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Original Contribution

The role of ALDH1A1 in contributing to breast tumour aggressiveness: A study conducted in an African population

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ABSTRACT

Aldehyde dehydrogenase 1 member A1 (ALDH1A1) is one of the most well studied breast cancer stem cells. Its expression has been associated with poor clinicopathological features and clinical outcomes in several studies. This paper studies the expression of ALDH1A1 and its combination with $CD44^{+}/CD24^{-/low}$ breast cancer stem cell and their association with clinicopathological parameters and molecular subtypes.

Method: Tissue Microarray was constructed from 222 Formalin Fixed Paraffin Embedded (FFPE) breast cancer tissues. The expression of ALDH1A1, CD44 and CD24 were assessed by Immunohistochemistry (IHC). The association of ALDH1A1 and its association with clinicopathological parameters, molecular subtypes, CD44 and CD24 were studied in an African population. The association between $CD44^{+}/CD24^{-/low}/ALDH1^{+}$ and the clinicopathological phenotypes were also studied.

Results: A high ALDH1A1 expression of 90% was recorded in this study. No association was found between ALDH1A1 and clinicopathological parameters. ALDH1A1 was positively associated with CD24 (r = 0.228, OR-4.599 95% CI- 1.751–12.076, $p = 0.001$) and CD44 (r = 0.228, OR-5.538 95%CI- 1.841–16.662, $p = 0.001$) but not associated with $CD44^{+}/CD24^{-/low}$ (r = 0.134, OR- 2.720 95%CI- 0.959–7.710, $p = 0.052$). $CD44^{+}/CD24^{-}/ALDH1^{+}$ however had significant associations with Age (*p- 0.020*, r = 0.161, OR- 2.771, 95%CI 1.147–6.697), Gender ($p = 0.004$, OR- 15.333 95%CI 1.339–175.54), Tumour grade ($p = 0.005$, r = 0.197, OR-3.913 95%CI 1.421–10.776) and clinical prognostic staging ($p = 0.014$, r = 0.182, OR-3.028 95%CI-1.217–7.536). There was no association between $CD44^{+}/CD24^{-}/ALDH1^{+}$ and the molecular subtypes.

Conclusion: The high expression of ALDH1A1 in breast cancer makes it an important target for targeted therapy. This study further confirms the increased tumourigenicity of $CD44^{+}/CD24^{-}/ALDH1^{+}$ combination phenotype and its association with increased tumour grade and clinical prognostic stage. Survival studies of ALDH1A1 and other breast cancer stem cells in African populations are strongly recommended to help further understand their effect on tumour aggressiveness.

1. Introduction

Despite advances in molecular techniques in cancer research, the role of cancer stem cells (CSC) in tumour initiation, differentiation, progression, therapy resistance and recurrence remain puzzling. This is partly because of their representation as a smaller but key subpopulation in the highly heterogenous tumour microenvironment with their ability to enter quiescence to evade regular therapeutic agents that target proliferating cells. The involvement of CSC in the aforementioned sequence of events in cancer development has been established [1-3] but the molecular interactions among themselves and with other intra-tumoral components is still under intense research. Targeting and

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eradicating CSC is crucial in the development of novel cancer therapies (Figs. 1 and 2).

One of the well-studied CSC marker is Aldehyde dehydrogenase 1 (ALDH1), a cytosolic ubiquitous detoxifying enzyme expressed in several tumours such as breast, laryngeal, ovarian, gastric and non-small cell lung cancer [4-7]. This enzyme converts aliphatic aldehydes and retinol into carbolic acid and retinoic acid respectively in an NAD(P) + dependent oxidation. Its increased expression has largely been associated with breast cancer aggressiveness and poor prognosis [1,8-11]. On the contrary, other studies such as that of Liu et al. reported that ALDH1 associated with better outcome in triple negative breast cancer [12] and still others did not find any association with clinicopathological features or clinical outcomes [13-15]. The role of ALDH1 in breast cancer outcomes therefore remains controversial and further investigation is warranted in the quest to unravel its 'for now' confusing role [16].

ALDH1 proteins consist of 3 main isozymes namely ALDH1A1, ALDH1A2 and ALDH1A3 with ALDH1A1 being the most specific which is largely reported to be related to poor prognosis [17]. The chemoresistance role of ALDH1 stems from its ability to detoxify anticancer drugs such as oxazaphosphorine *via* oxidation of aldophosphamide by activation of ALDH1 expression. The main stay of cancer treatment in Africa involves chemotherapy and radiotherapy. Such treatment regimens are limited in their inability to target cancer stem cells resulting in drug resistance and tumour recurrence *via* the aforementioned mechanism [18-20].

The role of ALDH1 related to cancer stem cell and ALDH1's association with poor prognosis in most tumours has been widely determined. $CD44^{+}/CD24^{-/low}/ALDH1^{+}$ cancer stem cell forms a phenotype with a higher tumourigenicity relative to the individual stem cell contributions. Evidence exist for this combined phenotype ($CD44^{+}/CD24^{-/low}/ALDH1^{+}$) having the propensity to achieve tumour initiation from as low as 20 cells as opposed to 100 cells by $CD44^{+}CD24^{-/low}$ alone in *in-vivo* studies [1,21]. With such enhanced tumourigenic potential, the role of the $CD44^{+}/CD24^{-/low}/ALDH1^{+}$ phenotype in contributing to the aggressiveness of breast cancers of African populations is not well understood. A study of breast cancer stem cells is crucial in improving breast cancer management and clinical outcomes in Africans. The aim of this study is to analyse the expression of ALDH1, and its combination phenotype $CD44^{+}/CD24^{-/low}/ALDH1^{+}$ and their associations with molecular and clinicopathological features of breast cancer in an African population.

2. Materials and methods

A retrospective study was carried out of some breast biopsies and reports of patients (n = 222) presenting with breast cancer at the departments of pathology, Korle-Bu Teaching Hospital, Accra and the Cape Coast Teaching Hospital, Cape Coast, two of the five teaching hospitals in Ghana between 2012 and 2018. The Korle-Bu Teaching Hospital department of pathology is the largest in Ghana, receiving specimens from the Korle-Bu Teaching Hospital, the largest referral hospital in Ghana and from other health facilities within the Greater Accra Region [22]. The department also receives specimen from all other regions of Ghana. The Cape Coast Teaching Hospital's pathology department receives specimen from mainly the Central and Western regions of Ghana. Clinical data was obtained from histopathology request forms. Two pathologists (PKA and LDK) reviewed histopathology slides of selected cases within the study period (2012–2018). Selection was done according to the quality of the FFPE blocks. Archival blocks of primary breast carcinoma from the two pathology departments were retrieved. Additional clinical information and histopathological features were obtained from the histopathology reports of patients. The information included the mean age of presentation, duration of symptoms, tumour grade, (based on mitotic count, nuclear grade, tubule formation). All cases were reviewed histopathologically and classified according to the recent WHO classification for breast tumours and histopathological grading done in accordance with the Nottingham criteria [23].

2.1. Tissue microarray (TMA) construction

Areas of tumour were selected after preparation of histopathology slides from archival formalin fixed paraffin embedded (FFPE) blocks' and staining with Hematoxylin and Eosin (H&E). Areas of normal tissue, necrosis, and haemorrhage were ignored. Using the TMA Grand Master® (3D HISTECH®, Budapest, Hungary), three cores 1 mm each (2 from peripheral tumour and 1 central tumour) were punched out from the representative selected areas and arrayed into a new recipient paraffin block. Four micrometer thickness of TMA sections were cut and mounted on Superfrost slides.

2.2. Immunohistochemistry (IHC)

TMA were stained using ALDH1A1 Rabbit Polyclonal antibody, Sigma Life Science (Prestige Antibodies) HPA002123, at dilution of 1:50. CD24 and CD44 staining was done with CD24 Monoclonal antibody (SN3), Thermofisher and CD44 monoclonal antibodies (156-3C11), Thermofisher in dilutions of 1:200 and 1:750 respectively and incubated in a black box for 1 h at room temperature. Immunohistochemical antibody labelling was done using the NOVOLINK polymer detection system (Leica, Newcastle, UK). Adhesion of tissue to the slide was done by pre-heating tissue microarrays at 60 °C on a hot plate for 20 min and cooled. Tissue sections were deparaffinised in xylene and rehydrated through a series of graded alcohols and rinsed in distilled water. Antigen retrieval was achieved by boiling slides in citrate buffer (27 mL of citrate in 123 mL disodium citrate and made up to 1.5 L with ddH2O) at pH -6.0 and microwaved (Whirlpool JT359 Jet Chef 1000 W) at full power for 20 min. Peroxidase blocking reagent from the NOVOLINK® kit was used to block the endogenous peroxidase activity for 5 min and rinsed with PBS for 15 min. Protein blocking was done for 5 min to minimize nonspecific binding and rinsed thoroughly with PBS for 15

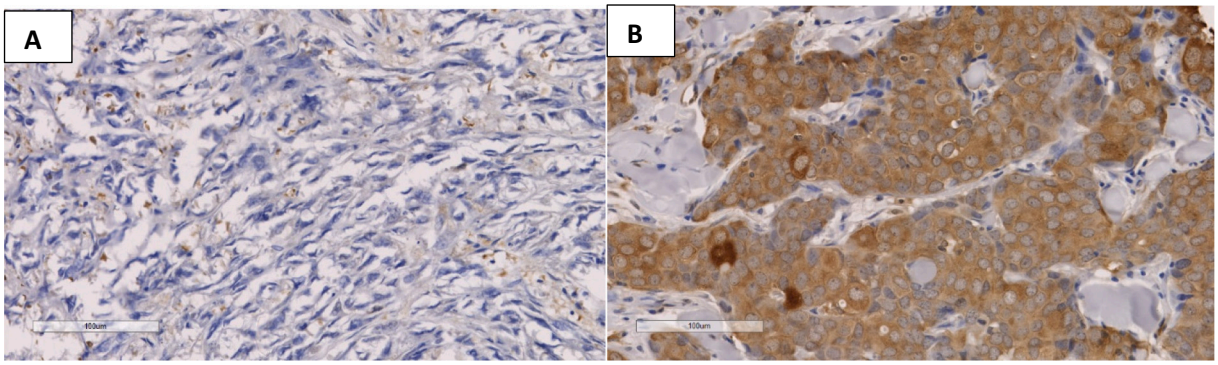

Fig. 1. A- Negative staining for ALDH1A1, B- Positive staining for ALDH1A1.

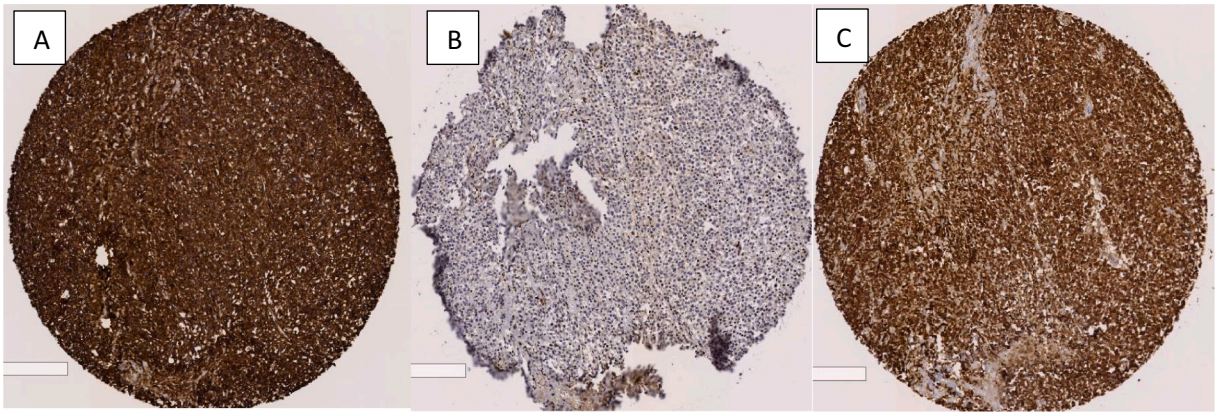

Fig. 2. CD44, CD24 and ALDH1A1 expression in breast cancer using IHC. A, B and C Same case stained positive for CD44 in A, negative for CD24 and positive for ALDH1A1.

min. Primary antibody was added in the following dilutions: ALDH1–1:50 and incubated in a black box for 1 h at room temperature. Positive control was Liver tissue, and negative control was obtained by omitting the primary antibody in the staining protocol. A thorough rinse was done for 15 min with PBS tween and then incubated with Post Primary Novolink reagent for 30 min in a black box. After a 15-minute thorough rinse, a polymer was added and incubated for 30 min. The reaction was then developed by incubating a 3,3′-diaminobenzidine chromogen solution (DAB) made up to 1:20 in dilution with DAB substrate buffer and incubated for 5 min. Counter staining with hematoxylin was done and incubated for 6 min. Dehydration and clearing were done using the Leica auto Stainer. Sections were then mounted with DPX. Evaluation of staining was done.

The semi-quantitative H scoring system was employed in scoring. The intensity of ALDH1 expression was scored as 0 (no expression), 1 (weak), 2 (moderate) and 3 (strong). The total score was calculated as the percentage of positive cells multiplied by the intensity giving a range of 0–300. A cut point of ≤40% score was designated as negative and >40% as positive.

For oestrogen and progesterone receptor staining, positive expression was considered as nuclear immunoreactivity in ≥1% of neoplastic cells. HER2 was analysed at the time of diagnosis according to the American Society of Clinical Oncology (ASCO)/College of American Pathologists (CAP) protocols [24].

The molecular subtypes were classified as Luminal A (ER+ and/or PR+ and Her2-), Luminal B (ER+ and/or PR+ and Her2+), Triple Negative (ER- PR- and Her2-) and Her2+ (ER- PR- and Her2+) [24].

2.3. Statistical analysis

IBM SPSS version 24.0 package program (SPSS Inc., Chicago, IL, USA) was used in the statistical analysis. The association between the markers and clinicopathological features were done with cross tables using chi-square test and odd ratios. Correlations were done with Pearson's correlation test. Statistical significance was set at 95% confidence interval.

3. Results

A high Aldehyde dehydrogenase 1A1 (ALDH1A1) expression of 90.2% was recorded in our cohort. There was no association of ALDH1A1 with any of the clinicopathological characteristics. Table 1 shows the association between ALDH1A1 and clinicopathological features. ALDH1A1 was positively correlated with CD24 (r = 0.228, OR-4.599 95% CI- 1.751–12.076, $p = 0.001$) and CD44 (r = 0.228, OR-5.538 95%CI- 1.841–16.662, $p = 0.001$) but not associated with CD44+/CD24- (r = 0.134, OR- 2.720 95%CI- 0.959–7.710, $p = 0.052$).

Table 1
ALDH1A1 Cytoplasmic expression and its relationship with clinicopathological features.

Parameters	ALDH1A1 cytoplasmic expression		Significance		
	Negative (%)	Positive (%)	OR (95% CI)	r	*p value*
Patient's age (n = 216)					
<50	11 (10.6)	93 (89.4)	1.171	0.024	*0.731*
≥50	10 (9.2)	99 (90.8)			
Grade (n = 206)					
1	3 (12.5)	21 (87.5)	1.714	0.056	*0.421*
2&3	14 (7.7)	168 (92.3)			
Tumour size (n = 190)					
≤2	1 (6.7)	14 (93.3)	0.664	−0.028	*0.699*
>2	17 (9.7)	158 (90.3)			
Gender (n = 215)					
Male	0 (0.0)	3 (100.0)		NA	*0.566*
Female	21 (9.9)	191 (90.1)			
Vascular invasion (n = 170)					
Yes	14 (12.5)	98 (87.5)	1.514	0.058	*0.447*
No	5 (8.6)	53 (91.4)			
LN stage (n = 108)					
1 (negative)	5 (19.2)	21 (80.8)	2.551	0.145	*0.131*
2 (positive)	7 (8.5)	75 (91.5)			
Mitosis (n = 159)					
≤10	7 (12.5)	49 (87.5)	1.492	0.060	*0.451*
>10	9 (8.7)	94 (91.3)			
NPI (n = 109)					
Moderate to good NPI (<3.4–5.4)	4 (12.1)	29 (87.9)	1.172	0.023	*0.807*
Poor NPI (>/=5.41)	8 (10.5)	68 (89.5)			
Clinical prognostic stage (n = 184)					
I&II	5 (7.5)	60 (92.3)	0.818	−0.026	*0.721*
III	11 (9.2)	108 (90.8)			

There was an inverse association with ER expression (r = −0.145, OR = 0.209, 95% CI- 0.047–0.928, $p = 0.025$) but no significant association existed between PR and Her2 (Table 2).

3.1. CD44/CD24/ALDH1 combination phenotypes

The predominant combination phenotype was $CD44^{+}/CD24^{+}/$

Table 2
Associations between ALDH1A1 expression, Hormone receptor status, Her2, CD24 and CD44 status.

Marker	ALDH1A1 cytoplasmic expression			Significance	
	Negative (%)	Positive (%)	OR (95%CI)	r	*p value*
ER					
Positive	2 (10.0)	67 (34.7)	1.0	−0.145	*0.025*
Negative	18 (90.0)	126 (65.3)	0.209 (0.047–0.928)		
PR					
Positive	4 (19.0)	67 (34.7)	1.0	−0.099	*0.148*
Negative	17 (81.0)	126 (65.3)	0.442 (0.143–1.368)		
Her2					
Positive	3 (15.8)	35 (19.0)	1.0	−0.024	*0.731*
Negative	16 (84.2)	149 (81.0)	0.798 (0.220–2.891)		
CD24					
Negative	9 (45.0)	11 (55.0)	1.0	0.228	*0.001*
Positive	29 (15.1)	163 (84.9)	4.599 (1.751–12.075)		
CD44					
Negative	6 (28.6)	15 (71.4)	1.0	0.228	*0.001*
Positive	13 (6.7)	180 (93.3)	5.538 (1.841–16.662)		
$CD44^+/CD24^-$					
Negative	6 (30.0)	14 (70.0)	1.0	0.134	*0.052*
Positive	26 (13.6)	165 (86.4)	2.720 (0.959–7.710)		
Molecular subtypes					
Luminal A	4 (20.0)	64 (36.7)	1		*0.080*
Luminal B	0 (0.0)	21 (11.2)	NA		
Her2+	4 (20.0)	18 (9.6)	1.481 (0.428–5.128)	0.058	
Triple Neg	12 (60.0)	80 (42.6)	0.0386 (0.119–1.253)	−0.165	

$ALDH1^+$ representing 72% of the total. $CD44^+/CD24^-/ALDH1^+$ was the second most occurring combination phenotype (12.3%). The least occurring combination phenotype was $CD44^-/CD24^+/ALDH1^-$ representing 0.9%. Table 3 shows the frequency of the combination phenotypes and Table 4 also shows the distribution of CD44/CD24/ALDH1 combination phenotypes across molecular subtypes.

From Table 5, $CD44^+/CD24^-/ALDH1^+$ had significant associations with age (*p- 0.020*, r = 0.161, OR- 2.771, 95%CI 1.147–6.697), gender (*p = 0.004*, OR- 15.333 95%CI 1.339–175.54), tumour grade (*p = 0.005*, r = 0.197, OR-3.913 95%CI 1.421–10.776) and clinical prognostic staging (*p = 0.014*, r = 0.182, OR-3.028 95%CI- 1.217–7.536). There was no association between $CD44^+/CD24^-/ALDH1^+$ and the molecular subtypes (Table 2).

There were significant inverse associations between $CD44^+/CD24^+/ALDH1^+$ and grade (*p = 0.003*, r = −0.206, OR-0.281, 95%CI 0.116–0.683) and mitotic count (*p = 0.023*, r = −0.182, OR-0.438 95% CI-0.212–0.909) (Table 5).

$CD44^-/CD24^-/ALDH1^+$ combination phenotype was only associated with mitosis (*p = 0.017*, r = 0.192) and NPI (*p = 0.028*, r = 0.212). There was however no association between $CD44^-/CD24^+/ALDH1^+$ and any of the clinicopathological parameters (Table 5).

This study recorded no association between the combination phenotypes and the molecular subtypes (*p = 0.555*).

Table 3
Frequency distribution of combination phenotypes.

Phenotypes	Frequency	Percent
CD44+/CD24-/ALDH+	26	12.3
CD44-/CD24-/ALDH1+	3	1.4
CD44-/CD24+/ALDH1+	10	4.7
CD44+/CD24+/ALDH1+	152	72.0
CD44+/CD24-/ALDH1-	7	3.3
CD44-/CD24-/ALDH1-	3	1.4
CD44-/CD24+/ALDH1-	2	0.9
CD44+/CD24+/ALDH1-	8	3.8
Total	211	100.0

4. Discussion

There is considerable evidence of ALDH1 as a breast cancer stem cell marker marker [5,25,26]. Breast cancer in Africans and those of African descent are known to be very aggressive with poor prognosis. This study explored the expression of ALDH1A1 and its association with $CD44^+/CD24^{-/low}$ and the effects of the combined phenotype ($CD44^+/CD24^{-/low}/ALDH1^+$) on the molecular and clinicopathological features of breast cancers in an African population.

A high expression of ALDH1A1 of about 90% was recorded in this current study. This percentage is higher than what has been reported in some earlier studies [8,27,28] but comparable to Althobiti et al. and Pan et al.'s studies which reported 71% and 93% ALDH1 expression respectively [10,29]. This high expression is however not consistent with the general assertion that CSC represent a minute subpopulation of cells in the tumour microenvironment [30,31]. Higher expression of ALDH1 has been associated with Triple negative breast cancer [16,32] and hence might explain the high expression in our cohort with a relatively high triple negative prevalence of 44.3%. This disparity may also be attributable to the varied range of cut off points and scoring systems employed by various investigators. This study used the semi quantitative H scoring method widely accepted both in research and in clinical practice.

It was observed from our African cohort that ALDH1A1 as a stand-alone breast cancer stem cell marker was not associated with any of the clinicopathological parameters. This finding was contrary to what has been reported some literature. For instance, Yao et al. analysed 137 paraffin embedded breast tissues and found an association with tumour grade, size and node metastasis in an Asian cohort [16]. A relatively larger Caucasian study (n = 930) recently published in early stage invasive breast cancer also revealed ALDH1A1 associated with high grade, high mitotic count, increased nuclear pleomorphism, poor NPI, advanced nodal stage (≥4 positive nodes) and lympho-vascular invasion. However at the protein level of this same paper, there was no association transcriptionally [29]. Furthermore, our finding also differed from an African study by Nalwoga and colleagues, who analysed 192 breast carcinomas in Uganda and had associations with tumour grade, high mitotic count, and high nuclear grade [33]. In their study however, there was no evidence of the use of the more specific ALDH1A1 isozyme used in this study which may account for the disparity.

Despite the non-association of ALDH1A1 with the clinicopathological parameters, this study recorded an association with ER negativity in keeping with Nalwoga et al.'s but not with PR and Her2 status as the latter concluded. There was no association between ALDH1 and triple negative breast cancer, a non-consistent finding to Nalwoga et al.'s study [33]. The difference in findings might also be attributable to the different scoring systems and the cut off points for the IHC.

Although ALDH1 as a stand-alone BCSC marker was not associated with clinicopathological parameters the combination phenotype $CD44^+/CD24^-/ALDH1^+$ was associated with increased age, higher histological grade, and higher clinical prognostic staging. This goes to affirm the assertion of $CD44^+/CD24^-/ALDH1^+$ phenotype having a higher tumourigenic potential as evidenced by high tumour grade [34] and poor prognosis [32]. It was interesting to note that $CD44^-/CD24^-/ALDH1^+$ phenotype also had features of aggression as an association was found with higher mitotic count and higher NPI (Table 5); a finding not yet reported in any literature to the best of our knowledge. This implies

Table 4
The distribution of CD24/CD44/ALDH1 combination phenotypes across molecular subtypes.

Hormonal status	$CD44^+/CD24^-/ALDH^+$	$CD44^-/CD24^-/ALDH1^+$	$CD44^-/CD24^+/ALDH1^+$	$CD44^+/CD24^+/ALDH1^+$	$CD44^+/CD24^-/ALDH1^-$	$CD44^-/CD24^-/ALDH1^-$	$CD44^-/CD24^+/ALDH1^-$	$CD44^+/CD24^+/ALDH1^-$	Total
Luminal A	11 (45.8)	2 (66.7)	3 (33.3)	52 (34.7)	1 (16.7)	1 (33.3)	1 (50.0)	1 (12.5)	72
Luminal B	2 (8.3)	0 (0.0)	3 (33.3)	16 (10.7)	0 (0.0)	0 (0.0)	0 (0.0)	0	21
Her2+	2 (8.3)	0 (0.0)	0	16 (10.7)	0 (0.0)	0 (0.0)	1 (50.0)	3 (37.5)	22
Triple negative	9 (37.5)	1 (33.3)	3 (33.3)	66 (44.0)	5 (83.3)	2 (66.7)	0 (0.0)	4 (50.0)	90
Total	24	3	9	150	6	3	2	8	205

Table 5
Association between CD44/CD24/ALDH1 combination phenotypes and clinicopathological features.

Parameter		$\%CD44^+CD24^-ALDH1^+$	$\%ofCD44^+CD24^+ ALDH1^+$	$\%ofCD44^-CD24^-ALDH1^+$	$\%ofCD44^-CD24^+ALDH1^+$
Age	<50 (n = 100)	69.2 (n = 18)	45.3 (n = 68)	33.3 (n = 1)	30.0 (n = 3)
	≥50 (n = 109)	30.8 (n = 8)	54.7 (n = 82)	66.7 (n = 2)	70.0 (n = 7)
	OR	2.771 (1.147–6.697)	0.700 (0.338–1.281)	0.540 (0.048–6.053)	0.451 (0.113–1.793)
	r	0.161	−0.080	−0.035	−0.080
	p	*0.020**	*0.246*	*0.612*	*0.247*
Grade	1 (n = 23)	28.0 (n = 7)	7.4 (n = 11)	33.3 (n = 1)	10.0 (n = 1)
	2&3 (n = 179)	72.0 (n = 18)	92.6 (n = 137)	66.7 (n = 2)	90.0 (n = 9)
	OR	3.913 (1.421–10.776)	0.281 (0.116–0.683)	4.023 (0.350–46.199)	0.859 (0.104–7.104)
	r	0.197	−0.206	0.085	−0.010
	p	*0.005**	*0.003**	*0.228*	*0.887*
Tumour size	≤2 (n = 15)	16.7 (n = 4)	6.7 (n = 9)	0.0 (n = 0)	10.0 (n = 1)
	>2 (n = 173)	83.3 (n = 20)	93.3 (n = 125)	100.0 (n = 3)	90.0 (n = 9)
	OR	2.782 (0.809–9.571)	0.576 (0.195–1.705)		1.302 (0.154–11.028)
	r	0.123	−0.073	−0.037	0.018
	p	*0.093*	*0.314*	*0.607*	*0.808*
Gender	Male (n = 3)	7.7 (n = 2)	0.7 (n = 1)	0.0 (n = 0)	0.0 (n = 0)
	Female (n = 208)	92.3 (n = 24)	99.3 (n = 151)	100.0 (n = 3)	100 (n = 10)
	OR	15.333 (1.339–175.54)	0.189 (0.017–2.122)		
	p	*0.004**	*0.130*	*0.834*	*0.670*
Vascular invasion	Present (n = 103)	68.8 (n = 11)	63.6 (n = 77)	66.7 (n = 2)	87.5 (n = 7)
	Absent (n = 55)	31.3 (n = 5)	36.4 (n = 44)	33.3 (n = 1)	12.5 (n = 1)
	OR	1.133 (0.374–3.438)	0.636 (0.298–1.357)	1.019 (0.090–11.481)	3.738 (0.448–31.163)
	r	0.017	*−0.091*	0.001	0.101
	p	*0.825*	*0.240*	*0.988*	*0.193*
Tumour weight	<1000 (n = 43)	40.0 (n = 2)	45.7 (n = 32)	100.0 (n = 2)	60.0 (n = 3)
	≥1000 (n = 49)	60.0 (n = 3)	54.3 (n = 38)	0.0 (n = 0)	40.0 (n = 2)
	OR	0.748 (0.119–4.70)	0.842 (0.323–2.197)		1.763 (0.280–11.078)
	r	−0.032	−0.307	0.159	0.064
	p	*0.756*	*0.725*	*0.063*	*0.541*
Lymph node stage	Negative (n = 26)	22.2 (n = 2)	21.3 (n = 17)	50.0 (n = 1)	25.0 (n = 1)
	Positive (n = 81)	77.8 (n = 7)	78.8 (n = 63)	50.0 (n = 1)	75.0 (n = 3)
	OR	0.881 (0.171–4.530)	0.540 (0.206–1.414)	3.200 (0.193–53.043)	1.040 (0.103–10.452)
	r	−0.015	−0.122	0.083	0.003
	p	*0.879*	*0.206*	*0.392*	*0.973*
Mitosis	<10 (n = 54)	44.4 (n = 8)	29.5 (n = 33)	100 (n = 3)	42.9 (n = 3)
	≥10 (n = 101)	55.6 (n = 10)	70.5 (n = 79)	0.0 (n = 0)	57.1 (n = 4)
	OR	1.583 (0.585–4.281)	0.438 (0.212–0.902)		1.426 (0.307–6.620)
	r	0.073	−0.182	0.192	0.037
	p	*0.363*	*0.023**	*0.017**	*0.649*
Nottingham prognostic index	<3.4–5.4 (n = 32)	30.0 (n = 3)	27.5 (n = 22)	100.0 (n = 2)	25.0 (n = 1)
	>5.4 (n = 76)	70.0 (n = 7)	72.5 (n = 58)	0.0 (n = 0)	75.0 (n = 3)
	OR	1.020 (0.246–4.220)	0.683 (0.273–1.706)		0.785 (0.079–7.844)
	r	0.003	*−0.079*	0.212	−0.020
	p	*0.485*	*0.413*	*0.028**	*0.863*
Triple negative status	Present (n = 91)	73.3 (n = 66)	73.3 (n = 66)	1.3 (n = 1)	3.3 (n = 3)
	Absent (n = 116)	26.7 (n = 24)	26.7 (n = 24)	98.7 (n = 89)	96.7 (n = 87)
	OR	0.741 (0.308–1.780)	1.015 (0.544–1.892)	0.635 (0.057–7.114)	0.626 (0.152–2.577)
	r	−0.047	0.003	−0.026	−0.046
	p value	*0.501*	*0.963*	*0.710*	*0.513*
Clinical prognostic staging	I & II (n = 65)	59.1 (n = 13)	32.8 (n = 44)	0.0 (n = 0)	33.3 (n = 3)
	III (n = 118)	40.9 (n = 9)	67.2 (n = 90)	100 (n = 3)	66.7 (n = 62)
	OR	3.028 (1.217–7.536)	0.652 (0.333–1.275)		0.903 (0.218–3.738)
	r	0.182	−0.093	−0.096	−0.010
	p value	*0.014**	*0.210*	*0.195*	*0.888*

* significant at 95% Confidence Interval

that in the absence of CD44 and CD24 expression, ALDH1A1 shows features of aggression and poor prognosis. To speculate, the expression of CD44 and CD24 may hinder or neutralize the aggressiveness conferred by ALDH1A1.

$CD44^+/CD24^+/ALDH1^+$ was the only phenotype among all combination phenotypes that did not relate to any feature of aggressiveness as

it was associated with lower histological grade and less mitotic count (Table 5).

5. Conclusion

This study has established that a high expression of ALDH1A1 in breast cancers in Africans and this is associated with adverse clinicopathological parameters. It further confirms the increased tumourigenic potential of the $CD44^{+}/CD24^{-}/ALDH1^{+}$ phenotype. The high expression of ALDH1A1 in Africans and its association with poor clinicopathological features makes it an important marker for targeted therapies among this race which is notable for more aggressive breast cancer. It is therefore highly recommended that survival studies are conducted in African populations to help further understand the role of ALDH1 in contributing to breast tumour aggressiveness.

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Ethical approval

This article does not contain any studies with human participants performed by any of the authors.

Consent for publication

'Not applicable'.

Availability of data

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

CRediT authorship contribution statement

Eric Gyan: laboratory work, writing the manuscript, data analysis and interpretation. **Linda Ahenkorah-Fondjo**: reviewing and editing the manuscript. **Patrick K. Akakpo and Leonard Derkyi-Kwarteng**: contributed by double scoring and reviewing the manuscript. **Michael S. Toss**: Laboratory work and reviewing the manuscript. **Ganiyu A. Rahman**: reviewing and editing the manuscript. **Andrew Jackson**: reviewing and editing the manuscript. **William Owiredu**: reviewing and editing the manuscript **Andrew Green**: reviewing and editing the manuscript. All authors read and approved the final manuscript.

Declaration of competing interest

The authors declare that they have no competing interests.

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Data file

Data to this work is available on reasonable request.

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