Association between Cyclin D1 G870A (rs9344) polymorphism and cancer risk in Indian population: meta-analysis and trial sequential analysis

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Introduction: Association between Cyclin D1 (CCND1) single nucleotide polymorphism (SNP) rs9344 and cancer risk is paradoxical. Thus, we performed a meta-analysis to explore the association between CCND1 variant and overall cancer risk in Indian population.

Methods: Data from 12 published studies including 3739 subjects were collected using PubMed and Embase. RevMan (Review Manager) 5.3 was used to perform the meta-analysis. OR with 95%CI were calculated to establish the association.

Results: Overall, the cumulative findings demonstrated that CCND1 polymorphism (rs9344) was not significantly associated with cancer risk in all the genetic models studied (dominant model: GG vs GA+AA: OR (95%CI) = 0.81 (0.60–1.09), P=0.17; recessive model: GG+GA vs AA: OR (95%CI) = 1.23 (0.96–1.59), P=0.11; co-dominant model: GG vs AA: OR (95%CI) = 1.35 (0.93–1.97), P=0.12; co-dominant model: GG vs GA: OR (95%CI) = 1.16 (0.85–1.59), P=0.34; allelic model: A vs G: OR (95%CI) = 1.20 (1.14–2.85), P=0.23; allelic model: G vs A: OR (95%CI) = 0.83 (0.62–1.12), P=0.23). Subgroup analysis according to cancer types presented significant association of CCND1 polymorphism and increased breast cancer risk in dominant model (GG vs GA+AA: OR (95%CI) = 2.75 (1.54–4.90), P=0.0006) and allelic model (G vs A: OR = 1.63, 95%CI = 1.22–2.19, P=0.001). An increased esophageal cancer risk in recessive model (GG+GA vs AA: OR = 1.51, 95%CI = 1.05–2.16, P=0.03) and co-dominant model (GG vs AA: OR = 2.51, 95%CI = 1.10–5.71, P=0.03) was detected. A higher risk for colorectal cancer was detected under both the co-dominant models (GG vs AA: OR = 2.46, 95%CI = 1.34–4.51, P=0.004 and GG vs GA: OR = 1.74, 95%CI = 1.14–2.67, P=0.01). However, in case of cervical cancer risk a non-significant association was reported under the recessive model (GG+GA vs AA: OR = 1.52, 95%CI = 0.60–3.90, P=0.38) with reference to CCND1 polymorphism (rs9344). The trial sequential analysis (TSA) showed that the cumulative Z-curve neither crossed the trial sequential monitoring boundary nor reached the required information size (RIS). Thus, present meta-analysis remained inconclusive due to insufficient evidence.

Conclusion: CCND1 polymorphism rs9344 may not have a role in overall cancer susceptibility in Indian population. However, this polymorphism acts as a crucial risk factor for breast, esophageal, and colorectal cancer but not for cervical cancer. Future studies with larger sample size are required to draw a reliable conclusion.

Introduction: Cancer is a major global health problem and it is worse in case of low- and middle-income developing countries. According to India’s National Cancer Registry Program (NCRP), 1.45 million cases would...
Table 1 Characteristics of the studies included in the meta-analysis

| S.No. | PMID    | Authors                  | Publication year | Country | Ethnicity | Source of control | Cancer type       | Genotyping methods |
|-------|---------|--------------------------|------------------|---------|-----------|-------------------|-------------------|-------------------|
| 1.    | 16488657| Sathyan et al.           | 2006             | India   | Asian     | Hospital based    | Oral cancer       | PCR-SSCP          |
| 2.    | 17011980| Sobti et al.             | 2006             | India   | Asian     | Hospital based    | Lung cancer       | PCR               |
| 3.    | 17561354| Jain et al.              | 2007             | India   | Asian     | Hospital based    | Esophageal cancer | PCR-RFLP          |
| 4.    | 18548202| Kaur et al.              | 2008             | India   | Asian     | Hospital based    | Cervical cancer   | PCR-RFLP          |
| 5.    | 19489683| Thakur et al.            | 2009             | India   | Asian     | Hospital based    | Cervical cancer   | PCR-RFLP          |
| 6.    | 20380574| Gangwar et al.           | 2010             | India   | Asian     | Hospital based    | Urinary bladder   | PCR-RFLP          |
| 7.    | 21268129| Hussain et al.           | 2011             | India   | Asian     | Hospital based    | Esophageal        | PCR-RFLP          |
| 8.    | 20822933| Mandal et al.            | 2012             | India   | Asian     | Hospital based    | Prostate cancer   | PCR-RFLP          |
| 9.    | 23354584| Sameer et al.            | 2013             | India   | Asian     | Hospital based    | Colorectal cancer | PCR-RFLP          |
| 10.   | 24604328| Wasson et al.            | 2014             | India   | Asian     | Hospital based    | Breast cancer     | PCR-RFLP          |
| 11.   | 24604328*| Wasson et al.           | 2014             | India   | Asian     | Hospital based    | Breast cancer     | PCR-RFLP          |
| 12.   | 25146682| Govatati et al.          | 2014             | India   | Asian     | Hospital based    | Colorectal cancer | PCR               |

Abbreviation: RFLP, restriction fragment length polymorphism. *PMID24604328 taken twice.

occur in 2016 with 0.74 million deaths in India. This is expected to rise to 1.73 million cases and 0.88 million deaths in 2020 [1,2]. Cancer is considered the disease of abnormal cell division. Besides, many environmental cofactors (smoking, use of alcohol, exposure to UV radiations, infections with certain viruses) and host genetic makeup has been recognized as a pivotal risk factor for human cancers.

India ranks third in the world in terms of incidence rate of cancer cases amongst women after China and the U.S.A. According to the Globocan report 2012, there were ~232000 breast cancer cases registered in the U.S.A., however in India, 145000 new cases were reported. The burden of breast cancer in India is approximately two-thirds of that of the U.S.A. and is growing progressively [3]. Breast cancer is one of the most common malignancies in women worldwide, and each year more than 1 million new cases are diagnosed [4]. The main risk factors for breast cancer are genetic predisposition, lifestyle, and environment [5–7]. Genetic polymorphisms have been identified as one of the crucial factor for determining inter-individual susceptibility to cancer [8]. The clinical importance of \textit{CCND1} gene lies in the fact that 5–20% of breast cancer cases present with either amplified or deleted version of the gene [9,10]. \textit{CCND1} is a key cell cycle regulatory gene which governs the G1/S checkpoint in cell cycle. It is one of the most frequently altered molecules in human carcinogenesis. A common G/A SNP \textit{dbSNP ID rs9344} was first described by Betticher et al. (1995) [18]. This SNP rs9344 is located at codon 242 in the exon-4/intron boundary of \textit{CCND1} and responsible for alternate splicing of transcripts with different half-lives [18]. Since then many case–control studies have been conducted to explore the potential association between \textit{CCND1} SNP (rs9344) and cancer susceptibility.
Table 2 Distribution of CCND1-G870A genotypes and allelic frequency in cancer cases and controls

| S.No. | PMID   | Cancer type          | Case n | Control n | Case GG | Case GA | Case AA | Control GG | Control GA | Control AA | A G | A G | A G |
|-------|--------|----------------------|--------|-----------|---------|---------|---------|------------|------------|------------|-----|-----|-----|
| 1.    | 16488657 | Oral cancer         | 146    | 137       | 36      | 71      | 39      | 40         | 61         | 36         | 0.51 | 0.49 | 0.49 |
| 2.    | 17011980 | Lung cancer         | 151    | 151       | 29      | 87      | 35      | 39         | 69         | 43         | NA  | NA  | NA  |
| 3.    | 17561354 | Esophageal cancer   | 151    | 201       | 22      | 76      | 53      | 37         | 111        | 53         | NA  | NA  | NA  |
| 4.    | 18548202 | Cervical cancer     | 150    | 150       | 33      | 64      | 53      | 30         | 65         | 55         | NA  | NA  | NA  |
| 5.    | 1948683  | Cervical cancer     | 200    | 200       | 39      | 94      | 67      | 47         | 119        | 34         | 228 | 172 | 217 |
| 6.    | 20380574 | Urinary bladder cancer | 212  | 250       | 48      | 85      | 79      | 58         | 119        | 73         | 243 | 181 | 265 |
| 7.    | 20622933 | Prostate cancer     | 192    | 224       | 38      | 65      | 89      | 58         | 93         | 73         | 243 | 141 | 239 |
| 8.    | 21268129 | Esophageal cancer   | 151    | 151       | 20      | 99      | 32      | 56         | 72         | 23         | 163 | 139 | 118 |
| 9.    | 23354584 | Colorectal cancer   | 130    | 160       | 19      | 70      | 41      | 41         | 76         | 43         | NA  | NA  | NA  |
| 10.   | 24604328 | Breast cancer       | 151    | 83        | 33      | 77      | 41      | 07         | 47         | 29         | 159 | 143 | 105 |
| 11.   | 24604328* | Breast cancer    | 54     | 134       | 15      | 31      | 08      | 18         | 78         | 38         | 47  | 61  | 154 |
| 12.   | 25146682 | Colorectal cancer   | 103    | 107       | 54      | 39      | 10      | 71         | 33         | 03         | 59  | 147 | 39  |

*PMID: 24604328 repeated twice in our study. NA, not available.

Table 3 Meta-analysis results based on different genetic models

| S.No. | Category                  | OR      | [95%CI] | P^2   | P_H  | I^2 (%) | Statistical method |
|-------|---------------------------|---------|---------|-------|------|---------|-------------------|
| 1.    | Dominant model (GG vs GA+AA) | 0.81    | [0.60–1.09] | 0.17  | <0.0001 | 72% | Random |
| 2.    | Recessive model (GG+GA vs AA) | 1.23    | [0.96–1.59] | 0.11  | 0.001 | 64% | Random |
| 3.    | Co-dominant model (AA vs GG) | 1.35    | [0.93, 1.97] | 0.12  | <0.0001 | 72% | Random |
| 4.    | Co-dominant model (GA vs GG) | 1.16    | [0.85, 1.59] | 0.34  | 0.0002 | 69% | Random |
| 5.    | Allele model (A vs G) | 1.20    | [1.14–2.85] | 0.23  | <0.00001 | 82% | Random |
| 6.    | Allele model (G vs A) | 0.83    | [0.62–1.12] | 0.23  | <0.00001 | 82% | Random |

Abbreviations: P_H, P value for heterogeneity; P^2, P value for Z-test.

Occurrence of this nucleotide variation has been found to be coupled with the risk of various cancers including cervical, breast, oral, esophageal, lung, urinary bladder, prostate, and colorectal [19–29]. The outcomes of these studies were inconsistent in different ethnic groups. To overcome this conflict, several meta-analyses have been performed worldwide to see the effect of CCND1 polymorphism and risk for different types of cancer [30–35]. To the best of our knowledge, no report is available from India addressing the impact of CCND1 SNP and overall cancer risk. Hence, we aimed to investigate the role of CCND1 polymorphism G870A (rs9344) in overall cancer susceptibility amongst Indian population by conducting this meta-analysis. The present data could be helpful in enriching the existing knowledge with respect to involvement of CCND1 polymorphism and cancer susceptibility in Indian population.

Methods

Literature search strategy

PubMed and Embase databases were searched with the keywords ‘CCND1’, ‘Cyclin D1’, ‘SNP’, ‘cancer’, ‘India’, and ‘polymorphism’ for literature published till September 2016. All studies included in the present meta-analysis met the following inclusion and exclusion criteria.
Inclusion criteria
(i) Prospective or case–control studies involving association analysis between CCND1 SNP G870A (rs9344) and cancer susceptibility, (ii) studies included Indian population, (iii) genotypic and allelic details are provided for both the cases and control groups, (iv) full text available, and (v) articles published in English language.

Exclusion criteria
(i) Studies published on populations other than Indian, (ii) articles published in languages except English, and (iii) articles not providing genotypic and allelic details.

Data retrieval
Data from all eligible studies were retrieved independently by two investigators (N.T. and S.K.). The retrieved data incorporated the following details: (i) PubMed IDentifier (PMID), (ii) name of the first author, (iii) year of publication, (iv) country, (v) sources of controls, (vi) methods for genotyping, and (vii) frequency of genotypic and allelic data.

Quality assessment
Quality of the included studies was assessed by assigning the quality scores as previously mentioned by He et al. (2014) [36]. The scores were assigned to each qualified studies between 0 and 10. Studies with >5 scores were included for the further analyses (Supplementary Table S1).

Meta-analysis
RevMan (Review Manager) is an easy tool to perform the meta-analyses and generate the graphs (forest plot, funnel plot) in publication standard. Meta-analysis of CCND1 gene G870A polymorphism (rs9344) was performed by RevMan 5.3 [37]. For statistical models, both fixed model and random model were included in the RevMan. For random models, DerSimonian and Laird random-effects models were used. Odds ratios (ORs) with 95% confidence intervals (95%CIs) were used to assess the strength of association between the CCND1-G870A polymorphisms and cancer risk. The pooled OR was evaluated by the Z-test and a P-value <0.05 suggests a significant association.

I² was used to estimate total variation across studies due to heterogeneity in percentage. A percentage of <25% was considered as a low level of heterogeneity, 25–50% as a moderate level of heterogeneity, and >50% as a high level of heterogeneity. I² > 50% could suggest heterogeneity and suggest using a random-effect estimate [38]. Otherwise, the fixed-effect model was used to calculate pooled ORs [39].

Software RevMan 5.3 used in this meta-analysis is freely available at http://community.cochrane.org/tools/review-production-tools/revman-5/revman-5-download

Statistical analysis
The association between CCND1 polymorphism and cancer risk was analyzed by OR with 95%CI in different genetic models: dominant (GA+AA vs GG), recessive (AA vs GG+GA), co-dominant (GA vs GG and AA vs GG), and allelic (A vs G and G vs A). The P-value <0.05 was considered statistically significant. Subgroup analysis was done after stratification of data according to various cancer types.

Heterogeneity was calculated by chi-square test and the extent of heterogeneity was measured by the value of I² statistic. The OR of different types of genetic models was evaluated by employing the fixed-effect model (when I² < 50%) or random-effect model (when I² > 50%). Egger's bias test and Begg's funnel plot was used to assess the publication bias [40,41]. It is a well-acknowledged fact that meta-analyses are vulnerable to random errors due to sparse data and repetitive testing of accrued data [42]. Hence, trial sequential analysis (TSA) was performed to minimize the type I error and random error as the present study had smaller sample size. TSA was performed as described previously by Fu et al. (2017) [43]. It was done by using TSA software version 0.9.5.10. (http://www.ctu.dk/tsa/) [44] to calculate the required information size (RIS) (meta-analysis sample size) by taking the control event proportion to 25.77%, experimental event proportion 21.55%, a relative risk reduction (RRR) 10%, power 80%, and type I error (α) 5%. The monitoring boundaries were constructed to determine whether present meta-analysis is sufficiently powered and conclusive. Therefore, it is able to reject false-positive reports from meta-analysis [45]. If the Z-curve crosses the TSA boundaries or futility area, there is sufficient information to support the conclusions and further trials are unlikely to change the findings. If the Z-curve does not cross the any of the boundaries or reach the RIS, evidence is insufficient to reach a firm conclusion.
Results

Study characteristics

Using the Pubmed and Embase database, a total of 12 studies were searched independently by two investigators (S.K. and N.T.) according to the methodology depicted in flow diagram (Figure 1).

Data from one study with PMID 24604328 was extracted twice. All the 12 studies including 1791 cancer cases and 1948 controls met our inclusion criteria. The characteristics of included studies for the present meta-analysis from different cancers are presented in Table 1.

Details of genotypic and allelic frequencies of CCND1 polymorphism is shown in Table 2.

Meta-analysis of CCND1 G/A polymorphism (rs9344)

A total of 12 studies were included in the analysis to evaluate the association between CCND1 polymorphism and cancer risk in Indian population. The results from meta-analysis of the association between CCND1 polymorphism (rs9344) and cancer risk in 12 case–control studies are shown in Figure 2 and Table 3. Values of ORs with 95%CI were as follows: dominant model (GG vs GA+AA: OR = 0.81, 95%CI = 0.60–1.09, P=0.17, I² = 72%); recessive model (GG+GA vs AA: OR = 1.23, 95%CI = 0.96–1.59, P=0.11, I² = 64%); co-dominant model (GG vs AA: OR = 1.35, 95%CI = 0.93–1.97, P = 0.12, I² = 72%); co-dominant model (GG vs GA: OR = 1.16, 95%CI = 0.85–1.59, P=0.34, I² = 69%); allele model (A vs G: OR = 1.20, 95%CI = 1.14–2.85, P=0.23, I² = 82%); and allele model (G vs A: OR = 0.83, 95%CI = 0.62–1.12, P=0.23, I² = 82%) (Table 3). If the values of I² were >50% then the random-effect model was applied, otherwise fixed-effect model was used to calculate the pooled ORs and 95% CI. In meta-analysis, P²<0.05 was considered statistically significant. Here, we demonstrate that CCND1 polymorphism G870A (rs9344) is not associated with the risk for overall cancers in Indian population.

On subgroup analysis stratified according to cancer types showed significant association of CCND1 polymorphism and increased breast cancer risk in dominant model (GG vs GA+AA: OR = 2.75, 95%CI = 1.54–4.90, P=0.0006), allelic model (G vs A: OR = 1.63, 95%CI = 1.22–2.19, P=0.001). A statistically significant association with esophageal cancer risk was observed in recessive (GG+GA vs AA: OR = 1.51, 95%CI = 1.05–2.16, P=0.03) and co-dominant model (GG vs AA: OR = 2.51, 95%CI = 1.10–5.71, P=0.03). An increased risk for colorectal cancer was detected under both the co-dominant models (GG+GA vs AA: OR = 2.46, 95%CI = 1.34–4.51, P=0.004 and GG vs GA: OR = 1.74, 95%CI = 1.14–2.67, P=0.01). Contrary to this, none of the genetic model reported a statistically significant association with cervical cancer risk. Although a non-significant association was observed in recessive model (GG+GA vs AA: OR = 1.52, 95%CI = 0.60–3.90, P=0.38) and co-dominant model (GG vs AA: OR = 1.45, 95%CI = 0.55–3.85, P=0.46) with reference to CCND1 polymorphism (rs9344) (Figures 3–6 and Table 4).
Figure 2. Forest plots describing the association of \textit{CCND1}-G870A polymorphism with overall cancer risk (Continues on next page)
Figure 2. Forest plots describing the association of CCND1-G870A polymorphism with overall cancer risk
(A) dominant model (GG vs GA+AA); (B) recessive model (GG+GA vs AA); (C) co-dominant model (GG vs GA); (D) co-dominant model (GG vs AA); (E) allele model (A vs G); (F) allele model (G vs A).

Heterogeneity measurement
Heterogeneity value depicted as $I^2$ was calculated for different genetic models and presented in Table 3. Heterogeneity was observed in all the genotypic and allelic models. For dominant model: GG vs GA+AA: $I^2 = 72\%$, $P$ for heterogeneity < 0.0001; recessive model: GG+GA vs AA: $I^2 = 64\%$, $P$ for heterogeneity = 0.001; co-dominant model: GG vs AA: $I^2 = 69\%$, $P$ for heterogeneity = 0.0002; co-dominant model: GG vs GA: $I^2 = 72\%$, $P$ for heterogeneity = 0.0001;
allelic model: A vs G: $I^2 = 82\%$, $P$ for heterogeneity <0.00001 and allelic model: G vs A: $I^2 = 82\%$, $P$ for heterogeneity <0.00001 were noted, respectively (Table 3).

**Publication bias**

Funnel plots were used in random-effect and fixed-effect models respectively to detect the publication bias. A relatively symmetric distribution in the funnel plot was observed, which indicates that there is no significant publication bias in the included studies (Figure 7).

![Figure 3](https://portlandpress.com/bioscirep/article-pdf/38/6/BSR20180694/809663/bsr-2018-0694.pdf)
Figure 3. Forest plots describing the association of CCND1-G870A polymorphism with breast cancer risk (A) dominant model (GG vs GA+AA); (B) recessive model (GG+GA vs AA); (C) co-dominant model (GG vs GA); (D) co-dominant model (GG vs AA); (E) allele model (A vs G); (F) allele model (G vs A).

TSA
The TSA for association between CCND1 polymorphism (rs9344) and overall cancer risk showed that only conventional boundary was crossed by Z-curve, however, it neither crossed the TSA boundary nor the futility area. And the total sample size (3739) did not reach the RIS (11375) (Figure 8). This result indicates that present meta-analysis is inconclusive at this level. Further studies/trials are needed to make this association valid.

Discussion
CCND1 is key driver of normal cell cycle regulation and genetic variation in this gene has been reported in many types of cancers. A SNP G870A (rs9344) located on exon-4–intron boundary of CCND1 has been studied extensively in several cancer types. Several reports from different parts of the world have been published with reference to CCND1 polymorphism and risk of various types of cancers including cervical, prostate, colorectal, urinary bladder, squamous cell carcinoma of the head and neck etc. [46–50]. Investigators from India also tried to explore the association of CCND1 polymorphism and susceptibility to different cancer types including cervical, breast, oral, esophageal, lung, urinary bladder, prostate, and colorectal [19–29]. However, these reports are conflicting thus we performed meta-analysis on the literature available in order to provide more accurate information on the role of CCND1 G870A (rs9344) polymorphism and overall cancer risk in Indian population. Although, various meta-analyses on individual cancer susceptibility have been published globally [30–35]. Pabalan et al. (2008) [51], performed a meta-analysis on role of CCND1 G870A polymorphism in different types of cancers and populations. However, a comprehensive data are lacking from India with overall cancer risk. Hence, we have designed the present study focussed on Indian population.

The present meta-analysis, contained a total of 12 studies comprising 1791 cancer cases and 1948 controls [19–29] showed the lack of significant association between CCND1 G870A polymorphism (rs9344) and overall cancer risk in all the genetic models. These findings are consistent with the result of another study by Luo et al. (2016) [52], which ruled out the involvement of CCND1 polymorphism (G870A) with the risk of hepatocellular carcinoma. In the similar lines, study by Zheng et al. (2015) [53] suggested that CCND1 polymorphism may not be associated with the risk of prostate cancer. Similarily, Wang et al. (2018) [54] also found no significant association between the let-7i rs10877887 and let-7a-1/let-7f-1/let-7d rs13293512 polymorphisms and overall cancer risk. In disagreement with our findings a meta-analysis by Pabalan et al. (2008) [51], showed an increased cancer risk associated with CCND1-A870G polymorphism in the human population. Another study by Qin et al. (2014) [55] also indicated that
Figure 4. Forest plots describing the association of $CCND1$-G870A polymorphism with colorectal cancer risk
(A) dominant model (GG vs GA+AA); (B) recessive model (GG+GA vs AA); (C) co-dominant model (GG vs GA); (D) co-dominant model (GG vs AA).
Figure 5. Forest plots describing the association of CCND1-G870A polymorphism with esophageal cancer risk

(A) dominant model (GG vs GA+AA); (B) recessive model (GG+GA vs AA); (C) co-dominant model (GG vs GA); (D) co-dominant model (GG vs AA).
Figure 6. Forest plots describing the association of CCND1-G870A polymorphism with cervical cancer risk
(A) dominant model (GG vs GA+AA); (B) recessive model (GG+GA vs AA) (C) co-dominant model (GG vs GA); (D) co-dominant model (GG vs AA).
Table 4 Subgroup analysis: meta-analysis results according to the type of cancer

| Subgroup                  | OR       | (95% CI)  | \(P^Z\) | \(P^H\) | \(I^2\) (%) | Effects model |
|---------------------------|----------|-----------|---------|---------|-------------|---------------|
| **Breast cancer**         |          |           |         |         |             |               |
| Dominant model (GG vs GA+AA) | 2.75     | (1.54–4.90) | 0.0006  | 0.73    | 0%          | Fixed         |
| Recessive model (GG vs AA) | 0.59     | (0.37–0.95) | 0.03    | 0.38    | 0%          | Fixed         |
| Co-dominant model (GG vs GA) | 0.41     | (0.23–0.74) | 0.003   | 0.60    | 0%          | Fixed         |
| Co-dominant model (GG vs AA) | 0.28     | (0.14–0.56) | 0.0003  | 0.81    | 0%          | Fixed         |
| Allele model (A vs G)     | 0.61     | (0.46–0.82) | 0.001   | 0.68    | 0%          | Fixed         |
| Allele model (G vs A)     | 1.63     | (1.22–2.19) | 0.001   | 0.68    | 0%          | Fixed         |
| **Colorectal cancer**     |          |           |         |         |             |               |
| Dominant model (GG vs GA+AA) | 0.53     | (0.35–0.80) | 0.002   | 0.78    | 0%          | Fixed         |
| Recessive model (GG+GA vs AA) | 1.81     | (0.66–4.99) | 0.25    | 0.13    | 56%         | Random        |
| Co-dominant model (GG vs GA) | 1.74     | (1.14–2.67) | 0.01    | 0.58    | 0%          | Fixed         |
| Co-dominant model (GG vs AA) | 2.46     | (1.34–4.51) | 0.004   | 0.32    | 0%          | Fixed         |
| **Esophageal cancer**     |          |           |         |         |             |               |
| Dominant model (GG vs GA+AA) | 0.44     | (0.15–1.26) | 0.13    | 0.010   | 85%         | Random        |
| Recessive model (GG+GA vs AA) | 1.51     | (1.06–2.16) | 0.03    | 0.98    | 0%          | Fixed         |
| Co-dominant model (GG vs GA) | 2.11     | (0.66–6.88) | 0.22    | 0.005   | 87%         | Random        |
| Co-dominant model (GG vs AA) | 2.51     | (1.10–5.71) | 0.03    | 0.09    | 64%         | Random        |
| **Cervical cancer**       |          |           |         |         |             |               |
| Dominant model (GG vs GA+AA) | 0.92     | (0.64–1.32) | 0.64    | 0.34    | 0%          | Fixed         |
| Recessive model (GG+GA vs AA) | 1.52     | (0.60–3.90) | 0.38    | 0.005   | 87%         | Random        |
| Co-dominant model (GG vs GA) | 0.93     | (0.63–1.37) | 0.71    | 0.88    | 0%          | Fixed         |
| Co-dominant model (GG vs AA) | 1.45     | (0.56–3.85) | 0.46    | 0.02    | 81%         | Random        |

Abbreviations: \(P^Z\), \(P\)-value for Z-test; \(P^H\), \(P\)-value for heterogeneity. Statistically significant values shown in bold.

Figure 7. Funnel plot assessing publication bias in recessive model (GG+GA vs AA)
Figure 8. TSA of association of CCND1 polymorphism (rs9344) and overall cancer risk in Indian population from 12 studies

The cumulative Z-curve was constructed by using random-effect model. We calculated α-spending adjusted RIS of 11375 patients using $\alpha = 0.05$ (two-sided), $\beta = 0.20$ (power = 80%). Note: Z-curve (blue); Conventional boundary (green); TSA boundary (red).

CCND1 polymorphism may increase the risk of non-Hodgkin lymphoma but it was not true in case of leukemia. On the identical lines, Lin et al. (2014) [56] too observed the lack of association between CCND1 polymorphism (G870A) and head and neck cancer, however; they found that smokers carrying ‘A’ allele or ‘AA’ genotype for rs9344 SNP located on CCND1 may be at higher risk to head and neck cancer development.

Our subgroup analysis showed an increased risk (1.52-fold) for cervical cancer development but this association could not attain the limits of statistical significance ($P = 0.38$). The possible explanation for this observation may be the small sample size of contributing studies. No promising association of this SNP has been established with the development of cervical cancer in Caucasian population by Yang et al. (2015) [57]. In another study, no significant association was reported between the CCND1 SNP (rs9344) and overall risk for cervical cancer in the Asian population but stratification analysis by race, individuals carrying the AA or AA/AG genotypes showed a significant higher risk in comparison with GG carriers [32].

Additionally, a significant association between CCND1 polymorphism and increased risk for breast and esophageal cancer has been established. Similar to our results, Sergentanis and Economopoulos (2011) [58] found that the ‘A’ allele of the CCND1 G870A polymorphism is associated with higher risk for breast cancer. These findings are further strengthened by another meta-analyses conducted by Lu et al. (2009) [59] and Cui et al. (2012) [60] that showed the association of AA genotype of CCND1 G870A polymorphism with breast cancer susceptibility. Similarly, Soleimani et al. (2016) [61] showed a significant association between CCND1 G870A polymorphism and breast cancer risk but in Caucasians. A meta-analysis conducted Wen et al. (2014) [62] supported our data that CCND1 G870A polymorphism is a potential risk factor in the development of esophageal cancer. Other related meta-analysis by Cai et al. (2013) [63] is not in agreement with our findings and showed lack of potential association between CCND1 G870A polymorphism and esophageal cancer risk. Likewise, Tang et al. (2015) [64], also observed similar results describing that CCND1 SNP rs9344 is not having role in esophageal squamous cell carcinoma. The present study suggests that there is a significant correlation between this polymorphism and increased risk of colorectal cancer amongst Indian population. Recently, Xu et al. (2016) [34] suggested that this SNP may increase the risk for developing colorectal cancer with special emphasis to sporadic colorectal cancer in Caucasian population. The study by Jiang et al. (2006) [65]
suggested that the CCND1 G870 AA genotype may increase the colorectal cancer risk compared with the GG+AG genotype (OR = 1.56, 95%CI = 1.10−2.21) in an Indian population. Similarly, Zhang et al. (2016) [33], suggested that CCND1 polymorphism is a risk factor for gastric cancer in Caucasians. According to the literature search, Dai et al. (2016) [35] also tried to establish the association between CCND1 polymorphism (rs678653) located on the 3′-UTR and susceptibility to cancer, but they have not studied the polymorphism under investigation G870A (rs9344).

The present study had some limitations, first, all of the included studies were hospital based which may not represent the true population. Second, environmental factors like smoking, use of alcohol, and infections with viruses were not included in the present meta-analysis. Finally, the sample size was reasonably small, which may be the reason for controversial results.

Conclusion
In conclusion, present meta-analysis showed that CCND1 SNP (rs9344) may not serve as a risk factor for overall cancer susceptibility in Indian population. However, a significant association between CCND1 SNP and increased risk for breast, esophageal, and colorectal cancer was found on subgroup analysis. Moreover, a non-significant increased risk for cervical cancer in relation to CCND1 polymorphism was observed in Indian population. Thus, CCND1 G870A (rs9344) polymorphism has a potential to be served as a prognostic biomarker for breast, esophageal, and colorectal cancer in Indian population. Still, larger and well-designed studies including other risk factors are warranted in future to validate the findings from present analysis.

Author contribution
NT: study design, literature survey, data extraction, analysis, interpretation of the results, manuscript writing. SK: literature survey, data extraction, analysis. RM: critically reviewed the manuscript.

Competing interests
The authors declare that there are no competing interests associated with the manuscript.

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Abbreviations
CCND1, cyclin D1; OR, odds ratio; PMID, PubMed IDentifier; RevMan, Review Manager; RIS, required information size; SNP, single nucleotide polymorphism; TSA, trial sequential analysis; 95%CI, 95% confidence interval.

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