18.1	81.9
	Cluster %	23.8	76.2	19.7	80.3	19.8	80.2	18.5	81.5

*NFE = No formal education; *PRE = Primary education.*SEE =Secondary education; TEE = Tertiary Education.

Table 7. Reported Pregnancy-related Illnesses by Women according to Level of Education (*n* = 647).

S/N	Parameter Illnesses	Level of Education							
		*NFE (<i>n</i> = 66)		*PRE (<i>n</i> = 83)		*SEE (<i>n</i> = 271)		*TEE (<i>n</i> = 227)	
		Yes (%)	No (%)	Yes (%)	No (%)	Yes (%)	No (%)	Yes (%)	No (%)
1	High blood pressure	27.3	72.7	31.3	68.7	16.2	83.8	26.9	73.1
2	STIs	33.3	66.7	14.5	85.5	20.3	79.7	4.8	95.2
3	HIV/AIDS	15.2	84.8	2.4	97.6	15.9	84.1	12.3	87.7
4	Severe vomiting	37.9	62.1	30.1	69.9	46.9	53.1	30.0	70.0
5	Anaemia	42.4	57.6	45.8	54.2	39.9	60.1	22.0	78.0
6	Malaria	60.6	39.4	66.3	33.7	68.3	31.7	49.8	50.2
7	Development of foetus outside the womb	12.1	87.9	18.1	81.9	6.3	93.7	3.1	96.9
8	Threatened abortion	36.4	63.6	27.7	72.3	22.9	77.1	15.0	85.0
9	Diabetes due to pregnancy	33.3	66.7	13.3	86.7	31.7	68.3	15.4	84.6
10	Morning sickness	62.1	37.9	65.1	34.9	61.6	38.4	49.8	50.2
	Cluster %	36.1	63.9	31.5	68.5	32.8	67.2	22.9	77.1

limited and, when available, they commonly define the type of medical conditions diagnosed at the hospital level (Assarag et al., 2013). However, many challenges plagued classification of maternal morbidities in developing nations including Nigeria where accurate diagnosis of maternal morbidities is indispensable to investigations (Graham and Campbell, 1992). These problems and weakness of conceptual framework underlying study of maternal health may explain why there is dearth of studies on maternal morbidities

(Graham and Campbell, 1992). This study is one of the few surveys conducted in south-east Nigeria studying incidence of pre-pregnancy illnesses and pregnancy-related morbidities in women within the population. Our results show that malaria (66.6%), STIs (28.6%), anaemia (15.8%) and pre-eclampsia (13.8%) were the most common pre-pregnancy illnesses in women as diagnosed by a physician while malaria (60.7%), morning sickness (58.0%), and nausea/severe vomiting (hyperemesis gravidarum) (39.7%) and anaemia (34.6%)

Table 8. Summary of Chi-square (χ^2) Analysis of Difference in Reported Pre-Pregnancy Illnesses in Women Based on Selected demographic Variables ($n = 647$).

Variables	Pre-Pregnancy Illnesses				Cal. χ^2	P-value
	Yes		No			
	<i>n</i>	%	<i>n</i>	%		
Age						
< 20 years ($n = 40$)	9	22.5	31	77.5	1.156	0.217*
21-29 years ($n = 307$)	57	18.7	250	81.3		
30-39 years ($n = 240$)	48	19.8	192	80.2		
> 40 years ($n = 60$)	21	35.0	39	65.0		
Level of Education						
No Formal Education ($n = 66$)	16	23.8	50	76.2	44.99	0.032*
Primary Education ($n = 83$)	16	19.3	67	80.7		
Secondary Education ($n = 271$)	54	19.7	217	80.3		
Tertiary Education ($n = 227$)	42	18.5	185	81.5		

Significant level: * = $P < 0.05$.

were the pregnancy-related illnesses mostly experienced by women. The incidence of these illnesses is higher than the reported incidence in a study in Niamey, Niger Republic (6.45%), and higher than that of Scotland (0.38%) (Prual et al., 1998; Brace et al., 2004). The higher occurrence of pre-pregnancy and especially pregnancy-related illnesses in our study may partly be due to poor access or uptake of ANC services and data assessment identifying more cases by using standardised definition in a large population. The disparity in occurrence of maternal morbidities may also be attributed to the general level of development and that of maternal health care delivery services. The fact that pre-pregnancy and pregnancy-related illnesses cases were higher in our study is robust proof that they constitute a significant threat to pregnant women in south-east, Nigeria. Thus, pre-pregnancy and pregnancy-related illnesses deserve to be considered priority targets for public health interventions.

We examined differences in pregnant women's experience of pre-pregnancy and pregnancy-related illnesses according to maternal factors of age and level of education. We found that there was a significant difference in the reported pre-pregnancy illnesses in women according to level of education (Table 8). Furthermore, we found that there were significant differences in the reported pregnancy-related illnesses based on maternal age and level of education respectively (Table 9). These findings are in tandem with the findings of a previous study conducted in northern Nigeria that found associations between maternal socio-demographic factors and maternal deaths from pregnancy

complications (Adamu et al., 2003). The authors reported that teenage mothers and mothers aged 40 years and above constituted the age groups at greatest risk. Adamu et al. (2003) further reported that the second most significant predictor of mortality was the educational level of mothers. They observed that as the level of education rose, the probability of the mother dying from delivery complications diminished in a dose-dependent fashion ($p = 0.02$).

Conclusion

The findings of this study will be useful to policy makers, healthcare professionals and public health experts. This study thus showed high prevalence of malaria, morning sickness and low prevalence of STIs, anaemia, pre-eclampsia and nausea/severe vomiting (hyperemesis gravidarum) in women. The incidence of these illnesses was significantly higher among pregnant women when compared to studies from other climes. The higher occurrence of pre-pregnancy and especially pregnancy-related illnesses in our study may partly be due to poor access or uptake of ANC services and data assessment identifying more cases by using standardised definition in a large population. The disparity in occurrence of maternal morbidities may also be attributed to the general level of development and poor maternal health care delivery services. Scaling-up of integrated maternal and child health (IMCH) services; access to high quality facility care; use of health systems approach in maternal health services provision are likely to provide a holistic

Table 9. Summary of Chi-square (χ^2) Analysis of Difference in Reported Pregnancy-related Illnesses based on Selected maternal characteristics ($n = 647$).

Variables	Pregnancy-related Illnesses				Cal. χ^2	P-value
	Yes		No			
	<i>n</i>	%	<i>n</i>	%		
Age						
< 20 years ($n = 40$)	12	29.5	28	70.5	35.36	0.045*
21-29 years ($n = 307$)	88	28.7	219	71.3		
30-39 years ($n = 240$)	73	30.4	167	69.6		
> 40 years ($n = 60$)	18	30.0	42	70.0		
Level of Education						
No Formal Education ($n = 66$)	24	36.1	42	63.9	10.39	0.023*
Primary Education ($n = 83$)	26	31.5	57	68.5		
Secondary Education ($n = 271$)	89	32.8	182	67.2		
Tertiary Education ($n = 227$)	52	22.9	175	77.1		

Significant level: * = $P < 0.05$.

improvement in the quality of care in the study area. This in turn will substantially reduce mortality and morbidity from these conditions. In addition, early identification and management of pregnancy-related complications, particularly pre-eclampsia, haemorrhage, premature rupture of membranes and STIs, identification and treatment of underlying or concurrent illnesses in pregnancy such as malaria, gestational diabetes, anaemia, STIs among others are vital to improved maternal and fetal outcomes in Nigeria.

Limitations of the study

Some inaccuracies in the classification of certain morbidities may be expected due to the use of admission diagnoses. Data collection did not extend to the medical wards as well as postpartum period. Therefore, data collected did not include postpartum obstetric conditions. Recall bias was another potential limitation because information on maternal morbidities based on recall spanned across pre-pregnancy period, pregnancy and perinatal and some women might not remember when they specifically had such morbidities. It is expected that inclusion of women around perinatal, childbirth and postpartum period may help minimize the effect of recall bias as recall period is shorter compared to using pre-pregnancy and early pregnancy periods. Furthermore, information that was obtained relied on women's self-report and pregnant women may underreport illnesses due to social desirability bias, hence, the observed occurrence of maternal illnesses may be underestimated. The incidence of maternal morbidity in this study may

depict the iceberg phenomenon. Thus, reported maternal morbidities may not be a true reflection of the burden of this problem in the sub-population as only a third of delivery takes place at the health facilities. Some women with these morbidities may not have access to PHCs or private or mission health facilities for several reasons, which include lack of transportation, ignorance, poverty, influence of traditional/religious beliefs and perceived negative attitude of health workers.

CONFLICT OF INTERESTS

The authors declare that they have no conflict of interest.

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Full Length Research Paper

Precision health contributions to public health: An integrative review

Vineeth Amba, Marina Celly Martins Ribeiro de Souza, Carole Kenner and Carolina Marques Borges*

Department of Public Health, School of Nursing, Health and Exercise Science, The College of New Jersey, USA.

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Precision health is an all-encompassing term, which can describe a type of care that shows the intersectionality of genomics, precision health or medicine and public health. This integrative review aimed to investigate how precision health strategies could contribute to the public health and improve health-related outcomes among populations. The search strategy included 5 main keywords combined with other 63 descriptors, resulting in 252 potential combinations. A total of 1,576 published articles were retrieved from the search. Fourteen articles met the inclusion criteria. Most addressed health-related outcomes were linked with chronic diseases like diabetes and cancer. The analyzed papers also discussed contextual effects and risk factors such as smoking under the scope of precision health and its interfaces with public health. Application of precision health to public health requires more collaborative work; use of science and technology to help individuals achieve better health outcomes is costly, although over time may result in more efficient, cost-effective resource allocation. The downside of it is the risk of excessive focus on genes and technology detrimental to other relevant determinants of health (e.g. social factors). It is important to give the population, government, health providers and other stakeholders equal voice in health innovation discussions.

Key words: Precision health, precision medicine, public health, health innovation.

INTRODUCTION

Precision health is a concept that is emerging in the field of public health, which shows a form of treatment in which the context of the condition of the patient is understood while finding the best intervention, promoting more personalized care (Feero, 2017). Precision medicine is an approach for disease treatment and

prevention that takes into account individual variability in environment, lifestyle and genes for each person. Precision medicine also differs from genomics, in the sense that genomics covers topics that do not include healthcare, like zoology, but also does not cover public health topics like the effect of wearable sensors on

*Corresponding author. E-mail: borgesc@tcnj.edu.

behavior (Feero, 2017). The terms “Precision Health” and “Precision Medicine” are often used interchangeably. Although “Precision Medicine” was coined first, broadening the scope of the term, switching to “Precision Health” seems to be more suitable once it is not limited to medical interventions or medical actions but it brings together different fields of knowledge and practice. This present study will adopt the term “Precision Health”. Therefore, “Precision Health” describes a type of care that discusses the intersectionality of genomics, Precision Medicine, and Public Health (Feero, 2017). By using the term “health” instead of “medicine”, we can couple the scientific aspects of medicine with the context of the conditions of patients, whether environmental effects, personal characteristics, or other factors that could be possibly detrimental to health, thus more aligned to with Public Health. Precision Health also includes an interprofessional health team approach to health promotion, disease prevention care instead of just the medical viewpoint that focuses on disease management and episodic care.

National initiatives have been conducted to promote the interdisciplinary concept of Precision Health. For example, an initiative led by a national organization, National Institutes of Health (NIH), called the “*All of Us Research Program*”, strives to extend precision medicine to all diseases by conducting continuous research on a cohort of over one million U.S. participants (National Institutes of Health, 2018). By doing so, it demonstrates how the general population, stakeholders who have an effect on policy, healthcare providers, and researchers can come together to improve public health.

Precision Health focuses on creating patient subpopulation and then administering specific intervention to each group appropriately (Feero, 2017). For example, both the United Kingdom 100,000 Genomes Project and United States Precision Medicine Initiative (PMI) will use patient data to create genomic sequences. In turn, this population data can be used to allow for understanding of diseases on specific molecular terms, thus allowing patients to gain more insight into the pathways of alleviating rare medical problems. For example, the United Kingdom 100,000 Genomes Project focuses on sequencing patients with rare disease, their families and cancer patients. As 80% of rare diseases are genomic, by understanding the family genomes of those who are affected, the causes can be identified, and individual care can be improved (Vaithinathan and Vanitha, 2017). The United States PMI uses a national group of 1 million people to investigate genetic and environmental determinants of health, to improve pharmacogenomics (how genes affect a human's response to drugs). In turn, those with knowledge of their respective alleles can use data-driven information to select effective treatments for their genotype. In doing so, both these projects involving cohorts can streamline medicine to be more cost-effective and avoid side effects, empowering individual care (Vaithinathan and Vanitha,

2017). Nevertheless, for large-scale studies to be successful, each individual must be compared to a diverse cohort, without convenience sampling, requiring an excellent epidemiological cohort structure (Khoury et al., 2016).

Additionally, it is important to give the public, government, health providers, as well as other parties in the healthcare system equal stake in decision-making, demonstrating the importance of public health and healthcare intersectionality. By having participation of all parties, it will allow for policy and resources to come together to create innovative approaches to fix the current populations' needs (Khoury et al., 2016). If the public is not given an active voice, an already imbalanced healthcare distribution may worsen health disparities (Khoury et al., 2012). It is important to highlight that even in genomic applications, a large cohort is needed as diseases are usually due to multiple factors. Additionally, large numbers of people are needed to make subgroup data for disease stratification and understanding of environment-gene relationships (Khoury et al., 2016). Cost and reimbursement from insurance companies may also become problematic over time, as sequencing DNA with new technology and deriving drugs and therapies for specific treatments will both be expensive (U.S. National Library of Medicine, 2017). Precision health focuses on prevention through not only encouraging lifestyle and environment choices, but by using a wide variety of biomarkers to diagnose risk of developing disease, like blood, saliva and urine, just to name a few (Vargas and Harris, 2016). Other resources such as wearables, smartphones applications (e.g. Apple partnership with Stanford Precision Health) are part of Precision Health strategy (Mach, 2017). The former United States administration encouraged governing bodies to implement policies that support Precision Health, such as the Precision Medicine Initiative (Dzau et al., 2016). From the Public Health perspective, the current challenge is still over health inequalities, which are not explained neither by the genes per se nor by improvement of technology itself but by social stratification and lack of basic conditions such as high quality education, decent housing, social support, clean water, among others.

This integrative review aimed to investigate how precision health strategies could contribute to public health and improve health-related outcomes among populations.

METHODOLOGY

This study is an integrative review that addresses experimental and non-experimental studies to understand the analyzed outcome, it combines data from theoretical and empirical literature, and has a wide range of purposes, such as definition of concepts, review of theories and evidence, and analysis of methodological problems of a particular topic (Whittemore and Knafl, 2005). The research question was “How can public health improve health-related outcomes based on precision health strategies?” Searches were conducted on US National Library of Medicine, National Institutes

of Health (PUBMED) on March 25th of 2017 by two authors of this study that searched independently on the same day. The PubMed "advanced search builder" tool and search strategy were used as follows for "Title/Abstract".

The authors searched for 63 descriptors (Medicine/ Health/ Healthcare/ Health Care/ Medicine 2.0 /Medicine 3.0/ Biomedical Technology/ Individual Treatment/ Personal Intervention/ Preventive Medicine/ Preventive Medicine/ Prevention/ Health Promotion/ Disease Prevention/ Disease/ DNA/ DNA Sequencing/ Phenotype/ Genotype/ Genomics/ Genetics/ Genetic Variation/ Molecular Diagnostics/ Molecular Phenotypes/ Molecular Classification/ Molecular/ Environment/ Environmental/ Data/ Data Science/ Data Application/ Big Data/ Targeted Therapy/ Medical Imaging/ Heterogeneity/ Pharmacogenomics/ Somatic Mutation/ MassARRAY/ Personalized Therapy/ Precision Therapy/ Predictive Factors/ Disease Taxonomy/ Disease Pathology/ Natural History of Disease/ Treatment Customization / Time-to-Subsequent-Disease-Progression/ Clinical Trials/ RCT/ Epidemiology/ Global Health/ Health Informatics/ Health Information Technology/ Health Technology/ Biomarker/ Biomarker Technology/ Clinical Decision-Making/ Risk Factors/ Chronic Disease/ Cancer/ Diabetes/ Cardiovascular/ Obesity/ Respiratory) that were individually combined with 5 main fixed keywords [(“Precision Health” OR “Precision Medicine” AND “Public Health” AND “descriptor X”) / (“Personalized Health” OR “Personalized Medicine” AND “Public Health” AND “descriptor X)], resulting in a total of 252 potential combinations of keywords. Example: [(“Precision Health” OR “Precision Medicine” AND “Public Health” AND “diabetes”) + (“Personalized Health” OR “Personalized Medicine” AND “Public Health” AND “diabetes”)]. The exclusion criteria for papers selection were: 1) papers in which abstract were not available by the date of search, and 2) study type reviews. The inclusion criteria for papers selection were: 1) texts with abstracts and full text availability, and 2) studies that involved humans and other animals.

When the searches were concluded, potential divergences were discussed between the two researchers responsible for this step. There was no limit for the year of publication. The search process retrieved 1,576 potential papers. The 1st phase of paper selection was according to “Title” (75 remaining papers), followed by “Abstract” (31 remaining papers). Titles and/or abstracts not related to the subject were excluded; 17 potential papers were fully printed for analysis due to the fact that they addressed the subject of this review. 14 papers met the inclusion criteria and were included in this integrative review.

RESULTS

The content of a diverse selection of 14 papers was extracted. The studies included were undertaken between 2008 and 2017. Papers ranged from long-term experiments to discuss obscure variables that correlated with certain diseases. Majority of the articles (79%) primarily addressed lifestyle and other contextual, public health interventions. Additionally, all papers reinforced the importance of prevention in public health and the benefits in moving to a health system model that focuses on prevention.

DISCUSSION

Addressing the population perspective

Population health is a term used to describe a group of

patients/families that have similar conditions such as diabetes, cardiovascular disease and asthma. Population health departments exist in some of the major health centers in effort to reduce the costs of care and produce better health outcomes for the populations served. Population health uses evidence-based interventions. Public health in precision medicine is through the use of evidence and scientific data, and then using this information in conjunction with the community/population of interest to make health decisions. These data can be used by health protection agencies like the Centers for Disease Control and Prevention (CDC) to sequence pathogens and then assist populations and individuals control diseases. On a smaller scale, data from family trees, including factors from lifestyle and behavior can be analyzed to guide the individual to precise screenings in order to make disease prevention to be more effective. Evidence-based public health is divided into three different types: Types 1, 2 and 3 (Khoury et al., 2011). Type 1 focuses on the risk factors of diseases and how to prevent them. On the other hand, Type 2 consists of comparing different interventions to create targeted solutions for specific diseases and risk factors. Finally, Type 3 focuses on the actual conditions the patients are under while administering the intervention. However, although Type 3 is utilized the least, it is also the most difficult to implement, as it depends heavily on clinical trials, rather than “general” information. Evidence-based analysis can also be applied to test whether an intervention (such as a change of diet) is actually benefiting a population, and can have signal when readjustments must be made (Khoury et al., 2011).

On the whole, the health of an individual is also based on the nearby environment, including family, community, and behavioral factors all functioning in unison. In turn, Precision Medicine treatments will not only include precise targeted drugs, but also include analysis of the population the individual is a part of, and form interventions using changes to the environment, health policy improvements, and education. By using population-based epidemiological studies to account for a variety of determinants at once, precision medicine can empower global public health by enabling risk factor prediction depending on the environment of an individual (McEwen and Getz, 2013).

Biological biomarkers can be used to create subpopulations of every disease for more targeted therapies, rather than having broad categories such as diabetes or hypotension. In turn, costs of medical care can be reduced, as useless screenings and treatments can be bypassed. With the addition of new subpopulations of diseases created by specific biomarkers, sample sizes for Randomized Clinical Control Trials (RCCTs) can also be reduced, leading to more efficient research. In turn, costs of individual care can be made lower, allowing for more health care to be more accessible (McEwen and Getz, 2013).

By collecting population-specific data effectively and

intervening with specific policy and environmental factors in mind, developing populations will have better access to the advantages of precision medicine. In this current age, most health care is focused on expensive treatments and technology usage after the onset of the medical condition. However, it is much more cost-effective to focus on prevention. This is done through analyzing biologic risk factors of populations, utilization of biomarkers, using molecular level characteristics of a population to assess the benefits and risks of an intervention, and allow the individual to have more say in care choices, as well as more access to at-home interventions (Downing, 2009).

Innovations involving precision medicine can make healthcare more affordable among all populations through focus on prevention. Through an important data bank of biological differences between populations, medical products can be made to identify vulnerability and create diagnostic tools to assess onset of a medical condition much earlier. In turn, late-stage treatment as well as trial-and-error approaches can be avoided. In addition, randomized control trials which contribute to health evaluation can be made economical. By utilizing health information exchange through new banks of data, evidence on a product can be obtained without expending an immense amount of resources with the RCCT (Downing, 2009). In addition, through genomic data and pharmacogenomics, adverse and aberrant effects of specific medical products can be found out sooner. By doing so, dangerous medications that are thought to be positive for certain populations, as well as extra costs for treatment can be avoided. Finally, the emphasis on patient participation in Precision Health can promote individual care using genomic data (Downing, 2009). "My Family Health Portrait", available through the U.S. Department of Health and Human Services, (<https://familyhistory.hhs.gov/FHH/html/index.html>) is a web tool that displays standardized information, and can be easily used by consumers to evaluate their own risks. Together with this innovative platform, new applications are being developed for the individual using information banks to allow the consumer to learn from home, instead of the "standard" healthcare environment (Downing, 2009).

Social and contextual effects

Studies demonstrate how non-medical variables are usually overlooked but can directly affect the overall health of an individual, and can be used in the Precision Medicine model to promote public health (Roman and Panduro, 2015; Vazquez AI et al., 2012). Common health problems that stem from lifestyle choices such as obesity, alcoholism, type 2 diabetes, brain disease, and liver damage are treated by specialists after they occur, instead of being prevented before they occur (Roman and Panduro, 2015). Typically, the induction of diabetes

started 20 to 30 years earlier before the diagnosis of the disease, as the sedentary lifestyle and high caloric intake lead to risk factors such as hyperglycemia and insulin resistance. The same can be said about non-alcoholic steatohepatitis (NASH), a nonalcoholic liver disease, in which liver damage can be predicted almost ten years prior to onset (Roman and Panduro, 2015). Common trends can also be seen in lifestyle choices such as alcoholism and unsafe sexual behavior. However, a patient who is expected to develop a certain disease will have varying susceptibility due to his/her own environment and genes. Even with lifestyle choices, the way in which an individual is affected will be based on innate genetics, as certain alleles are directly involved in controlling metabolism, appetite and the circadian cycle, which can affect the extent to which a complex disease will affect someone (Roman and Panduro, 2015). This intersection can be seen in Mexico, where the average diet is highly dependent on carbohydrates and saturated fats, and most of the populations are ApoE2/ ApoE4 carriers (which both increase the risk of high cholesterol, diabetes and liver damage). In turn, the population has a high rate of dyslipidemia (high amount of fat in blood) and is one of the most overweight and obese populations in the world. Future complex diseases can be avoided by physical exercise, even if genetic "disadvantages" are present. Studies show that future liver damage can be countered in the early stages through proper diet and regular exercise. Emotions also play a role in physical health, and can be influenced by not only the environment, but also the genes one has. For example, there are two variations in the catechol-O-methyltransferase gene, which makes dopamine and norepinephrine. The "Val" version increase resistance to stress, whereas the "Met" version creates a lower stress threshold, which can lead to unhealthier lifestyles and complex diseases (Roman and Panduro, 2015).

Lifestyle can also directly influence the brain of an individual, which can lead to disease. For example, those who are more stressed, either due to lifestyle or greater susceptibility, can have a hippocampus and medial prefrontal cortex with less sensory strength, leading to a greater chance of depression, Cushing's Disease, Type 2 Diabetes, and post-traumatic stress disorder (Vazquez AI et al., 2012). Additionally, the prefrontal cortex becomes less powerful with less exercise, which can cause higher stress levels and poorer decision-making. All these parts work together to control regular environmental adjustments such as hunger, thermoregulation and sleeping, and when these processes are compromised, health issues can arise. Studies have also shown that prenatal stress in mother can lead to impaired brain development in child, and poor maternal care or maternal anxiety can cause metabolic syndrome and begin the induction of diabetes (Vazquez AI et al., 2012). Poor childhood experiences can impair brain development, leading to low self-esteem and the gateway to poor habits such as overeating and risky sexual behavior, which in

turn can compromise the cardiovascular, metabolic, and immunologic body functions. By also lowering the self-esteem of the individual, there is a greater chance of having a smaller hippocampus, which will lead to elevated stress responses (Vazquez AI et al., 2012). In turn, the household as well as the environment of an individual becomes increasingly more important in the concept of precision health. By understanding the relationships between specific environmental detriments and tying them to specific health problems using the brain as a connector, the non-medical roots of certain issues can be analyzed and targeted.

Cancer prevention

The concept of precision medicine is beginning to be heavily utilized in the detection and prediction of cancer. Newfound biomarkers and other predictors in conjunction with new genetic data forms multiple breakthroughs in screening for potential risk for cancer by analyzing the proteins of an individual. Through the use of proteomics, protein biomarkers can be found in different specimens. Using the mass spectrometry, the entire protein product of a cancer cell, ranging from secretions to extracellular space, can be mapped out and analyzed (Hanash and Taguchi, 2011). Specimens used to find biomarkers can also vary. For example, the discharged blood of the lungs was analyzed and a biomarker that had the ability to detect lung cancer 30 months prior to original diagnosis (Hanash and Taguchi, 2011) was found. Liquid biopsies can also be conducted to find circulating tumor DNA even before genetic screening, by viewing the blood instead (Bertier et al., 2016). By analyzing a wide variety of specimens and unique sources for biomarkers, cancer can be more predictable. By predicting this medical condition well before the onset of disease, preventive strategies could be optimized.

The Human Genome Project is an important tool that is built towards precision medicine, because it works to determine the exact DNA sequences in a human genome (Hanash and Taguchi, 2011). Genetic material can determine regulation, coordination, and other human characteristics. Through new technologies such as protein profiling and the use of DNA chip, the effect of genes in the disease of an individual can be analyzed. More than 1100 genetic biomarkers have been discovered through these methods to work towards targeted cancer therapy (Bertier et al., 2016). Breast cancer risk can now be predicted using models that screen the BRCA1/ BRCA2 genes, which are responsible for breast cancer, as well as age, ethnicity, lifestyle, family history and environmental factors. In addition, the specific genetic mutations of cancer cells (like olaparib inhibiting BRCA1/ BRCA2/ BRCA3 in ovarian cancer) can be investigated (Bertier et al., 2016). The process becomes more feasible with the rise of genetic banks,

which can be used as comparison points to find driver mutations that contribute to cancer, rather than passenger mutations (which do not contribute to cancer) (Bertier et al., 2016). The microenvironment can also have an effect on the growth of harmful cancerous mutations. These stages of growth are called “driver” events or “driver” mutations. In primary melanomas (type of tumor), there are many progressive mutations before the end product is reached (Manamperi, 2008). Through studies done on 293 genes relating to cancer growth, it was found that the presence of abnormal tissue growth could be tied to harmful mutations stemming from ultraviolet radiation exposure (Vazquez AI et al., 2012).

The Precision Health trial design, emphasizing targeted, specific therapy, can also influence prevention by creating new interventions. For example, it was recently found that aspirin can assist in colorectal cancer prevention. Through studies conducted on colorectal cancer, it was found that urinary PGE-M (metabolite biomarker) levels were a risk factor indicated in the administration of aspirin. In turn, patients with high Mrna expression of 15-hydroxyprostaglandin dehydrogenase had lowered colorectal cancer risk after taking aspirin (Manamperi, 2008). Vaccinations also have an impact on cancer prevention- as it was shown that those with HPV-related cancers like oropharyngeal could dramatically reduce their risk factor by taking vaccines (Manamperi, 2008) HPV-associated oropharyngeal risk factors can also include childhood tonsillectomy and race. Vaccines that prevent non-viral cancer are also being created- these target immunogenic proteins and antigens (Manamperi, 2008). Additionally, through genomic practices, drug design (pharmacogenomics) can be improved. This will be done by analyzing unique individual information on how one is biochemically expected to respond to a drug leading to targeted interventions (Hanash and Taguchi, 2011). This research can also be directed at disease-causing microorganisms, as sequencing them will allow for understanding of how they can bypass the defenses of certain individuals. In turn, once again, targeted interventions can be improved (Hanash and Taguchi, 2011). This concept of Precision Health can be taken in developing nations for more enhanced and more effective control of common disease. By using affordable diagnostics for diseases that are specific to certain populations, individual care can be more accessible.

Chronic disease and risk factors

Smoking cessation

Smoking is a leading contributor to early death, with at least five million individuals dying each year from illnesses that stem from smoking. Through studies, it was found that genes of the alpha5-alpha3-beta4 nicotine

receptor contribute very strongly to nicotine dependence (20). Studies (n=73,000) have shown that the 15q25 chromosomal region that contains this receptor has a clear association with heavy smoking ($p=5.57 \times 10^{-72}$) (19). Low levels of alpha5 and other variations of the receptor can lead to a lower risk of developing nicotine dependence. The environment of an individual is also important, as genetic risks become exponentially more powerful if smoking begins at a young age. For example, parent monitoring and the number of adolescent peers around an individual that smoke both alter the power of the alpha5 subunit (Hanash and Taguchi, 2011). Even in pregnant women who smoke, smoking cessation was more likely to occur when there was a variation in alpha5 and there were environment and social factors that encouraged quitting smoking. In another study performed, there were three groups, one with a low-risk variation of alpha5, one with the high-risk variation of alpha5, and one group with the high-risk alpha5, but with pharmacological interventions (Bierut et al., 2014). It was shown that interventions like therapy and medications had a great impact on the occurrence of smoking cessation. In turn, by analyzing the genomics of each individual and looking for the presence of certain genes, one can predict the level of dependence one will have on smoking and nicotine. Although, a safe environment that encourages cessation should be produced for everyone, by using strong environmental influences and interventions (such as raising cigarette prices), it is possible to encourage people to quit smoking, even in high-risk variations of the genome. In addition, by coupling outside interventions with early genomic analysis of 15q25 chromosome in different populations, the potential risk for developing nicotine dependence in subgroups as a whole can be predicted (Bierut et al., 2014). In turn, future risk for more dangerous diseases can be avoided, promoting public health approaches and health risk communication campaigns to increase awareness of such problems.

Diabetes

Type 2 diabetes continues to be an important health issue that is affected by a variety of different factors. Although, this type of diabetes can be predicted through body mass index and obesity, due to other variables such as genetics and environment, discrepancies can arise (Vazquez Al et al., 2012). This can be shown through South Asian populations that obtain insulin resistance and eventual T2D at BMI levels not even marked as obese in some European populations (Spiegel and Hawkins, 2012). Primary prevention, including encouraging healthy foods and exercises in a world where there is an increased emphasis and processed food can allow for an intervention that is extremely cost-efficient and just as effective as drug treatments (shown through a meta-analysis of 21 trials) (Spiegel and

Hawkins, 2012). Additionally, risk for T2D carries over to offspring if the mother has gestational diabetes or is malnourished, so analyzing the state of the mother during pregnancy becomes increasingly important. Pharmacogenomic testing also is extremely important as it is found that those with family history of the disease have a risk that is up to six times greater than an individual without family history (Spiegel and Hawkins, 2012). Finally, metabolic profiles are also very important, as it was found that during the Framingham Offspring Study, having a combination of three specific amino acid could increase the risk factor of an individual by five (Spiegel and Hawkins, 2012). In turn, the creation of an efficient biomarker test could be a possibility, and could be a much greater predictor than factors such as BMI, which has high variability, based on the population.

Metabolically healthy obesity

In the world today, obesity is a leading epidemic, which can cause the onset of conditions such as metabolic syndrome, type 2 diabetes mellitus and cardiovascular disease. However, not all obese people are at the same risk of these diseases. A subpopulation of 'metabolically healthy obese' humans that have all the physical characteristics of an obese individual, but have little risk for dangerous medical conditions exist (Phillips, 2016). Stratifying obese populations based on metabolic health subtype can allow for improved diagnosis and treatment. However, metabolically healthy obese individuals can progress into becoming metabolically unhealthy obese. In Tehran lipid and glucose study, it was found that 43.3% of those tested went from healthy to unhealthy obesity, the main predictors being insulin resistance and overall lipid profiles (Phillips, 2016). The study also showed that metabolic health is the most important characteristic for determining cardiometabolic risk, and in turn, by stratifying those with different metabolic phenotypes into groups, personalized care can improve. Precision medicine can be empowered as those with greater risk of metabolic and cardiovascular problems can be identified earlier and can focus on improving metabolic health profile (including improving lifestyle and environment choices) (Phillips, 2016). This is important as lifestyle choices can influence one metabolic phenotype over another, as dietary quality and physical activity are more associated with MHO. Over time, this can make seeking interventions more efficient and more cost-effective (Phillips, 2016). This example reflects a case study, or a specific research example that is explored in a group, and thus may not be applicable to the entire population (Phillips, 2016).

Review limitations

This review has some limitations. Firstly, there are different databases available for research. PubMed used

in the search is one among several existing ones; thereby potential papers that would be suitable for this review were not included. Another aspect is that publications addressing precision health and public health just gained attention on research agenda few years ago, which explains the scarce number of papers on the topic. When the descriptors “Precision Public Health” were searched on PubMed by the time this article was finished (February 2018), 22 papers were retrieved, and only 9 addressed “Precision Public Health”. Majority of the analyzed papers in this review discussed the broad scope of Precision Health and potential applications in disease prevention and health promotion instead of presenting results of primary data analysis.

Costs and criticism

The great achievement of precision medicine for individual care for diseases such as cancer is undeniable (Kensler et al., 2016). It is important to point out the downsides of the excessive focus on genetics and technology plus the impact of precision health costs over society. Precision Health approach brings the advent of lowering the costs of healthcare in long term. Previously, some aspects were taken into consideration as the unsustainable costs of some drugs, principally the orphan drugs ruled by pharmaceutical companies. Ferkol and Quinton (2015) brought up this to discuss using the example of the drug Ivacaftor used to reduce pulmonary exacerbations, normalize sweat chloride concentrations, improve lung function together with the quality of life in patients with the G551D mutation, and cost approximately \$300 thousand dollars yearly. Although, the expectations are higher than the potential cost-benefit of precision health to preventative actions (16), focus on precision medicine may miss the point when it comes to public health. The enthusiasm for precision health and medicine initiatives is derived from the assumption that it will contribute to clinical practice and thereby advance the health of populations (Bayer and Galea, 2015). This enthusiasm has to be considered with caution, as agreed. Researchers, Public Health practitioners and other professionals who work in the health sector in general have to understand that the challenge of the century goes beyond genes, big data, and technology solely because the major current Public Health issues are social forces related (social disparities). Another point is that people that really need care are not getting the care that they need. Precision health could not receive all the credits as the solution to mitigate health inequalities principally due to the high costs and the uncertainty of Precision Health approaches will be translated to better health outcomes among populations (Bayer and Galea, 2015).

Conclusion

The application of Precision Health to Public Health

requires different resources (financial, interdisciplinary team of diverse stakeholders), work and time for its maturation. The use of science and technology to build genetic datasets as well as conduct clinical trials will be originally costly, although it might result in more efficient and cost-effective healthcare in the long run but this is still a black box. Most of the current precision health initiatives are individual-centered focus on the treatment of certain diseases rather than on prevention itself. High costs of Precision Health might be a relevant limitation factor when extended to Public Health. Considering the current challenges of Public Health worldwide, it is desirable that Precision Health be used to reduce health disparities. This is still not considered.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interest.

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Full Length Research Paper

Malaria outbreak and contracting factors in Afar Region, Ethiopia, 2016

Mitiku Bonsa Debela¹, Alemayehu Bayray Kahsay², and Taklu Marama Mokannon^{3*}

¹School of Public Health, College of Health sciences and Medicine, Madda Walabu University, Goba, Ethiopia.

²School of Public health, College of Health sciences, Mekelle University, Ethiopia.

³Department of Midwifery, College of Medicine and Health science, Wolaita Sodo University, Ethiopia.

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On July 5, 2016, Amibera District Health office was alerted of excess of malaria cases in two villages. Within July 5 to 17, 2016 malaria outbreak and associations factors were investigated. A malaria case is when a person with fever or fever with headache is confirmed either microscopically to have *Plasmodium* parasites or by Rapid Diagnostic Test (RDT) to detect the malaria antigens. In the last five years malaria data were reviewed from 2011 to 2015 at the district level. Cases were identified by using line list and house to house active case search was done on a daily basis. Unmatched case-control study was conducted in 1:1 ratio conveniently selected cases (117) and community controls (117). The control was the neighbor of those who have not developed symptoms of malaria in the last three months. Data were collected through a structured interview administered questionnaire, entered into Epi-info version7 and analyzed using SPSS version 20. A total of 415 confirmed malaria cases with no death was identified. The predominant species was *Plasmodium Falciparum* accounting for 95.5%. The median age was 27 years (ranges 2- 63 years). The highest age specific attack rate was above 15 years (63.7/1000 populations). Poor insecticide treated bed net utilization, absence of indoor residual spray, sleeping outside of their homes at nights and presence of stagnant water were factors associated with the disease contraction. In this study the current malaria outbreak was higher in magnitude than that of three years ago.

Key words: Amibera, malaria, outbreak, *Plasmodium Falciparum*.

INTRODUCTION

In Ethiopia, malaria transmission is generally seasonal and highly unstable because of the variations in topography, climate and rainfall patterns (Daddi and Abebe, 2012). Hence, large scale outbreak frequently occurs particularly in epidemic prone areas of the country. Generally outbreak occurs in places where

there is low and unstable malaria transmission, and where people have low or no immunity (Daddi and Abebe, 2012; Policy, 2013).

Other triggering factors like unusual local weather phenomena and activities resulting in environmental modifications that increase vector population increase

*Corresponding author. E-mail: taklu.marama@wsu.edu.et.

vulnerability of population to famine and malnutrition, and interruptions of anti-malarial measures which have kept malaria under control. However, there could be outbreak in high transmission areas if there is deterioration of health system, interruption of anti-malarial measures or migration of non-immune individuals (WHO, 2015; World Health Assembly, 2016).

Many localized but severe outbreaks of malaria occurred in Amhara and SNNP Regional States, leading to widespread epidemic malaria in highland and highland fringe areas (up to 2,500 m) in 2003 (Gemechu et al., 2015; Hurissa, 2015). Conventionally, in areas of high-endemicity, prevalence of malaria infection is known to peak at an early age with an increase up to the age of 5 years; followed by a sharp fall in age groups of 10-15 years and continuing on a slow decline with increasing age (Kevin and Baird, 2010; World Health Assembly, 2016).

Afar's geography and climate influence (seasonal) outbreaks of malaria epidemics. Peculiarities of this region (lowlands and seasonal heavy rainfall) lead to a high prevalence of mosquito breeding sites. The Afar Region is characterized by the lowland areas (≤ 1500 m altitude) with hot or warm climate. Malaria transmission in the region is generally seasonal and highly unstable due to variations in topography and rainfall patterns. Malaria transmission in the region is perennial due to the availability of large perennial river bodies and hot climate favoring the transmission throughout the year, with seasonal peak extending from August to December (AMREF, 2011; Daddi and Abebe, 2012).

The region is also prone to natural disasters such as droughts and floods and these have in the past contributed to increased malaria transmission, particularly along the banks of Awash River. Since the last decade, flooding of Awash River is on the increase, creating ideal conditions for vector breeding (AMREF, 2011). *Plasmodium Falciparum* (about 65%) and *Plasmodium vivax* (about 35%) are the two dominant malaria parasites prevailing in the region (Alemu, 2015; WHO, 2015).

There was a normal trend of malaria cases in Amibera District during the last five years. On the last week of June/2016 Werer health center of Amibera district reported an unusual increased number of malaria cases from Werer and Badhamo village. The aim of this investigation was to identify risk factors associated with this outbreak. The study aimed to describe the magnitude of morbidity and mortality due to malaria outbreak and investigate factors associated with an occurrence of malaria outbreak in Amibera, Ethiopia, 5-17 July/2016.

MATERIALS AND METHODS

The malaria outbreak investigation was conducted in Werer and Badhamo village of Amibera district from July 5 to 17th/2016. Amibera is bordered on the south by Awash Fentale, on the west by the Awash River which separates it from Dulecha to the southwest then on the northwest by the Administrative Zone 5, on the north by

Buromodaytu district, and on the east by the Oromia Region. The mean monthly temperature of the district was between 19 and 34°C, implying tropical temperature condition. The mean annual rainfall of the district is about 560 mm (AMREF, 2011).

Malaria was defined and identified as acute febrile illness with blood smear positive for malaria in Amibera district during this outbreak. We reviewed the previous five years (2011-2015) data of malaria from Amibera district health office and health facility to set epidemic threshold level and compare with similar week of this year (2016). The number of malaria cases was collected from health facilities on daily and weekly basis. Magnitude of outbreak was described by person, place and time. Slide positivity rate was calculated as those positive for malaria among total examined. Attack rates were calculated by person and place. An epidemic curve was constructed.

During analytical epidemiology, an un-matched case-control study was conducted to identify risk factors associated with malaria outbreak. A community control was selected for recently (not more than two weeks before interview) confirmed malaria case patients in 1:1 ratio basis. Controls were defined as having no malaria signs and symptoms for the last three months. A standard checklist was used to assess risk factors, including sleeping and staying area during the night, use of insecticide bed net, indoor residual spray, and presence of stagnant water or any other mosquito breeding area.

Regarding sampling method and sample size determination, the cases and control were recruited by convenience sampling method irrespective of the variables. Sample size determination was with a ratio of 1: 1 cases and control. The assumption taken from a previous study indicates that the proportion of controls exposed was 50% for a power of 80% with odds ratio (OR) of 2.2. The sample sizes which were conveniently taken from each group can be determined by the Epi-info version 7.2.1. Proposed sample size, therefore, 117 cases and 117 controls needed for the study was 234.

In the laboratory, laboratory technicians conducted thick and thin smears with a 100 × oil immersion microscopy at three health centers. Additionally, Rapid Diagnostic Test (RDT) was also used in this health center whenever they faced shortage of some reagents and during interruption of electric power. Health extension workers also used RDT to identify confirmed malaria cases at health post and community level during outbreak investigation case searching.

Data were collected in the presence of potential mosquito breeding sites. Selected case-patients and controls were interviewed about the presence of mosquito breeding sites in their compound and near home within 500 meters or less than it. In addition, availability of uncovered plastic water container, old tires and broken glasses in the home or outside the home were also critically assessed.

Quantitative data were collected using standardized face to face interviewer administered questionnaire that addressed socio-demographic characteristics, clinical manifestation, potential exposures, discussion with relevant bodies (task force), review of weekly integrated disease surveillance and response at different levels (District Health office and Health facilities), visiting of the affected village and interview of community members (patients) about knowledge of malaria transmission and control measure. Both RDT and Microscopic laboratory diagnoses were performed. Epi Info version 7.3.1 and SPSS version 20 were used to analyze the associated risk factors. The significance of risk factors for the outbreak was determined through bivariate and multivariate analysis by calculating Adjusted Odds Ratio and 95% Confidence Interval.

To ensure quality, the standardized questionnaire adopted was in English and translated into Afar local language, by experts. We reviewed and revised the questionnaire to ensure internal validity. We pre-tested it on 5% of the sample size. Data collectors and supervisors were trained for three days on the data collection tools

Table 1. Clinical manifestations among malaria cases in Amibera district, Afar-Ethiopia, July, 2016.

Symptom	Frequency; n (%)
Fever	44(88%)
Headache	44(88%)
Anorexia	23(46)
Vomiting	18(36%)
shivering/chills	13(26%)
Sweating	10(20%)
Diarrhea	5(10%)

and process of data collection. To ensure completeness, 5% of the collected data were checked and the investigators monitored the overall quality of data collection. We used line list for describing malaria cases in terms of time, place and person.

Case definitions

1. Community case definition: Any person with fever OR fever with headache, back pain, chills, rigor, sweating, muscle pain, nausea and vomiting OR suspected case confirmed by RDT.
2. Standard case definition: Any person with fever or fever with headache, rigor, back pain, chills, sweats, myalgia, nausea, and vomiting diagnosed clinically as malaria.
3. Suspected: Patient with fever or history of fever in the last 48 hours and lives in malaria endemic areas or has a history of travel within the past 30 days to malaria-endemic areas.
4. Probable: Any person with fever and one or more of major sign such as headache, rigor, back pain, chills, sweats, myalgia, nausea, and vomiting diagnosed clinically as malaria.
5. Confirmed: Any suspected case that is confirmed by microscopy or RDT for *plasmodium* parasites.

Inclusion criteria

1. Cases: Any residents of Werer and Badhamo village, who had symptoms of malaria and agreed to participate
2. Controls: Any residents of Werer and Badhamo village during the study who was a neighbor to a case and who did not develop signs and symptoms of malaria and agreed to participate.
3. Exclusion criteria
4. Cases: Those who refused to participate
5. Control: Those who refused to participate and did not fulfill inclusion criteria

Ethical consideration

All participants were informed about the objective of the study, confidentiality of the participant was assured and informed consent was sought from and given by the participants, with the knowledge they were free to withdraw at any time. Ethical clearance was obtained from the institutional review board of Mekelle University, College of health sciences and the support letter was written from Afar regional health bureau to Amibera district health office.

RESULTS AND DISCUSSION

Descriptive epidemiology by person

This study revealed that, among a total of 431 suspected

malaria cases, 198 (45.9%), 233(54.1%) were males and female respectively. Fever and headache were the two predominant clinical manifestations. Sweating and Diarrhea were less frequent, being present in approximately one quarter of the cases (Table 1).

The median age of suspected malaria cases was 27 years old (range- 2 to 63 year).The most affected age group was ≥ 15 years (63.6%) followed by 5-14 age groups (27.2%) and ≤ 4 years age group (8.2%) of all notified suspected malaria cases (Table 2).

The highest and lowest positivity rate was reported in the age group above 15 years (100%) and less than 4 years (78.5%) respectively (Table 3).

Among the total suspected malaria cases (431), 423 (98.1%) of them were examined by RDT/Microscopy and 8 (1.9%) were treated clinically. Of the total positive cases, *Plasmodium Falciparum* accounts for 404/423(95.5%) followed by *P. Vivax* 11/423 (4.5%). For the screened 415 febrile cases, RDT result comes out with 98.1% positivity rate. As the national guideline the outbreak threshold is 50% positive; these results confirmed the outbreak (Table 4).

The overall attack rate was 36.7 per 1000popn with a case fatality ratio of zero. Age group above 15 years was the most affected with an AR of 63.7 per 1000popn followed by age group 5-14 years which accounts for 11.4 per 1000 population (Table 5).

Descriptive epidemiology by place

Among the total suspected malaria cases, 349/423 (82.5%) were from Werer village and 74/423 (17.5%) were from Badhamo village, Amibera district. The most dominant species responsible for this outbreak were *P. Falciparum* followed by *Plasmodium Vivax*. Positivity rate was high in Werer village (82.5%) as compared to Badhamo village (17.5%)

The populations in Werer village were more affected by malaria outbreak followed by Badhamo village with an attack rate of 31 and 11 per 1000 population, respectively (Table 6).

Descriptive epidemiology by time

In both assessed villages, malaria outbreak was verified by comparing the current year data with a third quartile method (2nd largest number) during the previous 5 years (2011-2015). It was shown that the current case trend line crossed the threshold levels in both villages (Figure 1), peaked in second week and started to decline after the fourth week of July 2016 (WHO week 26 to 29/2016).

Epic curve showed that, district health office departed to the outbreak area lately, a week after the outbreak started. The epi-curve showed the outbreak was a propagated one with multiple peaks with a possibility of

Table 2. Distribution of suspected malaria cases by age group in Amibera district, Afar, Ethiopia, July 5-17, 2016.

Age group (years)	Frequency	Percent	Population at risk	Age specific AR/1000 population
≤4	14	3.2	1,703	8.2
5-14	47	10.9	3,785	27.2
≥15	370	85.8	5,809	63.6
Total	431	100.00	11,297	100

Table 3. Distribution of malaria cases by age and Plasmodium species tested in Amibera district, Afar-Ethiopia, July 5-17, 2016 .

Age group (years)	Total tested by RDT and Micro	Total positive	Positivity rate (%)	Plasmodium species	
				<i>P. Falciparum</i> ; n (%)	<i>P. Vivax</i> ; n (%)
≤4	14	11	78.5	10(90.9)	1
5-14	47	43	91.4	39(90.6)	4
≥15	370	370	100	370(100)	6
Total	423	415	98.1	404	11

Table 4. Distribution of malaria cases by sex and Plasmodium species tested in Amibera district, Afar, -Ethiopia, July 5-17, 2016.

Gender	Total tested by RDT and Micro	Total positive	Positivity rate (%)	Plasmodium species	
				<i>P. Falciparum</i> ; n (%)	<i>P. Vivax</i> ; n (%)
Male	190	189	99.4	185 (97.8)	4(2.5)
Female	233	226	96.9	219 (96.4)	7 (3)
Total	423	415	98.1	95.5	2.5

Table 5. Malaria attack rate by age in Amibera district, Afar, Ethiopia, July 5-17, 2016.

Age group (year)	Eligible population	Number of cases	Attack rate per 1000 population
≤4	1703	11	6.5
5-14	3785	43	11.4
≥15	5809	370	63.7
Total	11297	415	100

Table 6. Malaria attack rate by sex, village and age group in Afar-Ethiopia, July 5-17, 2016.

Name of village	Total population	Sex		Age group (in year)			Total cases	AR per 1000
		Male	Female	≤4	5-14	≥15		
Werer	11,297	7648	3648	1703	3785	5809	349	31
Badhamo	6,852	1523	1923	1284	2284	3284	74	11
Total	18,149	9571	5571	2987	6069	9093	423	42

person to person transmission (Figure 2). The weeks when the epidemic started were on March 6, 2016. However, the district health department was notified on July 5, 2016. The peak numbers of malaria patients were on 13th to 14th July, 2016. The proportion of *P. Falciparum* infections was higher than that of *P. viva*.

Epidemic preparedness and response

None of the district's health facility that we visited had an epidemic preparedness plan or an epidemic preparedness committee in place prior to the outbreak. There was no functional radio system for communication. They had to

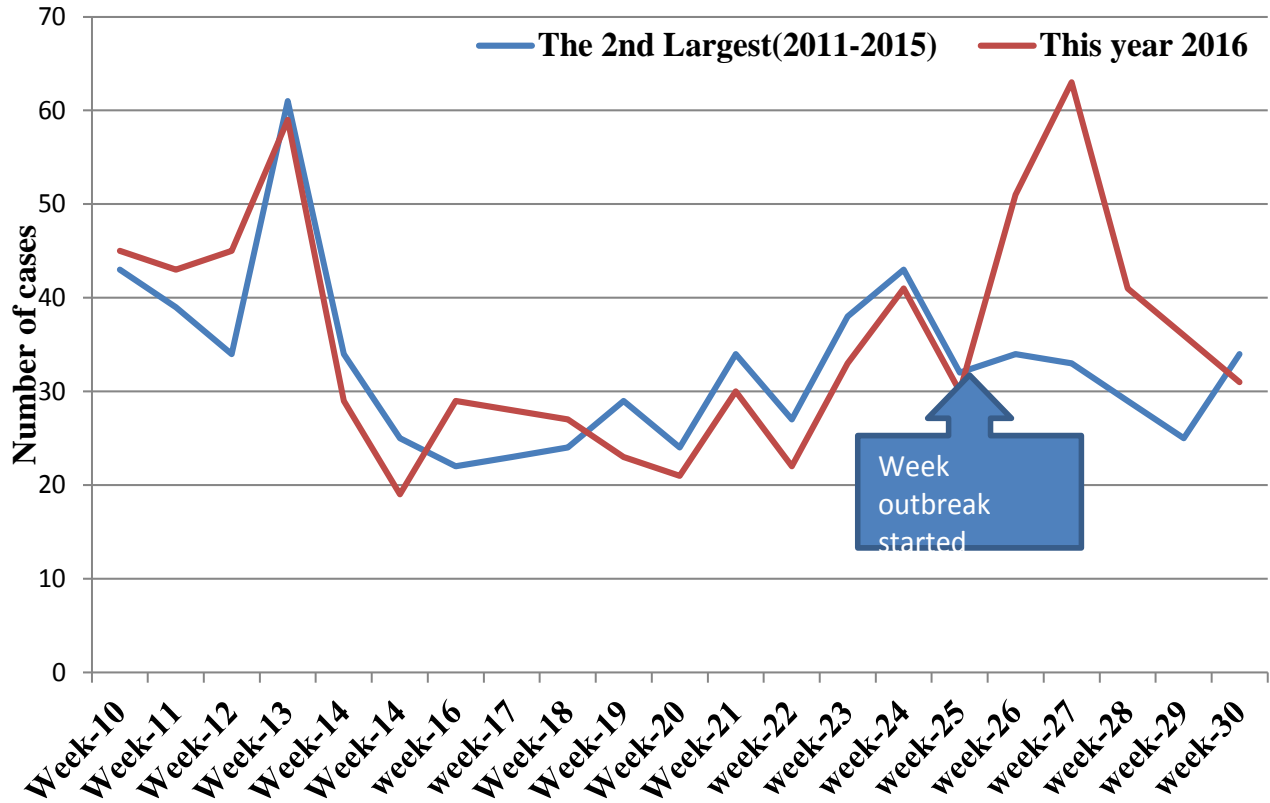


Figure 1. Epidemic weeks in current year above third quartile threshold from Werer and Badhamo village of Amibera district, Afar-Ethiopia, 2016.

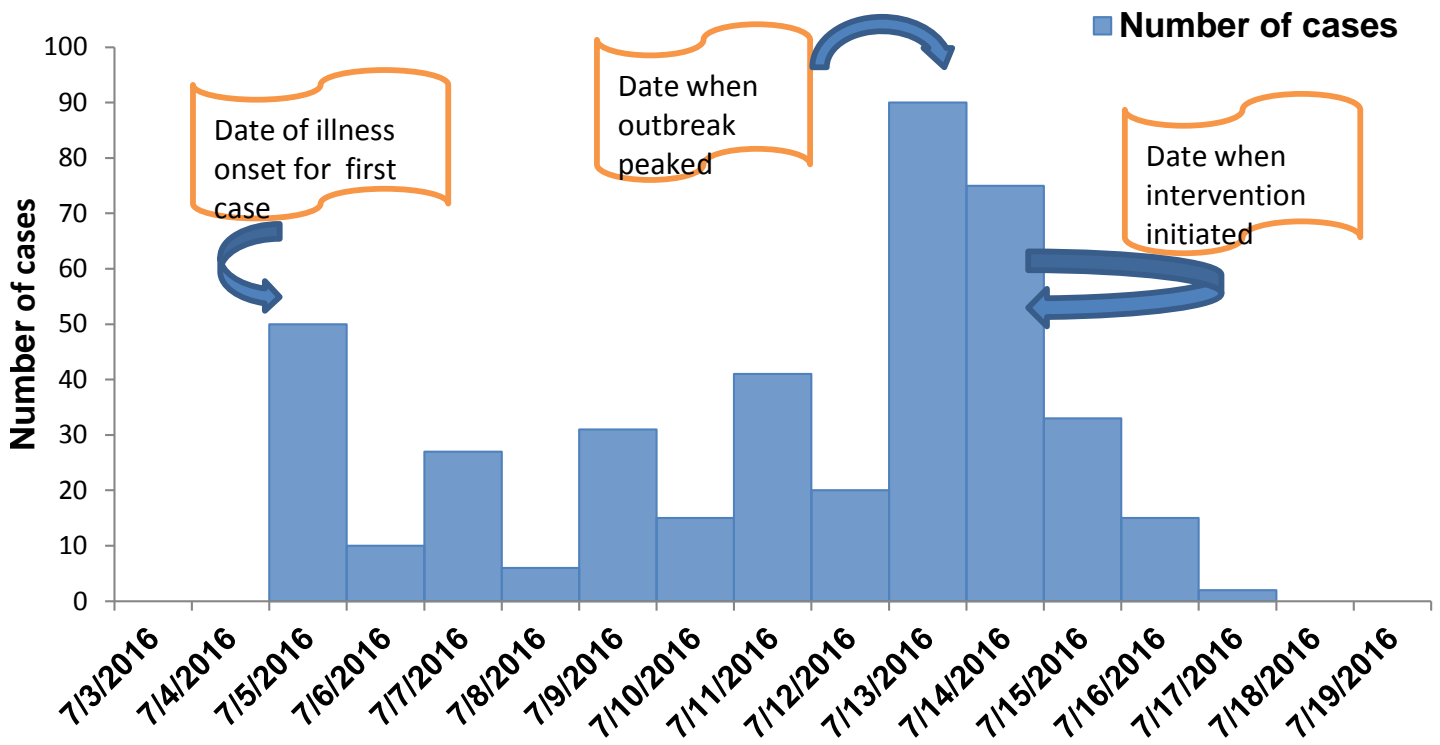


Figure 2. Epi-Curve showing Confirmed Malaria cases by date of onset in Amibera district, Afar-Ethiopia, 5-17 July 2016.

Table 7. Bivariate and multi-variate analysis of predictor variables related to malaria outbreak in Amibera district, Afar-Ethiopia, July 5-17, 2016.

Characteristic		Cases (n=117)	Control (n=117)	COR(95% CI)	AOR(95% CI)	P-value
Not using insecticide treated bed nets (every night)	Yes	81	37	5.00 (2.77,5.25)*	3.52 (3.33,4.12)**	0.002
	No	34	80	1		
Presence of stagnant water	Yes	99	83	2.25 (2.16,3.45)*	3.40(1.67,7.30)**	0.01
	No	18	34	1		
Sleeping outside of their home during the night	Yes	90	67	2.48.(1.96,2.64)*	2.16 (1.64, 7.28)**	0.002
	No	17	50	1		
Absence of chemical indoor residual spray	Yes	103	57	7.74 (3.84,8.42)*	3.16 (2.34, 5.28)**	0.003
	No	14	60	1		

*Significant at $P < 0.05$ bivariate analysis, ** Significant at $P < 0.05$ multivariate analysis, 1= Reference group.

travel almost 15 km by foot or bicycle to communicate with the health district. There were no epidemic management funds available in the country prior to the occurrence of the epidemic. No chemical was available in all the health districts that we visited. The public health surveillance system is run by one person in Amibera health facility. The system was not evaluated prior to the occurrence of the epidemic.

Risk factor analysis

In order to assess associated factors, 117 malaria case-patients and 117 community control were selected conveniently and interviewed from Werer and Badhamo village of the Amibera district. Of 117 case-patients and 117 controls, 87(73.2%) and 73(62.4%) were females for case-patients and controls respectively. The multivariable binary logistic regression analysis showed that, persons not using insecticide treated bed nets (every night) were 3.52 times more likely to be exposed to malaria parasite than those who use insecticide treated bed nets (every night) with (AOR=3.52 (3.33, 4.12) (Table 7).

In addition, persons who live in an area where there is stagnant water were 3.4 times more likely to be exposed to malaria parasite than those who do not live in an area with stagnant water (AOR=3.40(1.67,7.30). Moreover, sleeping outside at nights and absence of chemical indoor residual spray were risk factors for the occurrence of the outbreak and statistically significant with an AOR of 2.16 (1.64-7.28), 3.16 (2.34, 5.28) respectively (Table 7).

Environmental assessment

Thirty-three households from each affected village were arbitrarily selected and visited to search for new malaria cases and observe the status of insecticide treated bed nets utilization during night time. All households had at

least one insecticide treated bed nets in their house, but, only 36.3% (12) of the households hanged it in their ceiling directly to the bedding while the rest were put underneath the beds and other places in the house. However, 17/33(51%) of the places visited, household nets were damaged. About 14/33(42%) do not use their nets at all while of those who reportedly use their nets, about 23/33(69.6%) use their nets irregularly.

Public health interventions

A total of 137 (7%) households with 106 unit structures was sprayed with Propoxur and Bendiocarb chemical in Werer village. Abate chemical was sprayed as anti-larval on stagnant water with an estimated area of 46 m². A total of 18 volunteered people participated in this activity. Communities were mobilized and taught on prevention and control measures of malaria disease. Health professionals were mobilized and assigned to the affected village for active case search and early case management in the community.

These case-control studies confirmed existence of malaria outbreaks based upon believable five years of the 2nd largest number as a threshold to compare with 2016 on a weekly basis including laboratory diagnosed malaria data.

Malaria outbreak appreciated at the end of the week of June/2016 when it started to cross the threshold. The health facility had weekly malaria outbreak monitoring chart for early detection of an outbreak, but they were not reported to the district health office when the number of cases crossed the threshold. It was an exaggerated seasonal increase precipitated by interruption of vector control intervention. There were multiple potential mosquitoes breeding sites difficult for environmental management (Shalako Rivers) which surrounds the affected village and maybe the probable source of the outbreak.

Malaria outbreak in affected village was related to the national outbreak scenario; actually the outbreak occurred at different period depending on the weather condition of the region, but overall it is believed to have started in April, and lasted until the end of December. Many region of Ethiopia began reporting an abnormally increased number of malaria cases (Alemu, 2015; AMREF, 2008).

This study revealed that, the high proportion of *Plasmodium falciparum* cases shows difference as compared to the nationally registered proportion of *Plasmodium falciparum* and *P. vivax* which is 60 and 40%, respectively (Daddi and Abebe, 2012). This variation may be linked to high sensitivity of the malaria rapid diagnostic test. Since clients who get cured from malaria have also the chance to be positive for malaria if tested by the RDT within 14 days of treatment; this may increase the positivity rate falsely when clients visit health facility within 14 days of treatment. This is consistency with the case-study report from Oromia region (Alemu, 2015; AMREF, 2008).

In this study, the malaria outbreak lasted for two weeks (July 5-17/ 2016) due to inadequate vector control intervention in affected village. Heavy rain fall in affected village in mid-June was significantly attributed to the stagnant water bodies, and unusual temperature in affected village may also favore mosquito breeding site which is consistency with literature (Tarekegn, 2013).

Moreover, Amibera District is a place where agro-industry is under way both by private and government organization. Many unknown number of migrants come to work from different parts of the country; a lot of quarry works holding water bodies are suitable for mosquito breeding.

The results of analytical epidemiological study showed that, unusual heavy rainfall followed by high temperature is considered as one of the confirmed causes of malaria outbreak which agrees with the study from northeastern Ethiopia (Alemu, 2015; AMREF, 2008, 2011)

Besides this, using of bed net every night is associated with malaria parasite exposure and absence of timely chemical indoor residual spraying was associated with higher risk of febrile illness which is consistency with the study from Amhara Regional States (Workineh et al., 2015).

In addition, Stagnant water surrounding affected village and their compound was one of the dominant risk factor for malaria outbreak, which is consistent with previous reports in the literature (Alemu, 2015; AMREF, 2008; WHO, 2015); and study from Sri Lanka and India indicated that people living closer to vector breeding sites were at higher risk for malaria parasite exposure than those living farther away (Kiszewski and Teklehaimanot 2014).

This outbreak scenario has clearly showed that, in order to prevent and control malaria infection the sustainable implementation of vector control intervention through well organized malaria related strategies and programmes is crucial. Inter-sectoral collaboration and

close monitoring and evaluation of the vector control interventions are prerequisites for malaria control and elimination.

Limitation of the study

Mosquito breeding sites were visited in the village but observation of mosquito larva was not conducted due to lack of expert.

Conclusion

The malaria outbreak current situation is high in magnitude than three years ago. Inability to analyze and interpret the surveillance data at the district level delayed the outbreak investigation. This late notification of the outbreak shows that there is weak monitoring of malaria trends at district. This study revealed that, the attack rate was highest among above 15 years age groups (63.7 per 1000 of population) compared to the other age groups with sex difference. Sleeping outside of their homes during night, presence of stagnant water, absence of chemical indoor residual spray and poor utilization of insecticide treated bed net were attributed for this outbreak.

RECOMMENDATIONS

To prevent subsequent malaria outbreaks in the village it is recommended that Afar regional health bureau, Amibera district health office, District health facility and other sectors be interested in malaria prevention:

1. Since most of the village of the district are malarious area, insecticide treated bed net should be distributed for all households and utilization of bed net should be monitored and optimized.
2. Timely indoor residual spraying operations have to be planned as per required standard (twice per year) and applied before rainy season with appropriate chemical.
3. Trends of malaria cases should be monitored on weekly basis at all levels. This could help for early detection of malaria outbreak.
4. Community mobilization on disruption of potential mosquitoes breeding site.
5. It needs further study to evaluate validity and reliability of rapid diagnostic tests to avoid false positivity rate

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Genotypic variation, demographic characteristics and risk factors of hepatitis C virus in Scotland

Iveren Winifred Nyinoh

Department of Biological Sciences, Benue State University, 970001, Makurdi, Benue State, Nigeria.

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Knowledge on the epidemiology of hepatitis C virus (HCV) has implicit significance for the diagnosis, duration and treatment response of infected patients, as some genotypes are more responsive to therapy than others. In this paper, an examination of the possible association of hepatitis C virus (HCV) genotypes with demographic and risk factors for transmission was described. The study utilized routinely collected data of all persons diagnosed with HCV in Scotland and multivariate logistic regression was used to analyze genetic variability. The genotype variation was roughly distributed among genotypes 1 (45.6%) and 3 (47.9%), though genotype 2 (5.6%) and 'other' genotypes (0.89%) were also present. Furthermore, age less than 34 years, year of diagnosis between 2004 and 2008, Greater Glasgow and Clyde, Grampian, Lanarkshire and Lothian Health boards were sufficient to predict HCV status in Scotland, with Injecting Drug Use (IDU) behaviour being the most prevalent risk factor. These results will assist in the management of HCV infection in Scotland.

Key words: Epidemiology, genotypes, hepatitis C virus, risk factor, Scotland.

INTRODUCTION

Hepatitis C Virus (HCV) is a notable public health challenge. Globally, the prevalence rate is reported to be 2 to 3%, with 3-4 million newly infected cases worldwide, and an estimated 130 - 150 million individuals are infected with chronic HCV (Averhoff et al., 2012; Perz et al., 2006; WHO, 2015). The virus belongs to the family of single-stranded RNA viruses of the *Flaviviridae* family and is the sole member of the *Hepacivirus* genus (Ansaldi et al., 2014; Smith et al., 2016). At least, seven genotypes (1 to 7) and roughly 84 subtypes (Smith et al., 2014) have been identified. Individuals infected with HCV virus at the acute phase have no

obvious symptoms and 15 to 20% spontaneously recover. Nonetheless, nearly 65 to 80% of infected individuals become chronically infected with the possibility of developing acute liver diseases like cirrhosis and hepatocellular carcinoma (HCC) (Davis and Lau, 1997; Lauer and Walker 2001; Seeff, 2002; Jauncey et al., 2004). HCV is the prime cause of hepatic transplantation in liver failure patients in the USA and several Western nations (Bhamidimarri et al., 2017), accounting for 700 000 mortalities per annum, resulting from decompensated cirrhosis or hepatocellular carcinoma (Kanwal et al., 2011; Beste et al., 2015;

*Corresponding author. E-mail: inyinoh@bsum.edu.ng.

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Benvegnù et al., 2004).

The burden of infection of HCV in the West is established to differ across regions and nations, and is predominantly acquired through serologic surveys from the populace (Averhoff et al., 2012). The highest rate of HCV infection worldwide is in Egypt, estimated at >10%. Similarly, in the United States, like in Australia and other Western European countries, the burden is less, (<2%) (Alter, 2007; Sievert et al., 2011). On the contrary, in Eastern European countries, Latin America, former Soviet Union, certain African countries, Middle East and South Asia, the infection rates are ≥3% (Kerшенobich et al., 2011; Qureshi et al., 2010; Madhava et al., 2002; Shepherd et al., 2005).

In advanced countries, injecting drug use (IDU) accounts for the majority of HCV infections (Alter, 2007; Williams et al., 2011). In less developed countries, although IDU is also known to transmit HCV, healthcare-associated practices such as unsafe injections account for the majority of HCV transmission (Alter, 2007; Hauri et al., 2004; Prati, 2006). Across the globe, China tops the countries with the highest numbers of estimated HCV associated IDU infections (Nelson et al., 2011), greater than all of Europe or America (Sievert et al., 2011), while in Western European countries such as Scotland, the high occurrence of IDUs, account for the high proportion of individuals living with HCV in the country. Accordingly, 85 to 90% of all individuals that tested positive to HCV in Scotland have injected drugs (Hutchinson et al., 2006). As at 2006, an estimated one percent of the Scottish population (50 000 persons) were known to be infected (Hutchinson et al., 2006; Roy et al., 2007), whereas it is at least 200 000 cases in UK from 1986 to 2001 (Balogun et al., 2009).

Besides collecting epidemiological information, HCV genotyping and serotyping have clinical implications, and viral genotypes have been identified to predict therapeutic response to antiviral therapy assessed as the level at which HCV RNA is undetected following 24 weeks of treatment (Toyoda et al., 2017; Yee et al., 2015). In addition, the length of time to treat for, and the choice of antiviral agents to initiate are also dependent on genotype (Josephson F, Swedish Consensus Group 2016, Lagging et al., 2001; Yasin et al., 2011). Therefore, the knowledge on HCV infecting genotype is essential in tailoring treatment regimen. The aim of this study was to examine possible associations of hepatitis C virus genotypes with demographic characteristics and risk factors (for transmission) of any individual diagnosed with hepatitis C in Scotland.

MATERIALS AND METHODS

Epidemiological and demographic data of all diagnosed population of HCV in Scotland were electronically obtained and collected from the database of Health Protection Scotland (HPS). Data stored on the National Hepatitis C Diagnoses database is

expected to be representative of the study population taking into account, the fact that all the health board areas in Scotland are represented. The database was established in affiliation with microbiological laboratories and hospitals across Scotland (Shaw et al., 2003). From the information held on the database, only the genotypes, age group, gender, health board of residence, risk information, year of diagnosis and vital status were extracted for statistical analysis in this study. Information stored in the database has already been anonymised to ensure patient confidentiality and ethical approval for this study was obtained from the University of Glasgow Ethics Committee.

Transformation of the data prior to statistical analysis

In order to arrive at groups of sufficient size for the purpose of statistical analysis, additional groups were either created from the dataset or existing variables were collapsed. For instance, genotypes 4 and 5 were regrouped as 'others' while those patients for which genotyping was not carried out were classified as not known. Data on health board area of residence was reordered representing the geographical regions in Scotland such that the North was composed of Highland, Western Isles, Orkney and Shetland; the South was composed of Dumfries and Galloway, Borders, Ayrshire and Arran; and Central Scotland was now made up of Forth valley and Fife. Information on risk factor was broken down into injecting drug use, blood products (comprising of blood haemophiliacs and blood transfusion), and not known (NK) consisting of information from unconfirmed sources such as transmission sexually by contact with an IDU or a partner infected with HCV, tattoo/body piercing, needle stick, bite, blood spillage and perinatal risk. Individuals whose area of residence were not known, the health board area from where the individual's specimen was obtained was recorded and this occurred especially for prison convicts. A matching process was used in identification via the use of forename initial, Soundex code of surname, date of birth and gender in order to prevent duplication of records.

Statistical analysis

All analysis for this study was carried out using SPSS for Windows XP. Summary measures were utilized to describe the characteristics of the study population. Since the data are categorical, Pearson chi-square (χ^2) test was used to test for association between genotype and all the other factors listed, with the significance level set at $P < 0.05$. Clustered bar charts were used to show the pictorial representation of the main response variable and other explanatory variables. Furthermore, a multivariate analysis using binary stepwise logistic regression in SPSS was carried out in order to compare HCV genotypes in HCV diagnosed individuals in Scotland by covariates. The multivariate analysis was carried out using a backward stepwise method.

RESULTS

A total of 24419 records were held on the National Hepatitis C Diagnoses Database as at June 30, 2008. Of the HCV diagnosed population held on the National Hepatitis C Diagnoses Database, 73.6% had no information on genotype and were excluded from all the analyses performed. The characteristics of the study population according to genotype are shown in

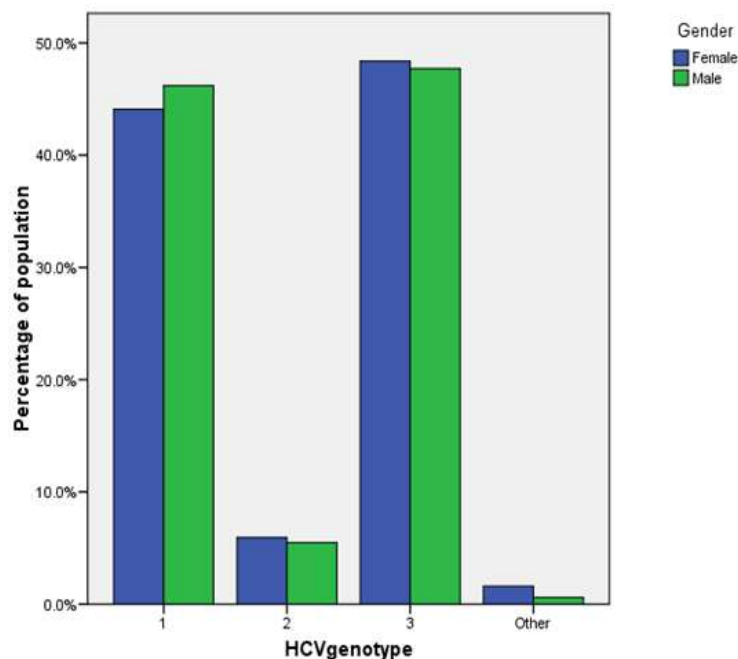


Figure 1. Bar chart showing the distribution of HCV diagnosed population by gender and HCV genotype.

Supplementary Table 1.

Results obtained indicate that in the study population, the genotype is roughly distributed equally into genotypes 1 and 3 (Figure 1). By gender, 44.1% of females with a known genotype were genotype 1, in comparison with 46.2% among males. For genotype 2, 5.9% were females in comparison with 5.5% males. In addition, 47.9% had a genotype of 3; 48.4% of that were females and 47.7% were males. For the 'other' category, there were 0.9% cases of which 1.6% were females and 0.6% males. Figure 1 shows the distribution of gender and HCV genotype. Pearson χ^2 test comparing these distributions found a statistically significant difference between males and females diagnosed with hepatitis C based on genotype alone ($\chi^2 = 16.198$, $P < 0.001$).

Next, the distribution of HCV diagnosed population by age group and reported risk information was evaluated. As shown in Figure 2, the 25-34 age group had a greater number of HCV diagnosed cases (42.7%), followed by the 35-59 (34.0%) and the 15-24 age groups (18.2%). The age groups with the least number of cases were the 60+ age group (3.3%) and the <15 age group (0.5%). Furthermore, 1.4% of cases had no known age group and was excluded from analyses. The number of injectors in the 25-34 groups was almost twice as much as that found in the other groups and Pearson χ^2 found a highly statistically significant difference ($\chi^2 = 3132.375$, $P < 0.001$).

Data also revealed that the reported risk information for HCV were: IDU (59.0%), blood products (2.9%),

not known (33.8%) and 'others' (4.4%) (Figure 3). A high proportion of genotype 1 (58.0%) was found among blood products (which comprise of haemophiliacs and blood transfusions) followed by 32.4% of genotype 3, 7.1% of genotype 2 and 6.0% of 'others' modes of transmission. This distribution was found to differ from the other reported risk information all of which were similar to the distribution of the other genotypes. 48.7% of the diagnosed HCV positive individuals that have ever injected drugs were infected with genotype 3, when compared with 46.1% infected with genotype 1. For the 'other' group, genotype 3 was more prevalent, 51.7% in comparison with 38.0% of genotype 1. Pearson χ^2 test was also found to be significant ($\chi^2 = 82.379$, $P < 0.001$).

An assessment of infecting HCV genotype by year of diagnosis was also performed. Data revealed that for genotype 1, the percentage of diagnosed cases fluctuated by year of diagnosis, though there was a steady increase in the diagnoses made for all the other genotypes. Of the diagnosed cases that had a genotype test, 50.2% of genotype 1 were identified in the period between 1994 and 1998, whereas there were more cases of genotype 2, 8.5% before 1994. Diagnoses for the most prevalent genotype 3 were between 2004 and 2008 (51.0%) (Figure 4). Pearson χ^2 carried out was significant ($\chi^2 = 45.115$, $P < 0.001$).

The question, what percentage of the diagnosed HCV population is dead? was asked. This was categorised by vital status. As indicated in Figure 5, the numbers of HCV diagnosed individuals who are not dead were 86.3%, and

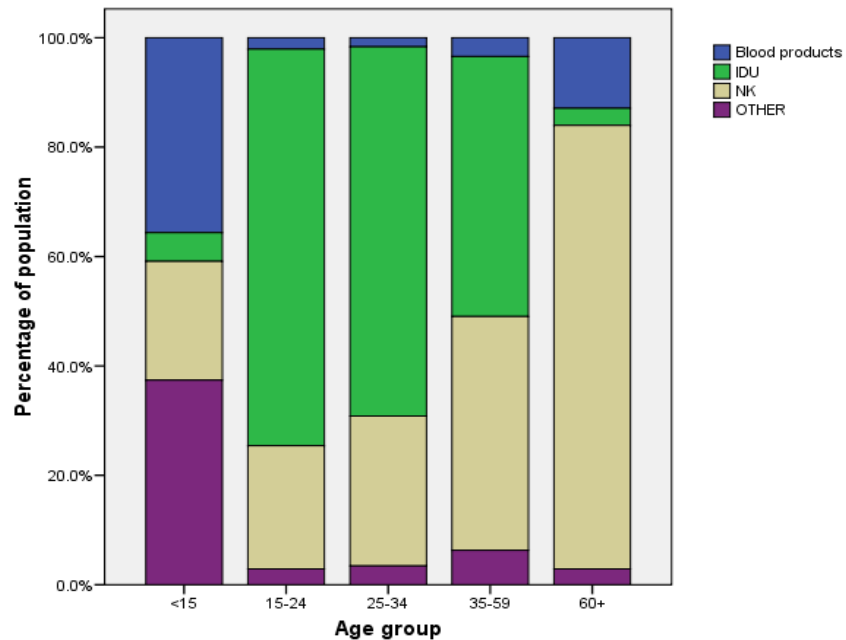


Figure 2. Bar chart showing the distribution of HCV diagnosed population by age group and reported risk information.

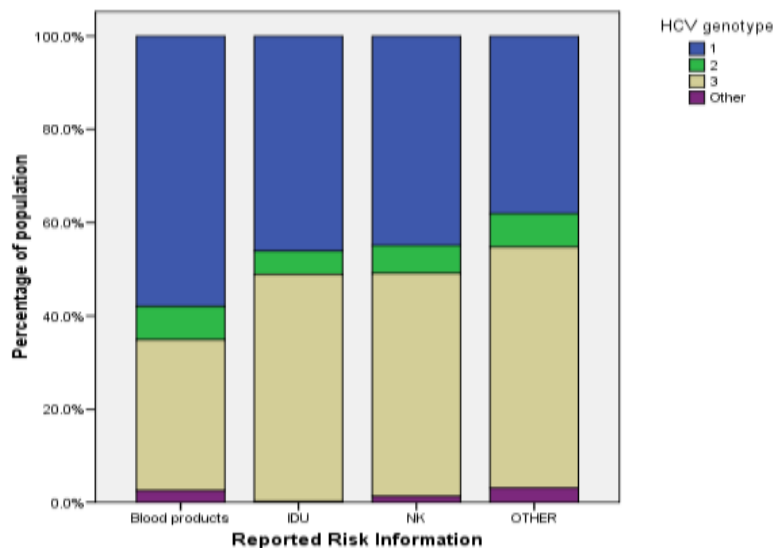


Figure 3. Bar chart showing the distribution of HCV diagnosed population by reported risk information and HCV genotype.

far outnumber those who are known to be dead (13.3%).

A logistic regression model was set up to identify parameters that are independently associated with HCV genotype. The results for the binary logistic regression model are displayed (Table 1). From the univariate analysis, all the factors were significantly associated with genotype and were therefore included in the model while in the multivariate analysis, gender,

age group and vital status did not contribute significantly to the model and were therefore excluded.

Further results identified that in the univariate analysis, women were more likely to be diagnosed with HCV genotypes 2 and 3 than men (odds ratio-OR: 1.232, 95% CI 1.122-1.352, $P < 0.001$). Furthermore, infecting genotype was not influenced by sex, thus $P > 0.05$ for both males and females. Patients in the 25-34

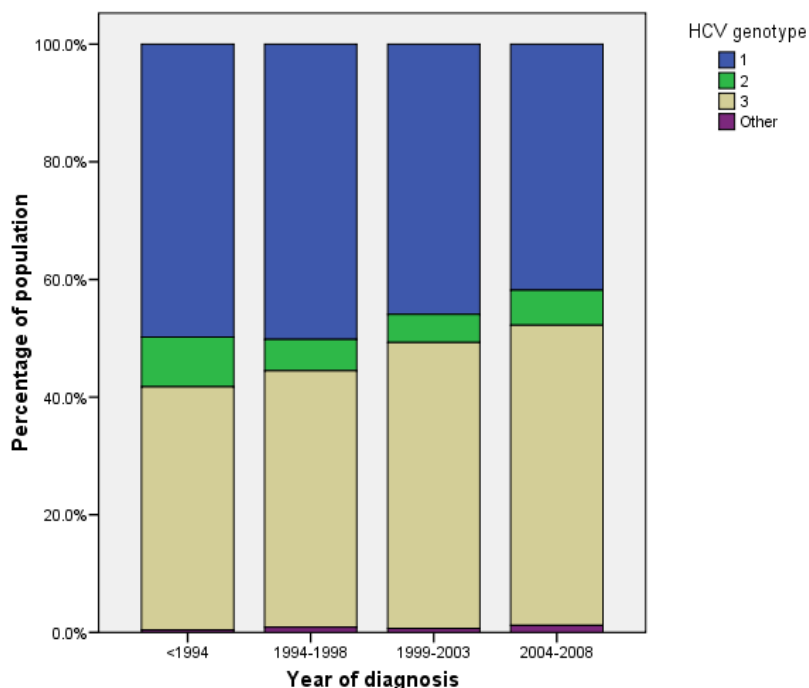


Figure 4. Bar chart showing the distribution of HCV diagnosed population by year of diagnosis and HCV genotype.

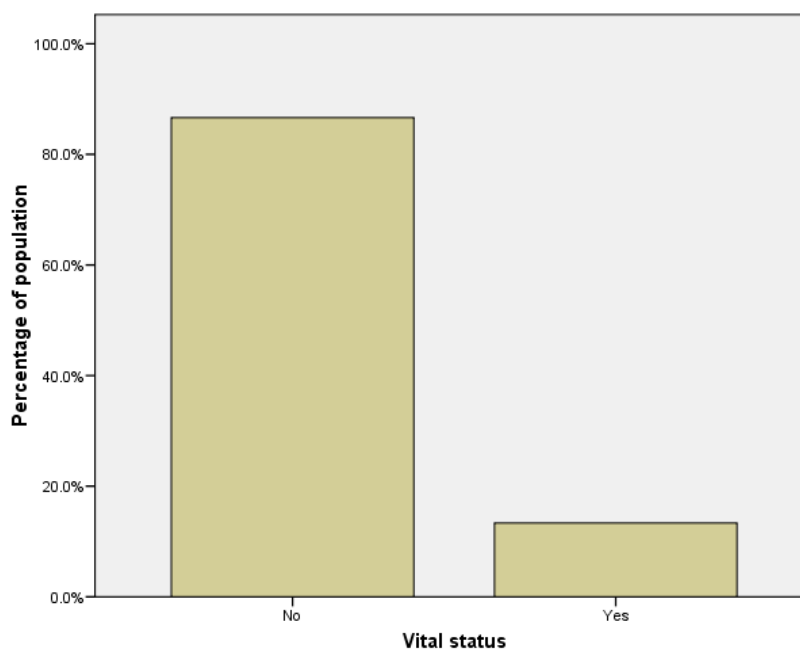


Figure 5. Bar chart showing the distribution of HCV diagnosed cases by vital status.

years age group (unadjusted OR: 1.194, 95% CI 1.031-1.382, $P=0.018$) and the 35-59 years age group (unadjusted OR: 1.162, 95% CI 1.005-1.343, $P=0.043$) exhibited a high and statistically significant risk of been diagnosed with HCV 2 and 3 rather than genotype 1 in

relation to the <15 and >60 age groups, whereas individuals in the greater than 60 years age group were less likely to be diagnosed with genotype 1 as compared to genotypes 2 and 3, and this result was not statistically significant (OR: 1.296, 95%CI 0.904-1.858,

Table 1. Results of logistic regression analysis with genotypes 1 vs. genotypes 2 and 3 as dependent variables.

Factor	Study population	Unadjusted odds ratio	95% confidence interval	P-value	Adjusted odds ratio	95% confidence interval	P-value
Sex	Male	1 (Baseline)					
	Female	1.232	1.122-1.352	<0.001			
Age group at diagnosis	<24	1 (Baseline)		0.097			
	25-34	1.194	1.031-1.382	0.018			
	35-59	1.162	1.005-1.343	0.043			
	60+	1.296	0.904-1.858	0.158			
Health board area	Greater Glasgow & Clyde	1 (Baseline)		<0.001	1 (Baseline)	0.456-0.667	<0.001
	Grampian	0.565	0.467-0.683	<0.001	0.552	1.131-1.667	<0.001
	Lanarkshire	1.378	1.136-1.671	0.001	1.373		0.001
	Lothian	0.748	0.640-0.875	<0.001	0.734	0.628-0.858	<0.001
	Tayside	1.000	0.773-1.295	0.998	1.030	0.791-1.341	0.828
	Rest of Scotland	1.141	1.005-1.297	0.042	1.127	0.991-1.283	0.069
Reported risk information	IDU	1 (Baseline)		<0.001	1 (Baseline)		<0.001
	Blood products	0.681	0.524-0.885	0.004	0.584	0.444-0.769	<0.001
	NK	1.198	1.107-1.297	<0.001	0.970	0.869-1.083	0.589
	Other	1.547	1.258-1.903	<0.001	1.274	1.021-1.589	0.032
Vital status	No	1 (Baseline)					
	Yes	1.220	1.005-1.481	0.044			
Year of diagnosis	<1994	1 (Baseline)		<0.001	1 (Baseline)		<0.001
	1994-1998	0.975	0.873-1.089	0.114	0.881	0.752-1.031	0.114
	1999-2003	1.162	1.072-1.260	0.452	1.054	0.920-1.207	0.452
	2004-2008	1.363	1.254-1.480	0.002	1.255	1.085-1.451	0.002

Results are considered as statistically significant at 5% level.

$P=0.158$).

All the health boards of residence posed a great risk of acquiring HCV. However patients residing in the Grampian HB had a lower odds of been diagnosed with genotype 1 than genotypes 2 and 3 (unadjusted OR: 0.565, 95% CI 0.467-0.683, $P<0.001$; Adjusted OR: 0.552, 0.456-0.667, $P<0.001$). There are higher odds and a statistically significant association between genotypes 2 and 3 and patients residing in Lanarkshire (unadjusted OR: 1.378, 95%CI 1.136-1.671, $P<0.001$; Adjusted OR: 1.373, 95%CI 1.131-1.667, $P<0.001$), while there is a significant association between genotype 1 and patients residing in Lothian (unadjusted OR: 0.748, 95%, CI 0.640-0.875, $P<0.001$; adjusted OR: 0.734, 95% CI 0.628-0.858, $P<0.001$). In Tayside, there was no statistically significant association and patients were more likely to be infected with genotypes 2 and 3 than 1 (unadjusted OR: 1.000, 95% CI 0.773-1.295; adjusted OR 1.030, 95% CI 0.791 -1.341, P value = 0.828). There were increased odds for patients residing in the rest of Scotland to be diagnosed with genotypes 2 and 3 than 1. This result was statistically significant in the univariate analysis (unadjusted OR: 1.141, 95%CI

1.005-1.297, $P=0.042$) but was not significant when adjusted for confounders in the multivariate analysis (adjusted OR: 1.127, 95% CI 0.991-1.283, $P=0.069$).

Both IDU and blood products carried a significant risk of anti-positive HCV status in the population. However, the lowest odds was found among the blood products and there was a significant association for patients who reported blood products as risk information and genotype 1 (unadjusted OR: 0.681, 95% CI 0.524-0.885, $P=0.004$; Adjusted OR: 0.584, 95% CI 0.444-0.769, $P<0.001$). Patients whose risk information was not known were significantly more likely to be infected with genotypes 2 and 3 than genotype 1 (unadjusted OR: 1.198, 95% CI 1.107-1.297, $P<0.001$), whereas in the multivariate analysis, the result was not statistically significant (adjusted OR: 0.970, 95% CI 0.869-1.083, $P=0.589$). There was however increased odds of been infected with genotypes 2 and 3 in patients who belonged to the 'other' risk category (unadjusted OR: 1.547, 95%CI 1.258-1.903, $P <0.001$; adjusted OR: 1.274, 95% CI 1.021-1.589, $P= 0.032$). Patients who were known to be dead were significantly more likely to have been diagnosed with genotypes 1

than 2 and 3 (unadjusted OR: 1.220, 95% CI 1.005-1.481, $P=0.044$). There was a statistically significant association for patients diagnosed with HCV between 2004 and 2008, to be infected with genotypes 2 and 3 than genotype 1 (unadjusted OR: 1.363, 95%CI 1.254-1.480, $P=0.002$; adjusted OR: 1.255, 95% CI 1.085-1.451, $P=0.002$).

These factors, age less than 34, IDU behaviour and blood products, year of diagnosis 2004- 2008 and the Greater Glasgow and Clyde, Grampian, Lanarkshire and Lothian health boards were sufficient to predict HCV status.

DISCUSSION

In this report, the description of the epidemiology of HCV in Scotland with respect to demographic characteristics and risk factors was carried out. The results obtained showed the most prevalent HCV genotypes as 1 and 3, and this distribution is found to be similar to what is obtained in Europe (Messina et al., 2015; Petruzzello et al., 2016). Data obtained from the Scottish population also revealed a complete absence of genotype 6, which was not surprising as this genotype is restricted to South China and Southeast Asia (Thong et al., 2014; Bunchorntavakul et al., 2013). However, genotype 6 has been identified to have a very low prevalence (0.1%) in Central and Western Europe (Petruzzello et al., 2016).

The percentage of HCV diagnosed males in the Scottish population is twice as much as that for females (Supplementary Table 1) but from the general population, it appears that there are more females to males. This difference could be as a result of more males indulging in risky behaviours like IDU that are known to transmit HCV. Correspondingly, of the participants that were found to attend the Needle Exchange Surveillance Initiative in 2007, less than 25% were females (HPS, UWS, 2008). Recent reports from 2008 to 2010 also suggest that only 28% of females attended the Needle Exchange Surveillance Initiative (HPS, UWS, 2012).

Similarly, although the distribution of HCV genotype is roughly equal among gender, females had a higher proportion (1.6%) of the 'others' genotype in comparison with males. However, this group has been found to be prevalent in the Middle East and Africa, especially, in Egypt; however, there is evidence of spread to several European countries possibly due to the transit of persons from endemic regions and also the movement of injectors (Nguyen and Keeffe 2005; Kamal and Naseer, 2008).

The distribution of HCV genotypes varies with the age of individuals in the Scottish population. HCV genotype 3 was predominant in young people <34. The strong association of genotype 3 infections with IDU was found in the population. This may be the reason for the age

dependence considering the fact that IDU is common amongst young adults. The increased prevalence of HCV genotype 3 in IDU has been reported from various countries (Wiessing et al., 2014; Salemovic et al., 2017; Ücbilek et al., 2016) and this is expected, as Scotland is one of the countries in Western Europe that are battling a drug problem.

Most historical infection of HCV infection in the UK was attributed to blood products. Thus genotype 1 particularly, subtype 1a, is found to be associated with hemophiliacs and receipt of blood transfusion (Watson et al., 1996; Harris et al., 1999). Apparently, IDU is the major source of acquiring HCV in the United Kingdom with an increased likelihood of transmission through sharing of injecting paraphernalia (Balogun et al., 2003; Palmateer et al., 2014). Tattooing has also been revealed to increase the chances of acquiring HCV and this is more frequent in the community (Carney et al., 2013; Tohme and Holmberg, 2012). Genotype 1 accounted for 58.0% in the blood products category and this coincides with 53.7% in the 15 years age group where blood products alone accounted for 35.7%. All these occurred in the 1994 diagnosis when Scotland had not introduced the treatment of clotting factor by heat for hemophiliacs, as such, many patients with clotting disorder were at increased risk of contracting HCV (Lowe 1987). Furthermore, it is possible that such people have transfused blood or blood products abroad (Patel et al., 2006). There was a significant decrease in the percentage of people contracting HCV by blood products from 19.8% in 1994 to 1.1% in 2004-2008. This suggests therefore that genotype 1 is more likely associated with blood products in the Scottish population than any other genotypes. The association between HCV and blood transfusion is likely to diminish with time due to a decreasing number of patients who received transfusion before blood screening and improved diagnostic methods. In comparison with the other genotypes, there is evidence to suggest that genotype 1 is correlated with a higher level of cirrhosis or chronic active hepatitis and this is particularly worrying because a large proportion of this genotype was seen among Scottish HCV diagnosed population (Harris et al., 2007; Dusheiko et al., 1994). Multivariate analysis revealed a statistically significant risk related to blood transfusion.

Treatment of patients who are chronically infected together with the rollover of preventive programs will assist in the reduction of HCV infection. It is thus essential to continually monitor the genotype distribution of HCV in order to identify drug-resistant genotypes and risk factors for transmission.

CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

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Supplementary Table 1. Characteristics of the study population in relation to genotype.

Characteristic	Genotype 1	Genotype 2 vs. 3	Other	Total (N)
Gender				
Female	802 (44.1%)	988 (54.3%)	29 (1.6%)	1819
Male	2128 (46.2%)	2450 (53.2%)	28 (0.6%)	4606
NK				11
Total	2930 (45.6%)	3438 (53.5%)	57 (0.9%)	6436 (100%)
Age group at diagnosis				
<15	22 (53.7%)	19 (46.4%)	0 (0.0%)	41
15-24	475 (49.2%)	488 (50.5%)	3 (0.3%)	966
25-34	1139 (44.9%)	1387 (54.6%)	11 (0.4%)	2537
35-59	1236 (45.2%)	1465 (53.6%)	32 (1.2%)	2733
>60	59 (39.9%)	78 (52.7%)	11 (7.4%)	148
NK				11
Total	2931 (45.6%)	3437 (53.5%)	57 (0.9%)	6436 (100%)
Health board area				
Central	194 (35.3%)	352 (64.2%)	3 (0.5%)	549
Grampian	312 (58.8%)	213 (40.1%)	6 (1.1%)	531
Greater Glasgow & Clyde	1267 (44.9%)	1531 (54.2%)	23 (0.8%)	2821
Lanarkshire	194 (37.3%)	323 (62.1%)	3 (0.6%)	520
Lothian	429 (51.7%)	388 (46.7%)	13 (1.6%)	830
North	110 (40.7%)	156 (57.8%)	4 (1.5%)	270
South	313 (47.6%)	343 (52.2%)	2 (0.3%)	658
Tayside	115 (44.7%)	139 (54.1%)	3 (1.2%)	257
Total	2934 (45.6%)	3445 (53.5%)	57 (0.9%)	6436 (100%)
Risk activity				
Blood products	138 (58.0%)	94 (39.5%)	6 (2.5%)	238
IDU	1529 (46.1%)	1781 (53.7%)	7 (0.2%)	3317
Other	148 (38.0%)	229 (58.9%)	12 (3.1%)	389
NK	1119 (44.9%)	1341 (53.8%)	32 (1.3%)	2492
Total	2934 (45.6%)	3445 (53.5%)	57 (0.9%)	6436 (100%)
Vital status				
No	2740 (45.7%)	3206 (53.5%)	51 (0.9%)	5997
Yes	186 (44.5%)	227 (54.3%)	5 (1.2%)	418
NK				21
Total	2926 (45.6%)	3433 (53.5%)	56 (0.9%)	6436 (100%)
Year of diagnosis				
<1994	241 (49.8%)	241 (49.8%)	2 (0.4%)	484
1994-1998	639 (50.2%)	623 (48.9%)	11 (0.9%)	1273
1999-2003	1086 (45.9%)	1262 (53.4%)	16 (0.7%)	2364
2004-2008	968 (41.8%)	1319 (57.0%)	28 (1.2%)	2315
Total	2934 (45.6%)	3445 (53.5%)	57 (0.9%)	6436 (100.0%)
Total				24419 (100%)

Full Length Research Paper

Prevalence and associated factors of undernutrition among school adolescents in Gobu Seyo District, East Wollega Zone, Oromia regional state of West Ethiopia, 2016

Kassahun Tegegne Bidu^{1*}, Tsedeke Wolde Hailemariam², Elias Legesse Negeri³ and Zalalem Kaba Babure⁴

¹Program Officer at USAID/JSI Transform, Primary Health Care Project, East Wollega Zone, Nekemte, Western Ethiopia.

²Population and Family Health Department, College of Public Health and Medical Sciences, Jimma University, P. O. Box 378, Jimma, Ethiopia.

³Department of Public Health, College of Medical and Health Sciences, Wollega University, P. O. Box 395, Nekemte, Ethiopia.

⁴East Wollega Zonal Health Department, Nekemte, Ethiopia.

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Adolescence is the transitional period between childhood and adulthood. During this, nutrient needs are greatest. There is so little data on adolescents' nutrition and research needs are immense. The objective of the study was to assess prevalence and associated factors of undernutrition in school adolescents aged 10 to 19 years. A cross-sectional study was conducted at GobuSeyo district in December, 2016. Using multi-stage sampling technique and interviewer administered questionnaire data was collected from 640 adolescents. Statistical package for social science version 20 for data entry and analysis and World health organization Anthroplus for determination of nutritional status of adolescents were used. Multivariable logistic regression analysis was used to identify independent predictors. Prevalence of stunting and underweight composed 17.0 and 18.8% respectively. Adolescents who were stunted and underweight were 22.9%. Severely stunted and underweight adolescents were 1.7 and 2.8% respectively. Single predictor of stunting was fathers' occupation (Adjusted odds ratio-AOR- 5.82; 95%; CI-1.15, 29.38). Sex and age of the respondents and fathers' occupation were significant predictors of undernutrition. Thus, adolescent nutrition program focusing on age and sex of adolescents needs to be designed and implemented to address nutritional problem specifically in the study area.

Key words: Adolescents, GobuSeyo, stunting, underweight, undernutrition.

INTRODUCTION

Adolescence is accompanied by dramatic physical, cognitive, social, and emotional changes that present both

opportunities and challenges for adolescents, families, health professionals, educators, and communities.

*Corresponding author. E-mail: kassahuntegegne@yahoo.com. Tel: +251911808112.

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Adolescence is a period of rapid growth: up 20% of final adult height and 50% of adult weight are attained, bone mass increases of 45% and dramatic bone remodeling occur. Soft tissues, organs, and even red blood cell mass increase in size. As a result, nutritional requirements peak during adolescence. Nutrition influences growth and development throughout infancy, childhood and adolescence; it is, however, during the period of adolescence that nutrient needs are the greatest (World Health Organization, 2002; Giuseppina, 2000).

Globally, malnutrition remains the most serious health problem and the single biggest thirty three (33) contributor to child mortality. In developing countries more than 30% of the population suffer from micronutrient deficiencies [Iodine Deficiency Disorder (IDD), Iron Deficiency Anemia (IDA), and Vitamin A Deficiency (VAD)] and almost one-third of children are either underweight or stunted in which the magnitude of the problem will hinder many countries from achieving Millennium Development Goals (MDGs) because problem of malnutrition and food insecurity revolves almost around all components of MDGs (The World Bank, 2006).

Worldwide, some 13 million infants are born each year with low birth weight (LBW) which has direct association with the nutritional status of their mothers before and during pregnancy and aggravated by teen age pregnancy. This problem causes lower intelligence and reduced physical capacity, which in turn reduce productivity, slow economic growth, and perpetuate poverty; and that malnutrition passes from generation to generation because stunted mothers are more likely to have underweight children. About 178 million children around the world are stunted. Of the estimated 178 million, 90% live in 36 countries, one of which is Ethiopia. Thus, if intervention is not taken, the problem goes through adolescence and adulthood (The World Bank, 2006).

Malnutrition continues to be a major public health problem in developing countries including Ethiopia. Ethiopia has witnessed encouraging progress in reducing malnutrition over the past decade. The baseline levels of malnutrition in this country still remain so high and then Ethiopia must continue to make significant investments in nutrition. In Ethiopia, 23% of adolescent girls were stunted while 9% severely stunted and underweight girls were 14% (National Nutrition Programme by Federal Ministry of Health of Ethiopia, June 2013-June 2015).

It has showed that IDA, IDDs, and stunting alone are projected to cost Ethiopia about 10% of Gross Domestic Product (GDP). Also total loss in productivity due to under nutrition for 2009 is estimated at approximately 55.5 billion Ethiopian Birr (ETB), which is equivalent to 16% of Ethiopia's Gross Domestic Product (GDP). World Health Organization (WHO) considers stunting and underweight prevalence rate of over 40 and 30%, respectively as very high and a major public health problem. This indicates that malnutrition remains a huge public health problem in Ethiopia (The World Bank, 2006; Federal Democratic Republic of Ethiopia MOH, 2009).

Study conducted in rural town of Ambo revealed that 27.2% was underweight and 4.4% was overweight (Bisai et al., 2011). Nutritional status of adolescents were studied in Jimma and Tigray, Ethiopia and found that 26.5 and 16.0% was stunted and 58.3 and 80.8% was underweight (Afework 2009; Huruy et al., 2013). These studies indicated that prevalence of underweight among adolescents were higher than that WHO indicator and needs attention for further research.

At present there are so little data on adolescents' nutritional and health status and micronutrient nutrition, eating pattern and underlying influences, and on impacts of nutrition intervention in adolescents that research needs are immense.

There were limited international reference data; the limited data available indicates that their nutritional status is considerably lower in developing than the industrialized world. Often, adolescents' health and nutritional status is a direct reflection of the cumulative efforts of childhood health and nutrition. At the same time, like children, adolescents also have specific and increased nutritional needs due to rapid physical growth and mental maturation.

Current information related to nutrition status for particular age group is needed for variety of purposes such as: identifying chronic nutritional problems and causes; predicting and detecting short term or acute nutritional problems; targeting population groups for both short-term relief efforts and long-term policy and program development; monitoring changes and evaluating the impact of interventions and development programs.

Therefore, the findings of this study were aimed to assess prevalence and associated factors of undernutrition among adolescents in the study area. The finding of the study will also serve as source of information for concerned bodies like planners, policy makers, governmental and nongovernmental organizations that need to know about nutritional status and associated factors among adolescents in the study area. It may also be used as a base line data and information for other researchers who will be interested in conducting a study on this topic. Besides, it is recommended that other investigators should conduct further study by adding more variables and qualitative types of data to assess the prevalence and the predictors of undernutrition among adolescents.

MATERIALS AND METHODS

Study setting and period

The study was conducted in Gobu Seyo District, East Wollega Zone from 1st to 26th December, 2016 among adolescents aged 10 to 19 years in the study area. Gobu Seyo is one of the 17 districts in East Wollega Zone, Oromia Regional State and located 250 km away from the capital city of Ethiopia, Addis Ababa to the West and 65 km from the capital of East Wollega Zone, Nekemte to the East. The main town of the woreda is Anno.

The district is geographically surrounded by: West Showa Zone and GudeyaBila district towards the East, Sibru Sire district towards the West, GudeyaBila district towards the North and BiloBoshe district towards the South. The climatic condition of the district is low land (kola) 78% and midland (WoyinaDega) 22 % with annual temperature of 15 to 31°C.

The district has 9 kebeles (1 urban, 1 semi urban and 7 rural) which is clustered into two clusters for administrative purpose. The total population of the district as projected from 2007/2008 census is about 50,366; from which 24,901 (49.44%) are males, and 25,465 (50.56%) are females. According to data obtained from district health office, there are 9,012 households in the district with different target group (Under one Year infants = 1,613; under five Year children = 6,403; pregnant women = 1,613; non pregnant women = 7,008, and 11,401 adolescents) (GobuSeyoWoreda Health Office, 2013).

Different ethnic group; Oromo, Amhara, Gurage, Tigre... etc live in the district. Different religion followers like Protestant, Orthodox, Muslim, and Wakefata live in the district. There are different government, private and non-governmental organizations and institutions in the district. Gobu Seyo district has two health centers (governmental), 9 health post, and 11 private clinics providing health services for the communities. The district has also different types of organizations, 1 kindergarten (private), 21 primary school (first and second cycle), 1 high school and 1 preparatory school.

Study design

A school based cross-sectional study design was employed.

Source and study population

All in school adolescents aged 10 to 19 years in Gobu Seyo district were the source population while a selected adolescents aged 10 to 19 years were taken as study population.

Inclusion and exclusion criteria

Adolescent students aged 10 to 19 years and from grades 4 to 8 who gave consent available during the study period were included in this study. Adolescent students with physical deformity and disability for anthropometric measurements were excluded from the study. Students from grades 1 to 3 were also excluded from the study because students at this level may not respond correctly to the prepared questionnaire and their age was most probably less than 10 years.

Sample size determination

The sample size of the study was determined using formula for a single population proportion with assumptions of 27.2% prevalence of underweight taken from study conducted in rural town of Ambo (37), 95% confidence level, 5% degree of desired precision or margin of error for sampling, a design effect of 2 due to multistage sampling and 5% for non-response rate. A Z-value of 1.96 was used at 95% confidence interval (CI) and d of 5% (n= sample size, p= prevalence, d= margin of error).

$$n = \frac{Z^2 \left(1 - \frac{\alpha}{2}\right) 2P(1 - P)}{d^2}$$

So with adjustment for non-response (5% contingency) n = (305+15) = 320, and multiplied by design effect 2, the final sample size was 640 adolescents.

Sampling procedures

Two stage cluster sampling technique followed by systematic random sampling was used to select adolescents from schools. From 21 primary schools found in the district, 10 of them are primary first and second cycle (1 - 8th grade). From these five schools was selected by probability proportional to size (PPS). Study participants were allocated to selected schools by proportionate allocation and from each selected schools they were selected by systematic random sampling based on frame existing in schools students' roster (Figure 1).

Data collection procedure and measurements

Instrument for data collection was developed based on conceptual frame work of undernutrition and associated factors on adolescents. Also some of the instruments for data collection was adapted and developed after review of literature from journals and different publication prepared by WHO, United Nation International Children Emergency Fund (UNICEF) and other organization to collect data on adolescent and school children nutritional status. In addition, some part of instruments was adapted from Ethiopian Demographic Health Survey (EDHS) data collection tool to capture data on dietary practice and micronutrient supplementation level for various age groups.

The data was collected through school visits from 640 adolescent students using structured and pre-tested questionnaire by interviewer which is prepared in English language and then translated to Afaan Oromo (local language). Questionnaire was pre-tested in the same study area of the schools which were not included in the actual data collection and checked for consistency and some modification was done. Anthropometric measurements were recorded for each study participants on the intended format attached to the questionnaire. For this purpose the following anthropometric information about the respondents was collected.

Measurements

Anthropometric assessment:

1. Height measurement: The measurement of height was done against a vertical wall with an attached measuring tape and a horizontal head board that could be brought into contact with the upper most point on the head. The adolescents' height was measured barefoot or in thin socks while they wear little clothing so that the position of the body can be seen. Each adolescent was asked to stand on the flat surface, with weight distributed evenly on both feet, heels together against the wall and the head positioned so that the line of vision is perpendicular to the body (Frankfurt position). The arms hanging freely to the sides, and the head, shoulder blade, buttocks and heels are in contact to the wall. The adolescents are asked to inhale deeply and to maintain a fully erect position. The moveable headboard brought on to the topmost point on the head with sufficient pressure to compress the hairs. The height is measured in meters and recorded to the nearest 0.1 cm.

2. Weight measurement: Well calibrated adult digital scale (described below in detail) was used to weigh the adolescents. The weighing scale was calibrated with the help of 10 kg weight. This calibration was done after each day measurements. The weighing scale placed on flat surface and the weight was measured with little clothing and bare feet. Weight was recorded to nearest 100 g. The age and sex specific height and body mass index (BMI) Z score of standard deviation (SD) for each subject was determined using the 2007 WHO growth reference for ages 5 to 19 years (61-228 months). The students were then classified into one of the following

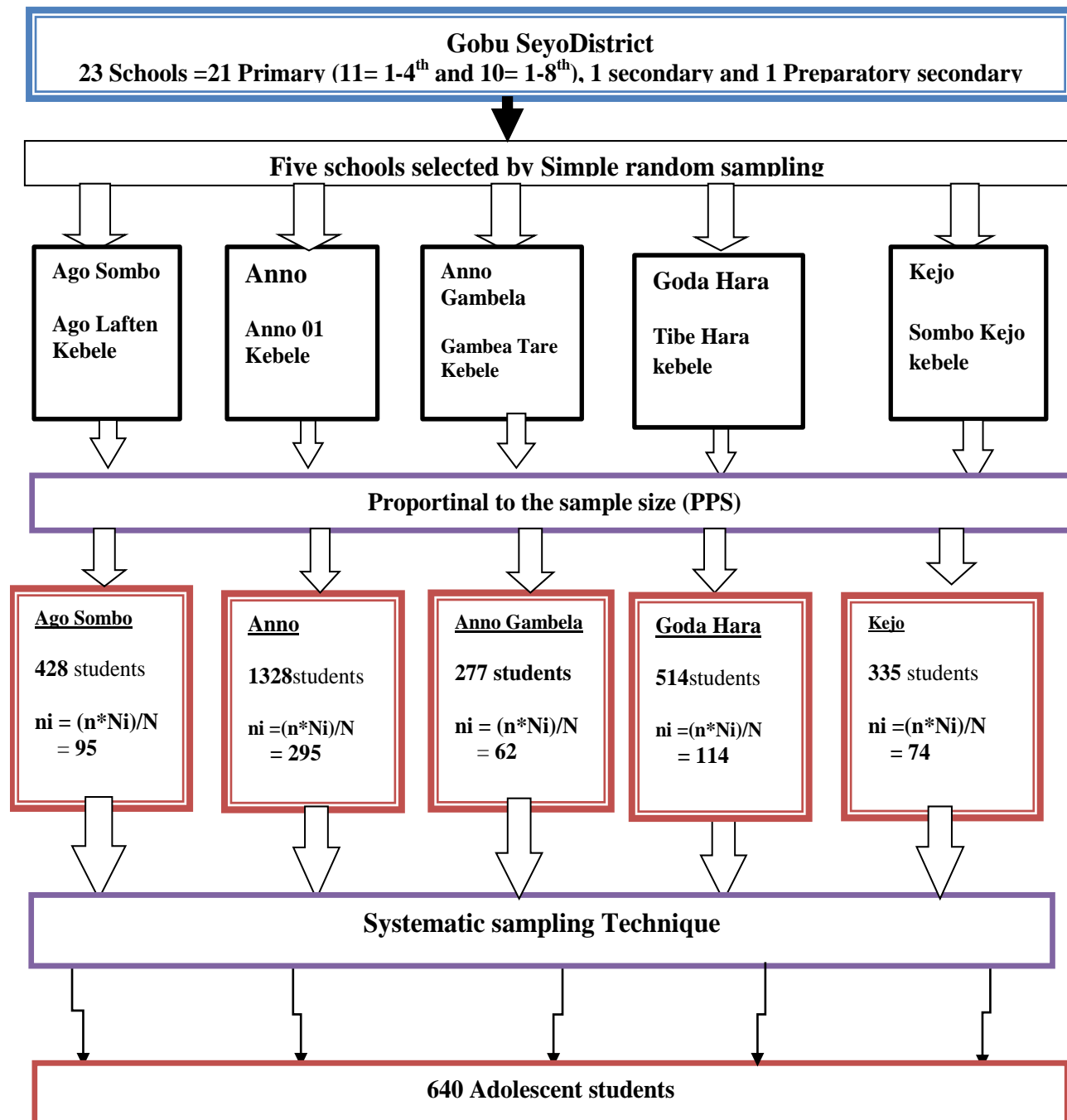


Figure 1. Schematic presentation of sampling procedures, Gobu Seyo district, December, 2016.

categories using previously used standards: Underweight (< -2SD), stunted (< -2SD), stunted (< -3SD) and severely underweight (< -3SD).

Dietary assessment:

1. Food frequency questionnaire: These were designed to assess usual eating habits, over recent months or years, and comprise a list of foods most informative about the nutrients of foods of interest. These generally have been of the type and

frequency of food item (FAQ) in which the subjects were asked to say how often they usually consume an item of food or drink and how much they typically have on the days they consume it in a month.

2. Dietary diversity score (DDS): These were designed to assess eating habits, over recent period of time, and comprise a list of foods most informative about the nutrients of foods of interest. These generally have been type of food eaten during the day and night at home or outside home by adolescents in which the subjects were asked to answer what types of food or drink they consumed in

the last 24 h. Dietary diversity score questionnaire was filled for each study participants by the interviewer.

Variables of the study:

- 1. Dependent variables:** Undernutrition indicated by underweight and stunting
- 2. Independent variables:** Socio-economic and demographic variables; residence, head of HHs, marital status, ethnicity, religion, family size, monthly income, decision making on use of money, education, occupation, ownership of livestock and farm land. Adolescent's characteristics: Age, sex, marital status, grade attending, autonomy in decision-making.
- 3. Environmental sanitation and hygiene:** Water supply, latrine and hand washing practice, waste disposal, sanitation and housing condition. Type and frequency of food item taken by adolescents in a month; dietary habits of adolescents, diversity of food consumed by adolescent;
- 4. Physical activities:** Level of activities performed by adolescent in a day;
- 5. Life style:** Healthy life style, unhealthy life style.

Data analysis

The data was checked for completeness, coded, entered into Statistical Package for Social Science (SPSS) a computer software version 20.0. After edited, cleaned, and processed, it was analyzed using SPSS for windows version 20.0. Descriptive statistics of mean and SD was used to examine the age and gender-specific anthropometric indices. Based on the WHO growth reference cut-off point, prevalence of stunting and underweight was calculated.

A binary logistic regression analysis was performed to determine the association of undernutrition (stunting and underweight) and associated factors. Statistical association was checked by 95% CI and crude odd ratio (COR). The significant variables (p -value < 0.05) observed in bivariate analysis was subsequently included in multivariate analysis. Finally, 95% CI and adjusted odd ratio (AOR) was checked and the significance variables were taken as associated factors of undernutrition. P -value less than 0.05 was considered as statistically significant.

Data quality management

Before data collection commence, training was given to data collectors and supervisors for two days. Pre-test of the questionnaire was done on 5% of the sample size. In the data collection process, diploma nurses from health center under which the selected school is found were recruited and data were collected by using questionnaire, adult digital scale for the weight and stadiometer for height. During data collection, supervisors were assigned in each cluster to assure the quality of data collection at spot. The measuring scales indicator was checked against zero reading after and before weighing every adolescent. On daily basis, collected information was reviewed and possible errors were returned to the collectors for correction.

Ethical considerations

Ethical clearance was obtained from Wollega University Institutional Review Board for ethical approval and permission. At the time of data collection, written informed consent was obtained from the

participants aged 15 years and above. For those study participants aged below 15 years of age, parents were invited to give ascent for their adolescents after they have been selected for the study to confirm whether they were willing to participate or not. Those not willing to participate in the study were given the right to do so. Confidentiality of responses was ensured throughout the research process. The study purpose was also explained to officials of Health department, Education office and Administrative of Gobu Seyo district for their permission and support after which district education office wrote a letter of support to selected schools for cooperation. Information was collected after securing informed consent from study participant and their parents (guardians) in the presence of a school teacher. Data obtained from each study participant was kept confidential and all who participated in the study were acknowledged.

RESULTS

Socio-demographic characteristics of the study participants

Six hundred forty adolescents were interviewed and anthropometric measurements (weight and height) were taken with a response rate of 100% using pretested data collection tools from five schools. For sex proportion of the participants, 326 (50.9%) were males and 314 (49.1%) were females. Of 640 adolescents who participated in the study, 445 (69.5%) were 10-14 years and 195 (30.5%) were 15-19 years old with a mean age of 13.32 years ($SD \pm 2.03$).

From all participants involved in the study, 398 (62.2%) adolescents were rural, 204 (31.9%) were urban and only 38 (5.9%) were semi-urban residents. Majority of the respondents were Protestant followed by Orthodox religion follower which is 312 (48.8%) and 234 (36.6%), respectively. Concerning ethnicity, majority 543 (84.8%) of the respondents were Oromo.

Regarding their marital status, all of them were single. For Educational status, study participants were classified into classes: 4th grade [128 (20.0%)], 5th grade [104 (16.3%)], 6th grade [103 (16.3%)], 7th grade [119 (18.6%)] and 8th grade [186 (29.1%)]. Concerning educational status of families, 84 (14.4%) of father and 184 (28.8%) of mother (guardians) were illiterate and 381 (65.6%) of fathers 168 (26.3%) of mothers were farmer while 328 (51.3%) of mothers were house wife by occupation.

Among adolescents involved in the study only 50 (7.8%) of adolescents have their own monthly income while majority, 590 (92.2%) did not have any monthly income and economically completely dependent on their family. From those who have their own monthly income 37 (74.0%) of adolescents earn ± 100 ETB. Majority of adolescents, 528 (82.5%) are living with their father and mother, 59 (9.2%) with their mothers only and the rest 53 (8.3%) with their relatives.

Majority of households [557 (83.0%)] have ≥ 5 family members in the household and the mean family size was [6.61 ($SD \pm 1.96$)]. Distribution of adolescents in the family varies from one to six and more than half [330 (51.5%)] of

Table 1. Socio-demographic characteristics of the study participants in Gobu Seyo district, East Wollega Zone, Western Ethiopia, 2016.

Characteristic (n = 640)		Frequency	Percent
Sex	Male	326	50.9
	Female	314	49.1
Age group in years	10-14	445	69.5
	15-19	195	30.5
Residence	Urban	204	31.9
	Rural	436	68.1
Religion	Orthodox	234	36.6
	Muslim	89	13.9
	Protestant	312	48.8
	Catholic	5	0.8
Ethnic group	Oromo	543	84.8
	Amhara	91	14.2
	Gurage	3	0.5
	Tigre	3	0.5
Grade level	Grade 4	128	20.0
	Grade 5	104	16.3
	Grade 6	103	16.1
	Grade 7	119	18.6
	Grade 8	186	29.1
Adolescent living style	Father and Mother	528	82.5
	Mother only	59	9.2
	Relatives	53	8.3
No. of adolescents in House hold(HH)	<3	330	51.5
	≥3	310	48.5
Father/guardian/occupation	Daily laborer	24	4.1
	Government employee	111	19.1
	Farmer	381	65.5
	Employed in private sector	30	5.1
	Private business	35	6.0
Mother/guardian occupation	House wife	328	51.3
	Daily laborer	33	5.2
	Maid servant	1	0.2
	Farmer	168	26.3
	Government employee	39	6.1
	Employed in private sector	21	3.3
Father's/guardians education	Private business	50	7.8
	Illiterate	84	14.4
Mother's/guardians education	Read and write only	23	3.9
	Grade 1-4	117	20.1
	Grade 5-8	166	28.5
	Grade 9-10	68	11.7
	Grade 11-12	36	6.2
	Diploma and above	87	14.9
Mother's/guardians education	Illiterate	184	28.8

Table 1 Contd.

	Read and write only	30	4.7
	Grade 1-4	182	28.4
	Grade 5 -8	133	20.8
	Grade 9-10	67	10.5
	Grade 11-12	9	1.4
	Diploma and above	35	5.5
Family size of household	<5	83	13.
	≥5-10	557	83.0

HH have <3 adolescents while the rest 310 (48.5%) of the household have three or more adolescents (Table 1).

Socio-economic characteristics of adolescents and households of adolescents

The mean monthly income of household of adolescents were 1215.64 (SD±1124.56) ETB with minimum and maximum of 100.00 and 6000.00 ETB (US\$ 5 and 300) respectively. Among households of adolescents, 270 (42.2%) have monthly income less than 750.00 ETB, one third, 226 (35.3%) have 750.00 to 1500 ETB and the rest of the household have income greater than 1500.00 ETB on monthly basis. Major source of monthly income of the family for the household was farming which accounts 431 (67.3%) of households followed by salary employment accounting 131 (20.5%) while other households obtain their monthly income from other sources.

Decision is made differently on how income earned by the family is utilized in the household. Majority, [387 (60.5%)] of the HH make decision both jointly (spouse and husband), 168 (26.3%) of HH decision is mainly made by the husband and in 18 (2.8%) of HH, decision is made only by husband. While the rest 57 (10.5%) of HH decision is made by mainly spouse; from whom 59 of the household are headed by females (Adolescents live with their mothers only). Only 76 (11.9%) of adolescents have control and power in decision making on HH income utilization and majority 564 (88.1 %) of adolescents do not have any decision making power and control on how income of the households is utilized in the family.

Household who own livestock, herds or farm animals were 521 (81.4%) and from those who have livestock, herds or farm animals, 90.8% of them have separate room for their animals while 9.2% of them do not have separate room for their animals. Concerning agricultural land ownership, 522 (81.6%) household of adolescents own lands. The mean size of the land for agriculture was 3.33 (SD±2.17) hectares varying from half a hectare to 15 ha which serve as main source of food for the household members including the adolescents.

Two hundred and fifty two (39.4%) of the household obtain their food from farm (produce food), 268(41.9%) of

them from both production and purchase of food. From all adolescents involved in the study majority (78.4%) did not miss their breakfast in a week (Table 2).

Major meals taken by adolescents ranges from two to four times per day. Majority of adolescents 520 (81.3%) took major meals three times per day while 78 (12.2%) and 42 (6.6%) of adolescents take major meals twice and four times per day respectively.

Majority of the study participants 527(82.3%) classified their level of physical activities as active and the rest [109 (17.0%) and 4 (0.6%)] of adolescents are classified as insufficiently active and sedentary, respectively. Concerning time taken from home to school in minutes (min), 383 (59.8%) adolescents came to school in less than 30 min distance and 257 (40.2%) of adolescents ≥30 min. The mean time taken from home to school is 24.57 min (SD ± 19.23 min) varying from school at premises to 90 min.

From all adolescents involved in the study, 355 (55.5%) do not have information on adolescent nutrition while others, 285 (44.5%) of the adolescents have awareness on adolescent nutrition from different sources.

The source of information according to decreasing order were mass media (TV/radio/newspaper), school teachers, friends and peers, health workers and family members with 83 (29.1%), 77 (27.0%), 66 (23.16%), 36 (12.6%) and 23 (8.0%), respectively.

Environmental health characteristics of study participants and house hold of adolescents

Main source of drinking water for more than 40% of household of adolescents were public tap followed by piped water which accounts for 22.5% of the households. Majority of the household of adolescents, [401 (62.7%)] do not treat their water for drinking using chlorine based solution. Mean time (minute) taken for fetching drinking water round trip was 12.22 min (SD ± 10.64 min) varying from water at premises to 60 min. Majority, [470(73.4%)] of HH of adolescents gets water in less than 30 min round trip. Regarding the HH latrine possession with type and usage of it by households six hundred twenty three (97.3 %) of them have latrine of different type and 17

Table 2. Socio-economic characteristics of the study participants in Gobu Seyo district, East Wollega Zone, Western Ethiopia, 2016.

Characteristic		Frequency	Percent
Income owned by adolescents	Yes	50	7.8
	No	590	92.2
Monthly income of adolescents	≤100 ETB*	37	74.0
	101 - 200 ETB*	7	14.0
	≥201 ETB*	6	12.0
Monthly income of HH	<750*	270	42.2
	750-1500*	226	35.3
	>1500*	144	22.5
Income source of HH	Farming	431	67.3
	Livestock and poultry raising	4	0.6
	Whole sale and retail trade	31	4.8
	Manufacturing and hand craft	15	2.3
	Salary employment	131	20.5
	Skilled laborer	20	3.1
	Daily/common laborer	8	1.3
Who decides on money earned in family	Mainly spouse	67	10.5
	Mainly husband	168	26.3
	Only husband	18	2.8
	Both jointly	387	60.5
Control and power in decision making on HH income	Yes	76	11.9
	No	564	88.1
Own any livestock, herd or farm animals?	Yes	521	81.4
	No	119	18.6
Have separate room for animals?	Yes	473	90.8
	No	48	9.2
Have land for agriculture?	Yes	522	81.6
	No	118	18.4
Agriculture land size HH own	<5	384	73.5
	≥5	138	26.4
Source of food for the HH	Farm (produced)	252	39.4
	Market (purchase)	120	18.8
	Both (produced and purchase)	268	41.9
Miss breakfast in a week	Yes	138	21.6
	No	502	78.4
How often missed breakfast per week	Once/week	60	43.4
	Twice/week	52	37.6
	Three or more times/week	26	18.8
Families provide additional food for adolescent?	Yes	360	56.2
	No	280	43.7

*US\$1 = 20.00ETB.

Table 3. Environmental health characteristics of adolescents and Household of adolescents, Gobu Seyo District, East Wollega Zone, Western Ethiopia, December,2016.

Characteristic	Response	Frequency	Percent
Main source of drinking water	Piped water	144	22.5
	Public tap	257	40.2
	Tube well/borehole	88	13.8
	Protected well	33	5.2
	River or stream	115	18.0
	Unprotected well	3	0.5
Main source of water for washing and other purpose	Piped water	113	17.7
	Public tap	208	32.5
	Tube well/borehole	82	12.8
	Protected well	56	8.8
	River or stream	178	27.8
	Unprotected well	3	0.5
Do you treat your drinking water?	Yes, using chlorine	198	30.9
	Yes, by boiling	6	0.9
	Yes, by filtration	35	5.5
	No	401	62.7
Time taken to obtain drinking water (Round trip)	Water on premises	90	14.1
	< 30 min	470	73.4
	30 min or longer	80	12.5
Possession and Type of latrine (Where do HH member go to toilet)	VIP latrine	109	17.0
	Traditional pit latrine	482	75.3
	Communal latrine	32	5.0
	No latrine (bush)	17	2.7
Hand washing after toilet	Always with soap	79	12.3
	Sometimes with soap	271	42.3
	Without soap	183	28.6
	Do not wash	107	16.7
Hand washing before eating	Always with soap	71	11.1
	Sometimes with soap	320	50.0
	Without soap	249	38.9
Hand washing before food preparation	Always with soap	65	10.2
	Sometimes with soap	357	55.8
	Without soap	218	34.1
How do you dispose garbage/waste	Open field disposal	215	33.6
	In a pit	308	48.1
	Common pit	17	2.7
	Composting	13	2.0
	Burning	87	13.6

(2.7%) household of adolescents do not have latrine at all and go to bush. Concerning waste or garbage disposal of household of adolescents nearly half (48.1%) of households of adolescents dispose waste in an individual

pit (Table 3).

Regarding hand washing practice of adolescents after toilet one hundred seven (16.7%) adolescents do not wash their hands after going to toilet (Figure 2).

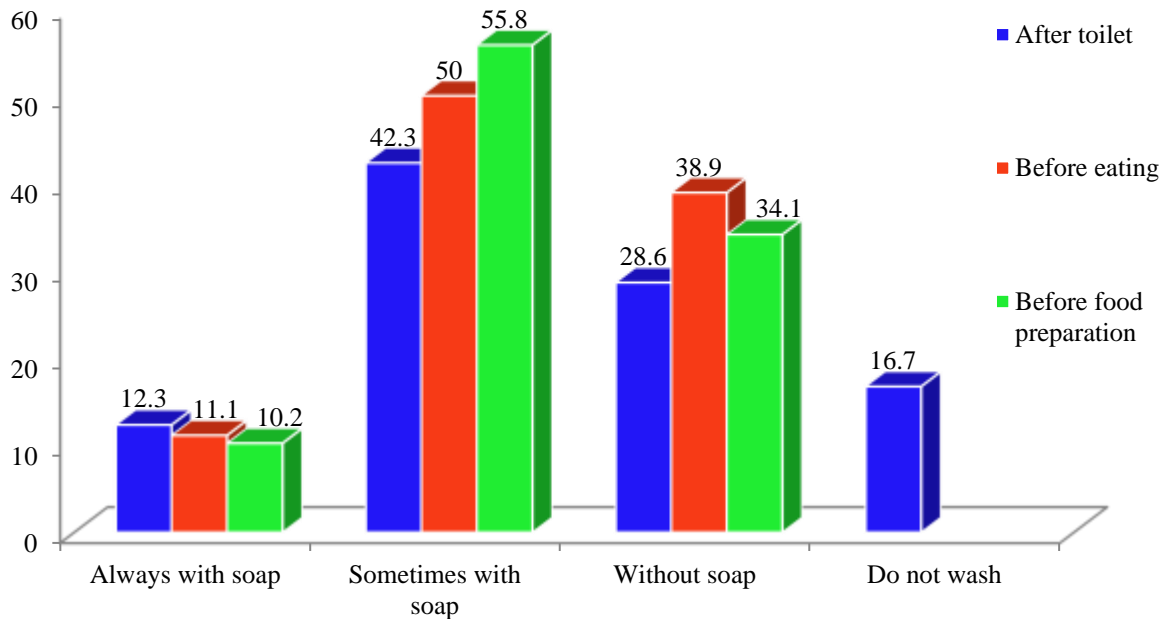


Figure 2. Hand washing practice of adolescents after toilet, before eating and food preparation, Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

Housing condition and information on adolescent nutrition of study participants

Number of room adolescents share in common among other household members were 1 to 2 rooms, 3 to 4 rooms, and 5 and above rooms excluding kitchen and store accounting 214(33.4%), 359 (56.1%) and 67 (10.5%), respectively. Households who have separate room used for kitchen were 572 (89.4%) and other 68(10.6%) do not have separate room used for kitchen and use single room as living room and kitchen. Type of fuel mainly used for cooking for the households of adolescents nearly all 620 (96.9%) of them use wood as a source of energy for cooking and only 20 (3.1%) households uses electricity as main type of fuel for cooking.

Semi-quantitative food frequency questionnaire (FFQ) of the adolescents

Semi-quantitative frequency of food eaten by adolescents in the last month at the time of the study was assessed using seven food items commonly used for assessing nutritional status of adolescents prepared in FFQ table and found that 446 (69.7%) of adolescents eaten food prepared from cereals and grains more than once per day. As indicated in Table 4, adolescents commonly consumed vegetables (dark green leafy vegetables) and fruits once or twice per week and twice per month or less.

Concerning consumption of meat of any type by adolescents, majority of them, 436 (68.1%) consumed twice per month or less and none of adolescents eaten

once per day or more frequent than once per day. Among adolescents involved in the study 112(17.5%) of them never eaten eggs in the last month and large number of adolescents 183 (28.6%) and 239 (37.3%) eaten an eggs once/twice per week and twice per month or less respectively. Surprisingly, all 640 (100.0%) of adolescents never eaten fresh or dried fish in the last month and even in the year or their life time. Lastly, frequency of any other food including tea or coffee, 438 (68.4%) of adolescents take more than once per day followed by 95 (14.8%) adolescents who took the food items at least once per day (Table 4).

Dietary diversity score of adolescents in last 24 h

Using eight food items dietary diversity score (DDS) assessed in the last 24 h among adolescents involved in the study, majority (93.6%) of adolescents ate grains, roots and tubers and nearly half 48.0% ate vitamin A rich foods. Adolescents who had eaten animal sources of protein meat and eggs was low which accounts for 78 (12.2%) and 198 (30.9%) respectively. Other food items consumed by adolescents are given in Table 5.

Prevalence of undernutrition in the study subjects

Prevalence of underweight

According to WHO growth reference 2007 with body mass index (BMI) for age cut off points $< -2SD$ the overall prevalence of underweight among adolescents

Table 4. Semi-quantitative Food Frequency Questionnaire(FFQ) in last one month response of the study population of Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

Food item	More than once per day		Once per day		3-6 times per week		Once or twice per week		Twice per month or less		Never	
	Freq.	%	Freq.	%	Freq.	%	Freq.	%	Freq.	%	Freq.	%
Bread, or any food made from cereals, grains (e.g. made of maize, sorghum, millet, wheat, barley, teff)	446	69.7	107	16.7	73	11.4	13	2.0	1	0.2	0	0.0
Any vegetable, dark green vegetables (kale, lettuce, cabbage)	14	2.2	55	8.6	141	22.0	192	30.0	157	24.5	81	12.7
Any fruit (mango, avocado, banana, etc)	11	1.7	38	5.9	113	17.7	218	34.1	211	33.0	49	7.7
Any beef, lamb, goat, chicken or other organ meat	0	0.0	0	0.0	22	3.4	82	12.8	436	68.1	100	15.6
Any egg	0	0.0	23	3.6	83	13.0	183	28.6	239	37.3	112	17.5
Any fresh or dried fish, or shell fish	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	640	100.0
Any other foods tea, coffee	438	68.4	95	14.8	44	6.9	37	5.8	20	3.1	6	0.9

aged 10 to 19 years in study area were 18.8% (95% CI; 15.6%, 21.9%) of which 2.8% (95% CI; 1.5%, 4.2%) were severely underweight (< - 3SD). The higher prevalence of underweight were seen in male 23.3% (95% CI; 18.6%, 28.1%) than female 14.0% (95% CI; 10.0%, 18.0%). Regarding age distribution of underweight among the study participants, it was more prevalent in early adolescence (10 to 14 years) than late adolescence (15 to 19 years) with prevalence of 20.2% (95% CI; 16.6%, 23.9%) and 13.9% (95% CI; 8.1%, 19.8%) respectively.

As presented in Figure 3, BMI for age of adolescents in the study area was assessed by sex distribution and compared with WHO growth reference 2007. For male adolescents the distribution was less peaked than both the WHO growth reference and those female adolescents but more skewed to the left side than WHO growth reference and the female adolescents. Regarding BMI for age distribution of female adolescents it was more peaked than both WHO growth reference of adolescents 2007 and those

adolescents in the same study area but it was more skewed to the left side than the WHO growth reference and less skewed to the left than that of male adolescent of the same study. These may show that growth pattern of both male and female adolescents in the study area lag behind when compared with WHO growth reference 2007 and this was true more for male adolescents than female adolescents in the study area. The peak of the distribution also showed that the spurt growth during adolescence occur nearly at the median age of adolescents for the female (Figure 3).

Prevalence of stunting

Prevalence of stunting among study subjects were 17.0% (95% CI; 14%, 20%) of which 1.70% (95% CI; 0.6%, 2.8%) were severely stunted. Similar to prevalence of underweight among adolescents, stunting were more prevalent on male [20.0% (95% CI; 15.7%, 24.8%)] than females [13.7% (95% CI; 9.7 %, 17.7 %)] [Figure 4].

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Age distribution of stunting were 16.45% (95% CI; 13%, 19.7%) and 19.2% (95% CI; 12.6%, 25.8%) in early and late adolescents respectively (Figure 5).

Like BMI for age of adolescents, height for age of adolescents were assessed and compared with WHO growth reference 2007 as indicated in Figure 6. The distribution of height for age Z-score (Figure 6) of both male and female adolescents were almost similar to each other and less peaked and moiré skewed to the left than that of adolescents on WHO growth reference 2007. But heights for age Z-score of male adolescents were slightly skewed to the left than that of female adolescents in the study area.

This might indicate that height growth of adolescents in the study area was less than that of adolescents in WHO growth reference 2007 which may hinder physical capabilities and work opportunity by adolescents when compared with normally growing adolescents of the same age

Table 5. Dietary diversity score of adolescents in last 24 h, Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

Food group	Frequency	Percent
Grains, roots and tubers	599	93.6
Vitamin A-rich plant foods	307	48.0
Other fruits and vegetables	387	60.5
Meat, poultry, fish and sea food	78	12.2
Eggs	198	30.9
Legumes, pulses and nuts	530	82.8
Milk and milk products	357	55.8
Miscellaneous(tea, honey, sugar, soft drink etc)	571	89.2

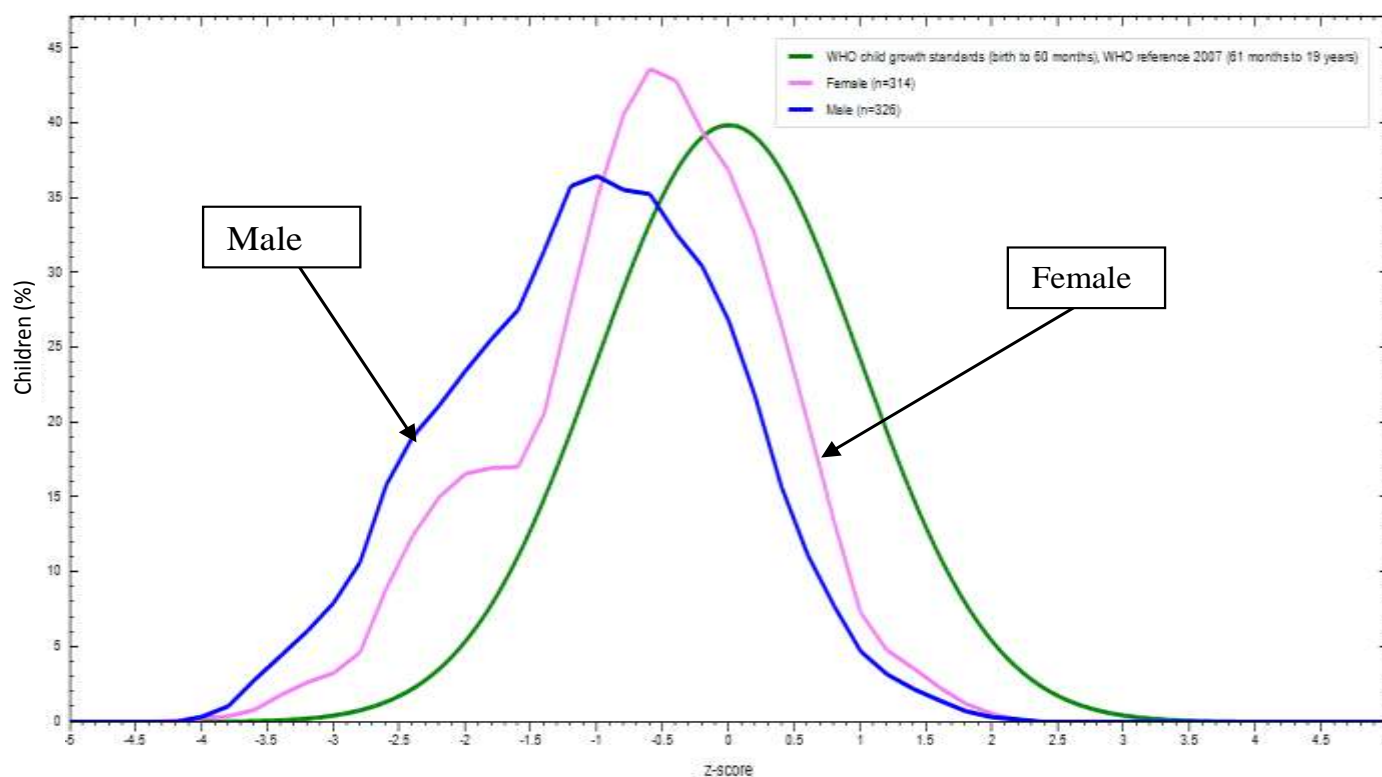


Figure 3. BMI for age of adolescents by sex, WHO growth reference 2007, Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

and sex. The spurt growth of height for both male and female adolescents occurs at similar age in the study area with SD of -1 when compared with WHO growth reference (Figure 6).

Factors associated with undernutrition of adolescents

Associated factors of underweight

Binary logistic regression analysis for factors of

underweight among study participants were performed and found that sex and age of the respondents, level of grade attended by adolescents and fathers' occupation were statistically associated with underweight of adolescents. As indicated Table 6, sex and age of the respondents and father's occupation were significantly associated with underweight in final multivariate logistic regression analysis.

Analysis of this study showed that, female adolescents were about 1.6 times more likely to be underweight than male adolescents (AOR = 1.62; 95% CI = 1.05, 2.49). Adolescents in age group 10 to 14 years were less likely

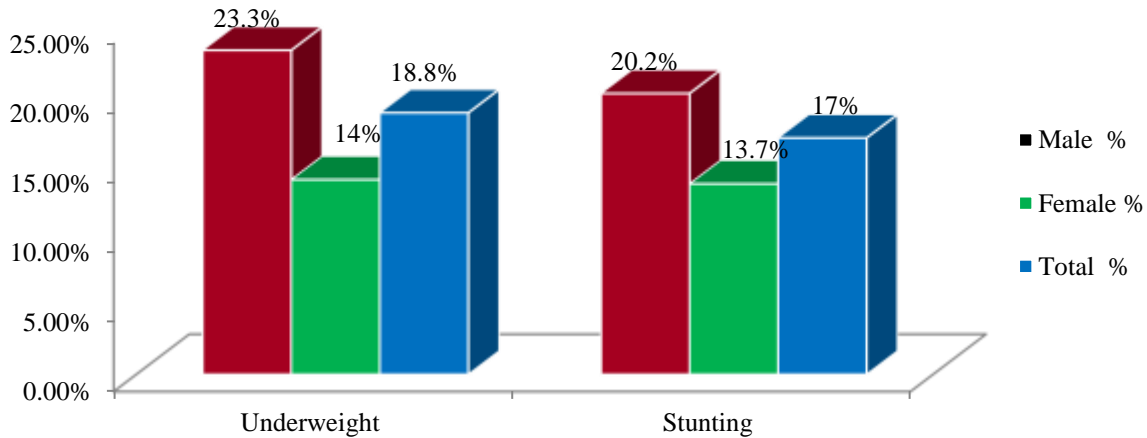


Figure 4. Distribution of undernutrition among adolescents by sex at Gobu Seyo District, East Wollega Zone.

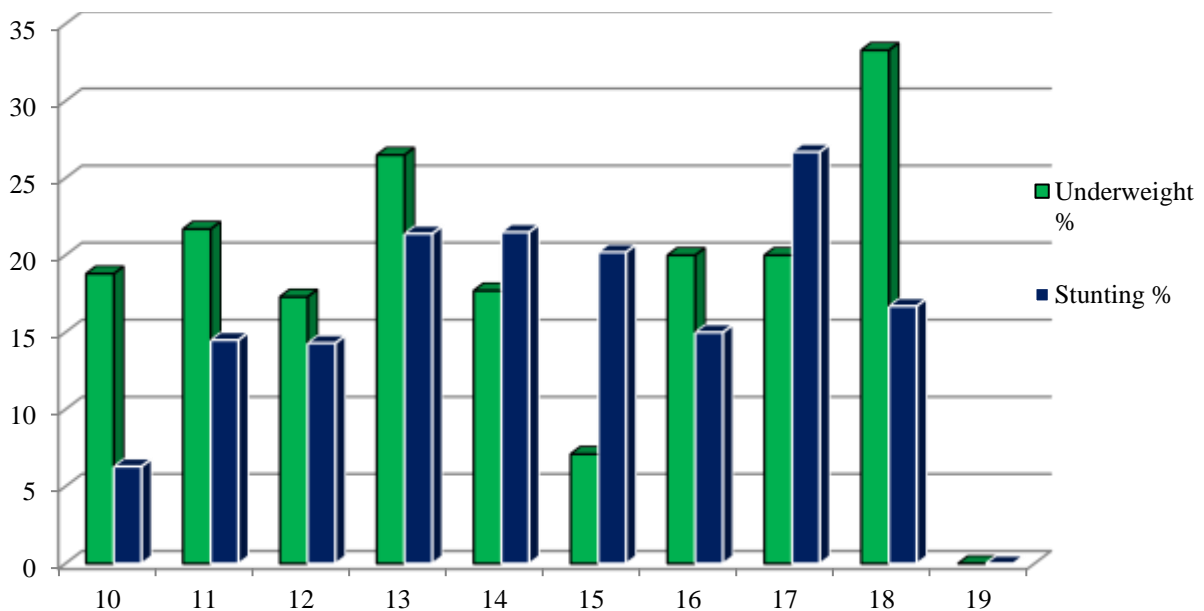


Figure 5. Distribution of undernutrition among adolescents by age at Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

to be stunted when compared with adolescents in aged group of 15 to 19 years of age (AOR = 0.43; 95% CI = 0.25, 0.73). Adolescents which their fathers were employed in private sectors were almost six times more likely to be underweight than those adolescents whose their father run their own private business (AOR = 5.90; 95% CI = 1.16, 30.13) (Table 6).

Associated factors of stunting

Based on binary logistic regression analysis of this study residence, fathers’ occupation, income source of

household, ownership of agriculture land, source of food, latrine ownership, number of rooms for HH and time to obtain water (round trip) were significantly associated with chronic undernutrition nutrition (that is stunting). But on multivariate logistic regression analysis only fathers’ occupation was statistically associated with stunting of adolescents. Adolescents whose fathers are employed in private sectors were nearly six times more likely to develop stunting when compared with adolescents whose father have their own private business (AOR = 5.82; 95% CI = 1.15, 29.38). Adolescents who did not have latrine were 3 times more at risk to be stunted than adolescents who have ventilated improved latrine but also this was

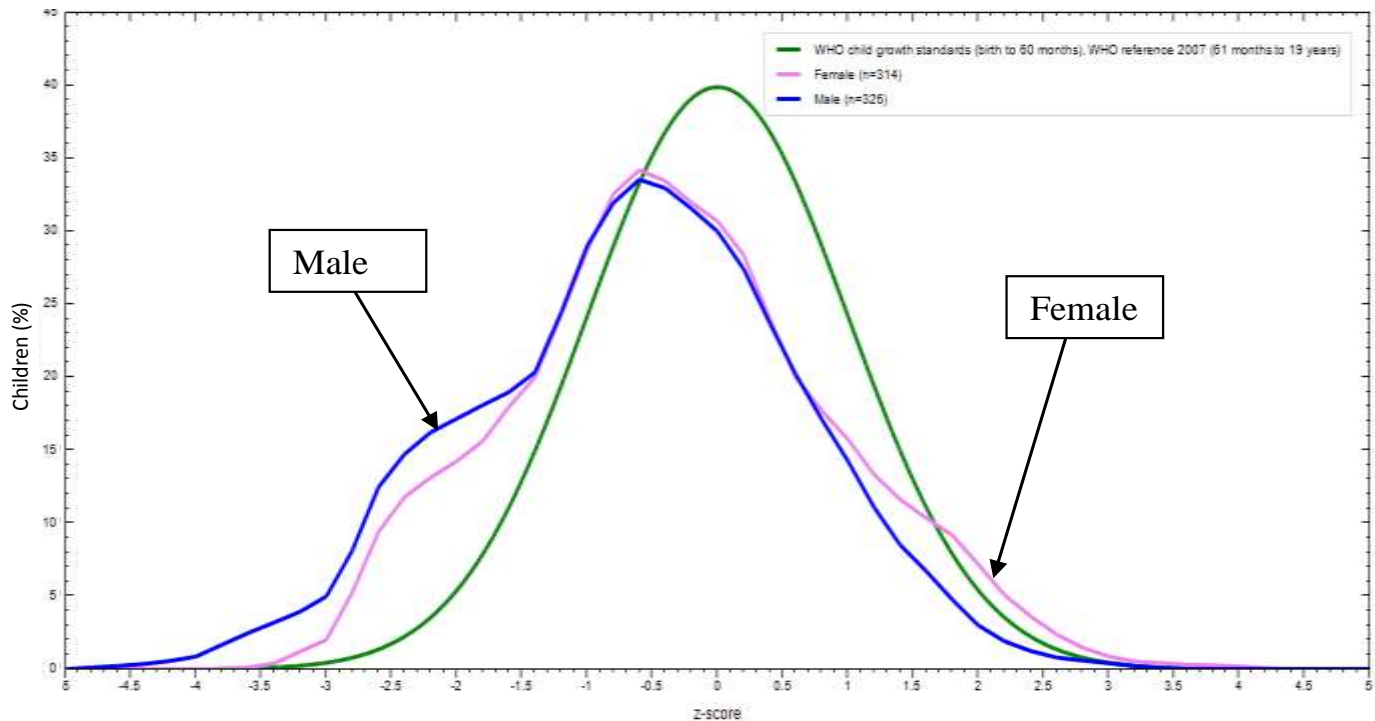


Figure 6. Height for age of adolescents by sex, WHO growth reference 2007, Gobu Seyo District, East Wollega Zone, Western Ethiopia, December, 2016.

Table 6. Bivariate and multivariate analysis showing impact of selected independent variables on underweight among adolescents age 10-19 years at Gobu Seyo district, East Wollega Zone, Western Ethiopia, December 2016 (n=640).

Variable	Underweight		Crude odds ratio (COR;95%CI)	Adjusted odds ratio (AOR;95%CI)	
	Yes	No			
Sex	Male	72(11.3%)	254(39.7%)	1	1
	Female	48(7.5%)	266(41.5%)	1.57(1.05-2.35)	1.62(1.05-2.49)*
Age (year)	10-14	96(15.0%)	349(54.5%)	0.51(0.31-0.83)	0.43(0.25-0.73)**
	15-19	24(3.8%)	171(26.7%)	1	1
Adolescent educational level	Grade 4 th	27(4.2%)	101(15.8%)	0.58(0.32-1.05)	0.80(0.37-1.72)
	Grade 5 th	17(2.6%)	87(13.6%)	0.79(0.40-1.55)	1.08(0.47-2.49)
	Grade 6 th	24(3.7%)	79(12.3%)	0.51(0.27-0.95)	0.70(0.32-1.48)
	Grade 7 th	27(4.2%)	92(14.3%)	0.53(0.29-0.96)	0.66(0.31-1.37)
	Grade 8 th	25(3.9%)	161(25.1%)	1	1
Fathers' occupation	Daily laborer	2(0.3%)	22(3.8%)	4.40(0.86-22.29)	4.46(0.87-22.98)
	Gov't employee	24(4.1%)	87(15.0%)	1.45(0.61-3.43)	1.50(0.62-3.60)
	Farmer	72(12.4%)	309(53.1%)	1.71(0.78-3.73)	1.88(0.85-4.15)
	Employed in private sector	2(0.3%)	28(4.8%)	5.60(1.12-28.04)	5.90(1.16-30.13)***
	Private business	109(18.7%)	25(4.3%)	1	1

p-value * = 0.028, ** = 0.002 and *** = 0.03 Backward LR was used in multivariate analysis

not statistically significant.

Unlike others study, this result showed that residence of adolescents, income source of HH, ownership of agriculture land, source of food, latrine for household, time

to obtain drinking water (round trip), and number of rooms for household members were not statically associated with stunting by multivariate analysis (Table 7).

Table 7. Bivariate and multivariate analysis showing impact of selected independent variables on stunting among adolescents age 10-19 years at Gobu Seyo District, East Wollega Zone, Western Ethiopia, December,2016(n=640).

Variable	Stunted		Crude odds ratio (COR;95 % CI)	Adjusted odds ratio (AOR;95% CI)	
	Yes	No			
Residence	Urban	53(8.3%)	151(23.6%)	1	1
	Rural	56(8.7%)	380(59.3%)	2.38(1.56-3.62)	0.77(0.37-1.56)
Fathers' occupation	Daily laborer	1(0.2%)	23(3.9%)	10.75(1.10-105.26)	4.22(0.82-21.61)
	Government employee	29(5.0%)	82(14.1%)	1.35(0.54-3.41)	1.47(0.61-3.52)
	Farmer	52(8.9%)	329(56.6%)	2.55(1.05-6.19)	1.55(0.69-3.47)
	Employed in private sector	7(7.0%)	23(3.9%)	1.49(0.48-4.62)	5.82(1.15-29.38)*
	Private business	11(1.9%)	24(4.1%)	1	1
Income source of HH	Farming	58(9.0%)	373(58.3%)	1	1
	Livestock and poultry raising	1(0.2%)	3(0.5%)	0.05(0.51-5.05)	0.12(0.01-1.130)
	Whole sale and retail trade	9(1.4%)	22(3.4%)	0.40(0.17-0.94)	0.33(0.82-1.34)
	Manufacturing and hand craft	4(0.6%)	11(1.7%)	0.45(0.13-1.51)	0.61(0.09-3.95)
	Salary employment	33(5.1%)	98(15.3%)	0.62(0.34-1.15)	0.43(0.10-1.92)
Land for agriculture	Skilled laborer	4(0.6%)	24(3.7%)	0.65(0.20-2.08)	0.54(0.09-3.25)
	Yes	80(12.5%)	442(69.0%)	1	1
Source of food for HH	No	29(4.5%)	89(13.9%)	0.55(0.34-0.89)	1.17(0.33-4.06)
	Farm (production)	29(4.5%)	223(34.8%)	1	1
	Market (purchase)	30(4.7%)	90(14.0%)	0.39(0.22-0.68)	1.95(0.49-7.66)
Time taken to fetch water(round trip)	Both	50(7.8%)	218(34.0%)	0.56(0.34-0.92)	1.54(0.92-2.11)
	On premises	24(3.7%)	66(10.3%)	1	1
	<30 min	70(10.9%)	400(62.5%)	2.07(1.22-3.54)	0.96(0.44-2.11)
Latrine for HH	≥30 min	15(2.3%)	65(10.1%)	1.57(0.76-3.27)	0.76(0.28-2.01)
	VIP latrine	29(4.5%)	80(12.5%)	1	1
	Traditional pit latrine	73(11.4%)	409(63.9%)	2.03(1.24-3.32)	1.66(0.86-3.20)
	Communal latrine	6(0.9%)	26(4.0%)	1.57(0.58-4.20)	1.27(0.98-21.99)
No of rooms for HH members	No latrine(bush)	1(0.2%)	16(2.5%)	5.8(0.74-45.71)	3.00(0.82-71.04)
	1-2 rooms	31(4.8%)	183(28.6%)	2.00(1.03-3.91)	0.91(0.41-2.02)
	3-4 rooms	61(9.5%)	298(46.5%)	1.66(0.89-3.07)	0.90(0.44-1.83)
	≥5 rooms	17(2.6%)	50(7.8%)	1	1

* = p - value = 0.03, Backward LR was used in multivariate analysis

DISCUSSION

In developing countries, adolescents have higher demographic weight compared to the world adolescents accounting about 26 and 20%, respectively. Africa continent is expected to see its adolescent population growth much more rapidly than other developing countries in the world like Asia and America with a lower fertility control (World Health Organization, 2005).

During adolescence there is rapid and dramatic physical, cognitive, social and emotional changes that increases nutritional requirements and present both opportunity and challenges for adolescents, families, health professionals, educators and communities (World

Health Organization, 2002; Giuseppina, 2000).

In developing countries, large numbers of adolescents suffer from different form of malnutrition and anaemia which adversely affect their health and development particularly in adolescent girls contribute to increased risk of pregnancy related complication and giving birth to low birth weight (World Health Organization,2006).

In most developing countries, nutrition initiatives and programs have been focusing on children and women (specially pregnant and lactating) thus neglecting adolescents. Addressing the nutrition needs of adolescents could be an important step towards breaking the vicious cycle of intergenerational malnutrition, chronic diseases and poverty (World Health Organization, 2006).

Worldwide it is well recognized that anthropometric measurements are indispensable in diagnosing under-nutrition among children and adolescents and BMI is the most appropriate variables for determining nutritional status of adolescents (Mukhopadhyay et al., 2005). The current study enabled us to know about the current nutritional status in this very important age group.

A study conducted in Bangladesh, Khagrachari district and India, West Bengal Purulia district on nutritional status of adolescent girls have similar finding to each other on prevalence of underweight (41.3%) which was almost three times higher than prevalence of underweight in this study area which were 14.0% (Hossain et al., 2013). A cross-sectional study conducted on nutritional status of adolescents in India, West Bengal rural area including both male and female adolescents found that prevalence of stunting and underweight was 27.8 and 28.3%, respectively and distribution of underweight by sex was higher on male (31.0%) than female (24.2%) adolescents (Bisai et al., 2011). This result showed that it was higher both for stunting and underweight in adolescents of Gobu Seyo district. There is particularly higher prevalence of underweight in male than female relates with current study even though the percentage of the finding differ from each other. As clearly known, the two countries are developing countries with high prevalence of undernutrition among adolescents and children aged less than 5 years. The higher prevalence of undernutrition in these two developing when compared with current study area can be due to socio-economic status, dietary pattern and educational status of families of adolescents.

Another cross-sectional study conducted in urban and rural Rohtak, Haryana on nutritional status of adolescents found that prevalence of stunting among male and female adolescents were almost similar male (10.7%) and female (10.8%) but stunting in this study was higher both for male and female with prevalence of 20.0 and 13.7% male and female respectively when compared with Rahtak, Haryana study. Prevalence of underweight (male 21.9 to 34.1% and female 11.5 to 19.8%) in Rahtak, Haryana accommodates prevalence of underweight in study area which is 23.3% for males and 14.0% for female (Vashist and Goel, 2009).

Also other similar cross sectional studies conducted in India rural area of Punal and Varanasi district on nutritional status of adolescents found that prevalence of underweight was 70.6% (38.8% for male and 63.6% for female) and 27.0% respectively which was much higher than prevalence of underweight when compared with this study. Between the two districts there is a significant difference on prevalence of underweight even if they are in developing countries of India (Mankar et al., 2016; Sweta Singh et al., 2012). Data collection period, method of assessment and standard growth reference could be a factor for the difference of prevalence of undernutrition in between the two countries and as well as with the current

study.

In this study, prevalence of stunting among adolescent girls were 13.7% which was much lower than prevalence of stunting (34.61%) among adolescent girls residing at Hills of Garhawa rural area, India and another cross-sectional study conducted in India, Karnataka on prevalence of stunting found that 40.5% of boys and 24.5% of girls were stunted which was two times higher for boys and nearly two times for girls than in this study (Yogesh and Vartika, 2010; Rajaretnam and Hallad, 2012). Higher prevalence of stunting among adolescent boys goes similar with higher prevalence of stunting in GobuSeyo woreda. This difference in the prevalence might have various factors such as socio economic condition, cultural difference on dietary practice, geographical disparity and genetic variation among the adolescents.

In Dhaka city, Bangladesh, nutritional status and associated factors were assessed among school and college adolescents aged 10 to 19 years of age using height for age, weight for height and weight for age and found that prevalence of stunting was 17.6% and those adolescents who were stunted and wasted were 16.2%. The finding of current study also revealed that prevalence of stunting (13.7%) among adolescent girls were lower than study conducted on nutritional status and associated factors among adolescent girls as measured by height for age in urban Bangladesh (Monira and Khyrunnisa 2003).

Also similar study was conducted to assess nutritional status of adolescents in Islamabad city, Pakistan and revealed that overall prevalence of underweight and stunting among adolescents were 17.0 and 12.2%, respectively. When compared with current finding of Gobu Seyo district it was slightly lower with prevalence of underweight (18.8%) and much lower with prevalence of stunting (17.0%) (Hajra, 2009).

In addition, similar study was conducted in Rawalpindi, Pakistan, among adolescent college girls and come up with a finding of prevalence of underweight was 20.0% which is somewhat lower than that of the current study (Shahid et al., 2009). On adolescent school girls of Rawalpindi, Pakistan, prevalence of stunting and underweight were 6.8 and 17.3%, respectively that indicated prevalence of stunting and underweight was higher than that of current study conducted in Gobu Seyo district (Arshad, 2005).

In Africa, nutritional statuses of adolescents were neglected by some initiatives and programs where focused on children and pregnant and lactating women. Due to this, research finding on adolescent nutrition was not as much as needed for intervention and policy development. The finding of this study on prevalence of stunting among male adolescents were slightly lower and female were higher when compared with prevalence of stunting among adolescents in Nigeria, semi urban area with a prevalence of 23.8 and 4.7% for male and female, respectively. Regarding prevalence of underweight, the

same study found that 4.8 and 2.3% of male and female were underweight respectively which was nearly five and six times lower for male and female, respectively than current study conducted in Gobu Seyo district which were 23.3 and 14.0% (Chukwunonso et al., 2010).

In Nigeria, Osun State, cross-sectional study on prevalence of underweight a matter of concern among adolescents was conducted and found that overall prevalence of underweight was 20.1% which was slightly higher than prevalence of underweight in the current study. In both study prevalence of underweight was higher among adolescent boys than girls with a finding of 25.8 and 15.1% in Nigeria and 23.3 and 14.0% in the current study, respectively (Olumakaiye, 2008).

In this study the overall prevalence of underweight and stunting among adolescents were 18.8 (male 20.0 and female 13.7%) and 17.0% (male 23.3% and female 14%), respectively. The results of this study revealed that the prevalence of stunting was lower and that of underweight was exactly similar when compared with a Ethiopian National Nutrition baseline survey conducted in 2010 on adolescent girls, 23% stunted and 14% were underweight (Federal Democratic Republic of Ethiopia MOH, 2009; Literature Review, January 2011). Since the base line survey was conducted in different regions of the country there might be variation in socio demography, economy, culture and dietary patterns among adolescents as well as access to food and information on adolescent nutrition for adolescents and their families that could make difference on prevalence of stunting through long run; as stunting is long run effect of undernutrition among adolescents and rooted in childhood age.

Finding of this study also revealed that prevalence of stunting among adolescents aged 10 to 19 years in the study area was almost similar with community based cross-sectional study conducted among adolescents of Jimma zone, South West Ethiopia with a prevalence of 16.0%. But prevalence of underweight in study of Jimma zone was four times higher (80.83%) when compared with that of this study (Huruy et al., 2013). The study might have similar geographic area to each other but their culture and dietary pattern and practice as well as study design could make discrepancy on prevalence of underweight among adolescents because study design of Jimma was a community-based cross-sectional study in which adolescents were enrolled to the study in the second round of the five-year longitudinal study of adolescents in Jimma zone, South west Ethiopia.

Although prevalence of underweight in this study area was far below than that of Jimma zone it was higher than study conducted in Gondar, North Ethiopia with a prevalence of 12.9% (Bemnet, 2012). Similarly prevalence of underweight among elementary adolescent students of 10 sub-cities of Addis Ababa was lower (13.0%) when compared with prevalence of this study (Zelege, 2007). This difference might be due to socio economic and educational status of adolescents and their families and

also exposure to information on adolescent nutrition through mass media and adolescents in Addis Ababa have more access to food than adolescents in this study area.

Prevalence of stunting and underweight in this study were much lower than community based cross-sectional study conducted on prevalence of stunting and underweight in rural communities of Tigray, Northern Ethiopia, which was 26.5 and 58.3%, respectively (Afeework, 2009). This discrepancy could be due to socio cultural and geographical variation between the study areas. Additionally dietary pattern of adolescents of the study area and attention towards awareness on adolescent nutrition for adolescent and their families could differ.

Similar institution based cross-sectional study was conducted on factors affecting BMI of adolescent students aged 10 to 19 years in rural town of Ambo, West Oromia, Ethiopia and found that prevalence of underweight was much higher than prevalence of underweight in this study with 27.2%. Even though the prevalence of underweight among adolescents in both studies was different, gender distribution of underweight was higher in males (29.8%) than females (24.6%) when compared with the current finding (23.3%) for males and (14.0%) for females in the study area (Yetubie et al., 2010).

Dietary pattern are determinant factors of nutritional status among adolescents and other age groups. This pattern can be assessed by means of dietary diversity and frequency of selected food items consumed by adolescents. Food items used in the dietary pattern was locally available and food source indicator for balanced diet. Accordingly dietary diversity score of adolescents in the study area was assessed by asking whether adolescents consumed listed food item within 24 h at home and outside home and found that statistically not associated with nutritional status of adolescents and there was no difference between male and female dietary pattern of adolescents.

Frequency of food consumed by adolescents within one month during the study period was clearly described by adolescents based on list of selected common staple food items and found that food made from cereals and grains were commonly consumed more than once per by 446 (67.9%) of adolescents as a source of heat and energy for them and none of adolescents never consumed food made from cereals and grains. This could be due to production crop of food items locally and tradition of households and adolescents on consumption such food as a staple food.

Fruits and vegetables are food groups very important for human health and disease prevention. Eating these food items will favor health and wellbeing of adolescents by making them to avoid junk and fast food eaten. In this study, frequency of fruits and vegetable consumed by adolescents were commonly once/twice per week or

twice/less per month.

Different socio demographic and economic characteristics variables were included in the study to identify factors of undernutrition among adolescents in the study area. Variables statistically associated with undernutrition of adolescents were age and sex of adolescents and fathers' occupation for underweight and only residence of adolescents were statistically associated with chronic undernutrition (stunting) on multivariate analysis. On other studies conducted on nutritional status and associated factors of adolescents various variables of study were associated with undernutrition in which some of the variables did not associate with undernutrition of the current study.

Among variables associated with underweight and stunting of adolescents in other studies major meals per day, missing breakfast, income of household and educational status of families were significantly associated (Shahid et al., 2009; Afework 2009; Yetubie et al., 2010; Huruy et al., 2013). Some cross sectional studies found that associated factors of undernutrition in adolescents were age and sex of adolescents which had similar finding with current study conducted in GobuSeyo woreda (Monira and Khyrunnisa 2003; Yetubie et al., 2010; Huruy et al (2013).

Lack of latrine, distance of drinking water, agricultural land and ownership of cattle significantly associated with stunting and underweight of adolescents particularly in our countries. But in this study environmental factors did not associate statistically with under nutrition except number of rooms shared with household members of adolescents.

Limitation of the study

Due to the cross-sectional nature of the study, it is weak in elucidating cause and effect relationship of variables. Frequency food questionnaire was collected on items consumed by adolescents only for frequency with which adolescents eat listed food. So, it did not include the quantity of food item consumed by adolescents and this may be the limitation of the study to identify calories and nutritional value of food eaten.

Conclusion

This study revealed that the prevalence of undernutrition was high. Sex and age of the respondents and father's occupation were significantly associated with underweight and only fathers' occupation was statistically significant variable associated with chronic malnutrition (stunting) of adolescents on multivariate analysis. Dietary diversity of food for adolescents was below the standard for normal growth and development of adolescents to attain nutritional requirements during adolescence when compared to food pyramid for frequency of food taken.

Frequencies of food item consumed by adolescents were majorly cereals and grains and food for protein source were very low when compared with other food items. Therefore, community based nutrition program should be established to tackle the problem of intergenerational cycle of malnutrition at community level depending on the severity of malnutrition identified in this study. Nutrition education by health extension works should be strengthened to improve the attitude of parents on dietary pattern of adolescents' particularly dietary diversity and frequency of food eaten by adolescents according to food pyramid of nutrition. Age and gender specific nutrition education program should be provided in the study area for better behavioral changes among adolescents and their families on adolescent nutrition. Continued attention will be mandatory to adolescent dietary practices to meet their nutritional requirements for their spurt physical and mental growth according to their age, sex and residence. District government sectors should strengthen and established income generation activity and saving at households like credit and saving process with collaboration of stake holders to improve family income particularly fathers' income. Nutrition surveillance needs to be done continuously and special attention should be given to vulnerable groups such as poorest and the most severely malnourished adolescents. Further study should be done to see other unexplored associated factors that were not included in the present study.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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