

# SOX Transcription Factors Control Cervical Cancer Development: Uncovering Therapeutic Strategies and Signalling Networks

Gerald Devault\*

Department of Health Sciences, Division of Forensic Medicine, University of Florence, Italy

## Abstract

Cervical disease is the fourth normal gynaecologic malignant growth and is considered as second driving reason for death among ladies. Different procedures are applied in therapy of cervical malignant growth including radiotherapy, chemotherapy and medical procedure. Be that as it may, cervical disease cells show forceful conduct in cutting edge stages, requiring novel methodologies in their disposal. Then again, SOX proteins are record factors equipped for directing different sub-atomic pathways and their demeanour shifts during embryogenesis, infection improvement and carcinogenesis. In the current audit, our point is to uncover job of SOX record factors in cervical disease. SOX record factors play like a blade that cuts both ways in malignant growth. For example, SOX9 has both growth silencer and cancer advancing job in cervical disease. Hence, definite job of each SOX individual in cervical malignant growth has been examined to coordinate further analyses for uncovering different capabilities. SOX proteins can manage multiplication and metastasis of cervical malignant growth cells. Moreover, reaction of cervical malignant growth cells to chemotherapy and radiotherapy is firmly controlled by SOX record factors. Different downstream focuses of SOX proteins, for example, Wnt flagging, EMT and Hedgehog have been recognized. Furthermore, upstream arbiters, for example, microRNAs, lncRNAs and circRNAs can manage SOX articulation in cervical malignant growth.

**Keywords:** Cervical cancer • SOX transcription factor • Biomarker • Chemoresistance • Cancer therapy • Non-coding RNAs

## Introduction

One of the most widely recognized gynecological malignancies, cervical disease accounts for 311,000 deaths annually. From the 13170 cases that were analyzed, malignant growth measurements indicated that cervical disease was the cause of 4250 new deaths. Women between the ages of 20 and 39 typically suffer from cervical cancer, which accounts for nine deaths per week in this age group. The fourth most common gynecological malignancy and the second leading cause of female death is cervical cancer. Contamination with human papillomavirus (HPV), particularly HPV16 and HPV18, is the primary risk factor for cervical disease. Imperatively, cervical malignant growth is more common in metropolitan areas than in provincial ones, and it has been established that an increasing number of women are suffering from cervical disease in both metropolitan and rural areas. Radiotherapy and chemotherapy are the standard treatments for the majority of patients with cervical disease. Notwithstanding the way that inoculations have been delivered for treatment of cervical harmful development, two or three people simply seek immunizer for cervical infection treatment. Prophylactic antibodies are the best vaccines for treating HPV-interceded cervical malignancy. The HPV test, cytologic test, and colposcopy are among the various tests used for cervical malignant growth determination and screening. These tests have been effective in reducing mortality caused by cervical disease. Nevertheless, screening and early detection of cervical precancer are becoming even more important. The non-

curable metastasis cervical disease is one issue, regardless of whether its diagnosis occurs in the early stages and medical procedures are performed to remove it. As a result, cervical cancer is a potentially fatal condition that should be taken into account when developing risky methods for identifying it and discovering novel treatments [1].

## Description

The therapy systems for cervical malignant growth are different in view of stage and nodal status. The therapy technique for neighborhood cervical malignant growth and analyzed at first stages is careful, yet as illnesses movement happens and nodal-positive cancers structure, notwithstanding medical procedure, radiotherapy and chemotherapy are used. Notwithstanding huge advancement in therapy of cervical malignant growth patients utilizing multimodal treatments, it actually causes high demise and 5-year generally speaking endurance is 65%, 40% and 15% for stages II, III and IVA stages, separately. Moreover, repeat is likewise a rising test in cervical disease, so 30-40% of cervical malignant growth patients show repeat cervical disease, and this number is critical in cutting edge cervical malignant growth. An assortment of biomarkers is applied as prognostic variables for cervical disease including stage, histology, growth volume, and lymph hub metastasis and single-quality markers. Ongoing tests play shown part of hereditary and epigenetic factors in cervical malignant growth movement. The DNA methylation, hydroxymethylation, demethylation, chromatin rebuilding, histone change, non-coding RNAs and quality engraving are considered as elements engaged with cervical malignant growth improvement. In the current survey, our point is to give a robotic conversation of SOX record factors job in cervical malignant growth. For this reason, we initially give a presentation of SOX relatives and their basic jobs in physiological and obsessive occasions. Then, we partition conversation area into various parts in light of SOX family and depict what SOX relatives can mean for movement of cervical malignant growth. As SOX relatives have double job as growth advancing or cancer silencer, their contribution in cervical disease is more convoluted, and uncovering their relationship with cervical malignant growth progression is fundamental [2].

\*Address for Correspondence: Gerald Devault, Department of Health Sciences, Division of Forensic Medicine, University of Florence, Italy, E-mail: devaultg@gmail.com

**Copyright:** © 2022 Devault G. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Received:** 01 November, 2022, Manuscript No. jfr-22-84258; **Editor assigned:** 03 November, 2022, Pre-QC No. P-84258; **Reviewed:** 15 November, 2022, QC No. Q-84258; **Revised:** 22 November, 2022, Manuscript No. R-84258; **Published:** 29 November, 2022, DOI: 10.37421/2157-7145.2022.13.525

## SOX record factors

The SRY-related High Versatility Gathering (HMG)- box (SOX) record factors have potential and essential physiological jobs including advancement of cardiovascular framework and lymphatic pipes. The main separation and recognizable proof of SOX record factors gets once again to 1990, and it was found that the individuals from SOX family share a typical trademark known as High Portability Gathering (HMG)- box protein space that is correlated with sex-deciding district Y (SRY). The HMG space is an exceptional locale containing 79 amino acids and individuals from a specific gathering show half homology around here corresponding to SRY. The SOX individuals are considered as record factors and their appearance happens in different tissues during embryogenesis, sickness improvement and tumorigenesis. The HMG space is liable for DNA restricting of SOX record factors in a grouping explicit way. This limiting happens through three alpha helices in HMG spaces that produce an L-formed space equipped for communicating with DNA minor score. The DNA succession theme ATTGTT is basically impacted by SOX record factors. The collaboration of SOX individuals through HMG space with DNA prompts conformational modifications in DNA, bowing it and empowering effect of SOX individuals. The job of SOX record factors is more confounded, as these individuals can collaborate with pre-twisted DNA present in nucleosomes, showing their job as trailblazer factors. By and large, HMG space is a deciding element for communication of SOX record factors with different cofactors and no cross-over between bunches. The SOX record factors capability in a tissue-explicit and setting explicit way, convoluting our insight towards disease science. It has been accounted for that SOX record factors control movement and remedial reactions. As of late, much consideration has been coordinated towards job of SOX record factors in malignant growth. Expansion and metastasis of disease cells are firmly directed by SOX record factors. Treatment reaction of malignant growth cells including chemotherapy reaction is controlled by SOX record factors [3,4].

SOX1 is a notable individual from SOXB1 family with possible job in various diseases. It appears to be that SOX1 has an enemy of growth action in disease, so SOX1 down-guideline by microRNA (miRNA)-155 by means of restricting to 3' - untranslated area (3' - UTR) essentially upgrades metastasis and relocation of gastric disease cells. In bosom malignant growth, SOX1 overexpression restrains Wnt/ $\beta$ -catenin flagging pathway to weaken metastasis and attack of cells. In this segment, we give a robotic conversation of SOX1 job in cervical malignant growth to make ready for creating novel therapeutics for focusing on this variable. Like different malignant growths, SOX1 is a cancer silencer considers cervical disease. The actuation of Wnt/ $\beta$ -catenin flagging pathway is supportive of cervical disease movement and medication opposition. In hindering cervical malignant growth multiplication and metastasis, SOX1 restrains Wnt/ $\beta$ -catenin flagging pathway in a TCF-subordinate way. The methylation status of SOX1 modifies in cervical malignant growth that can be considered as a biomarker for identification of this dangerous sicknesses. It has been accounted for that hypermethylation of SOX1 happens in cervical malignant growth and is a positive component for antecedent sores. As a matter of fact, methylation status of SOX1 can work as a helper biomarker for cervical disease conclusion and further develops precision for this situation. The methylation status of SOX1 progressively upgrades in cervical malignant growth, and a meta-examination has shown particularity and pooled responsiveness of 0.72 and 0.75, separately for SOX1 in cervical disease. Until this point, a couple of studies play analysed part of SOX1 in cervical disease. In any case, at present led tests feature the way that SOX1 has a growth silencer job in cervical disease, and its hypomethylation expands chance of cervical malignant growth improvement. More examinations are expected to uncover downstream and upstream arbiters of SOX1 in cervical malignant growth [5,6].

## Clinical application and biomarker

This audit expected to investigate job of SOX record factors in cervical disease. The positive place of tests is the examination of SOX proteins job in pre-clinical and clinical investigations. In this manner, an achievement progress has been made in deciphering pre-clinical discoveries, and following stage is involving such encouraging outcomes in therapy of cervical malignant growth patients in clinical course. As SOX relatives are considered as record factors,

it is hard to target them utilizing hostile to cancer specialists, notwithstanding utilizing such methodology. This is because of absence of restricting site in record factors for growing little particles focusing on them, and regulating record factor action requires focusing on DNA-protein and protein communications. Consequently, it is smarter to utilize hereditary apparatuses like little meddling RNA (siRNA), short-clip RNA (shRNA) and CRISPR/Cas9 for focusing on SOX record elements to acquire most noteworthy and best outcome in therapy of cervical disease patients. As both enemy of growth specialists and hereditary devices require designated conveyance at growth site, and crossing a few hindrances like blood-cancer boundary (BTB) and other natural obstacles, it is recommended to utilize vectors, both organic transporters and nanoparticles to get improved brings about therapy of cervical disease patients. Moreover, SOX record elements can be considered as biomarkers for determination and anticipation of cervical malignant growth. Such potential was talked about in the fundamental text and has been examined for various SOX relatives, for example, SOX1 and SOX2 in cervical disease [7].

## Discussion

The methylation status of SOX record factors goes through changes in ordinary and harmful cells and tissues. For SOX1, its advertiser shows hypermethylation in cervical disease to fundamentally hoist growth stage and movement. Furthermore, methylation status of SOX record elements can be investigated with different variables to further develop forecasts about analysis and visualization of cervical malignant growth. For example, SOX1, TERT, LMX1A and hsa-miRNA-124-2 exhibit hypermethylation in cervical malignant growth and are potential symptomatic apparatuses. The DNA methylation status has been additionally examined in different sorts of SOX proteins. For example, SOX9 exhibits no total methylation in typical tissues, yet it shows total methylation in cervical disease cells and tissues. Besides, overexpression of SOX9 can intervene unfortunate visualization in cervical malignant growth. Conversely, there are SOX record factors with hostile to growth action like SOX6. The down-guideline of SOX6 intercedes cervical disease movement. Thusly, articulation level of SOX record factors is different in light of their capability in cervical disease that ought to be viewed as involving them as analytic and prognostic devices in cervical malignant growth [8-10].

## Conclusion

The current audit objective was to research job of SOX record factors in cervical disease and their relationship with various perspectives including expansion, metastasis and treatment reaction. The sub-atomic pathways engaged with cervical disease movement are muddled, since SOX record elements might have both growth silencer and growth advancing job in cervical malignant growth like SOX9. In this way, use of hereditary apparatuses for down-directing articulation of such SOX individuals ought to be definitively chosen, in the wake of uncovering precise job in cervical malignant growth movement/hindrance. SOX record variables can direct both development and intrusion of cervical disease cells, and reaction of malignant growth cells to radiotherapy and chemotherapy is firmly tweaked by SOX record factors. Different upstream and downstream focuses of SOX record factors have been uncovered in cervical disease. ncRNAs including miRNAs, lncRNAs and miRNAs are most notable upstream middle people of SOX individuals in cervical disease. Essential, SOX record elements can shape a criticism circle with ncRNAs and going about as their upstream go between in cervical disease. Drug carriers, Wnt/ $\beta$ -catenin flagging and EMT are a couple of downstream focuses of SOX individuals in cervical disease. The fascinating point is that job of SOX record factors in cervical disease patients as prognostic and demonstrative elements has been explored, and future tests can zero in on uncovering more SOX-related atomic pathways in cervical malignant growth to make ready for powerful treatment of this danger.

## Acknowledgement

None.

---

## Conflict of Interest

None.

---

## References

1. Ptashne, Mark and Alexander Gann. "Transcriptional activation by recruitment." *Nature* 386 (1997): 569-577.
2. Lee, Tong Ihn and Richard A. Young. "Transcriptional regulation and its misregulation in disease." *Cell* 152 (2013): 1237-1251.
3. Lambert, Samuel A., Arttu Jolma, Laura F. Campitelli and Pratyush K. Das, et al. "The human transcription factors." *Cell* 172 (2018) 650-665.
4. Look, A. Thomas. "Oncogenic transcription factors in the human acute leukemias." *Science* 278 (1997): 1059-1064.
5. Wilson, Garrick K., Daniel A. Tennant and Jane A. McKeating. "Hypoxia inducible factors in liver disease and hepatocellular carcinoma: Current understanding and future directions." *J Hepatol* 61 (2014): 1397-1406.
6. Calissi, Giampaolo, Eric W-F. Lam and Wolfgang Link. "Therapeutic strategies targeting FOXO transcription factors." *Nat Rev Drug Discov* 20 (2021): 21-38.
7. Yu, Hua, Heehyoung Lee, Andreas Herrmann and Ralf Buettner, et al. "Revisiting STAT3 signalling in cancer: New and unexpected biological functions." *Nat Rev Cancer* 14 (2014): 736-746.
8. Liang, Zhenxing, Jing Xu and Chunhu Gu. "Novel role of the SRY-related high-mobility-group box D gene in cancer." *Semin Cancer Biol* 67 (2020): 83-90.
9. Kamachi, Yusuke and Hisato Kondoh. "Sox proteins: Regulators of cell fate specification and differentiation." *Development* 140 (2013): 4129-4144.
10. Zaret, Kenneth S. and Jason S. Carroll. "Pioneer transcription factors: Establishing competence for gene expression." *Genes Dev* 25 (2011): 2227-2241.

**How to cite this article:** Devault, Gerald. "SOX Transcription Factors Control Cervical Cancer Development: Uncovering Therapeutic Strategies and Signalling Networks." *J Forensic Res* 13 (2022): 525.