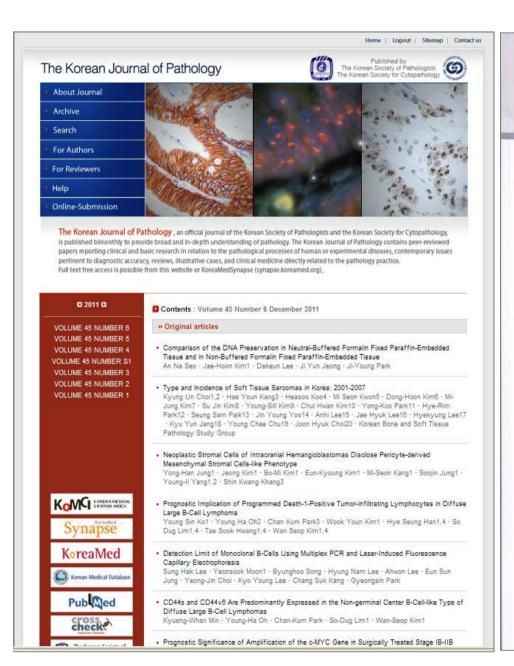


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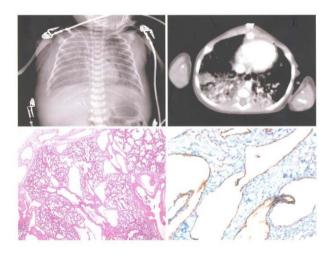
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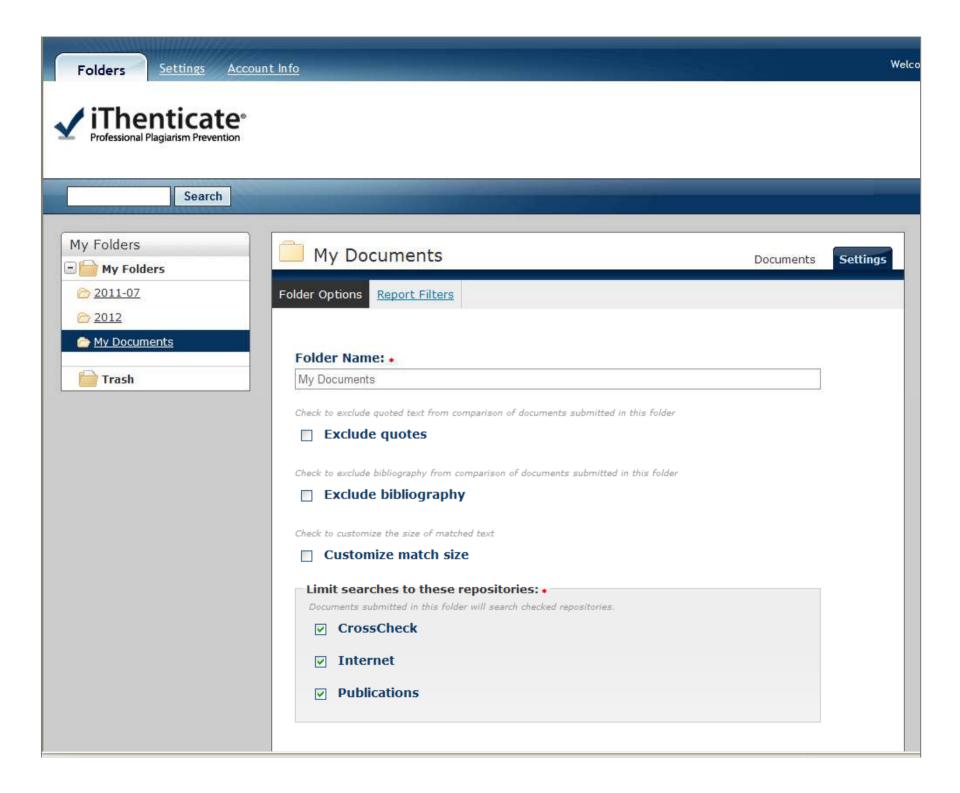






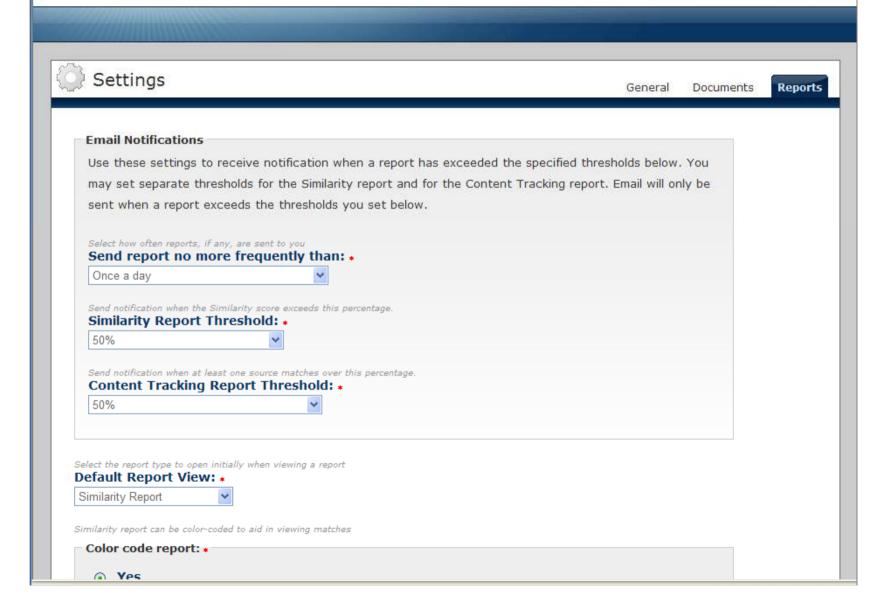
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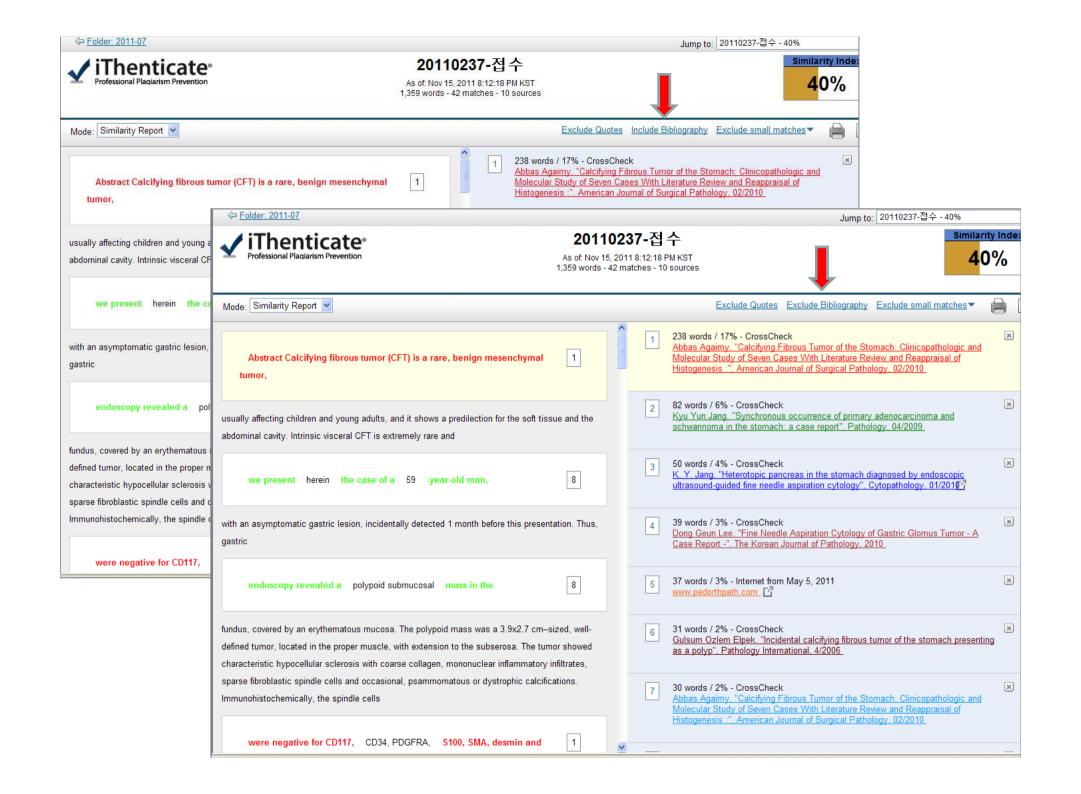
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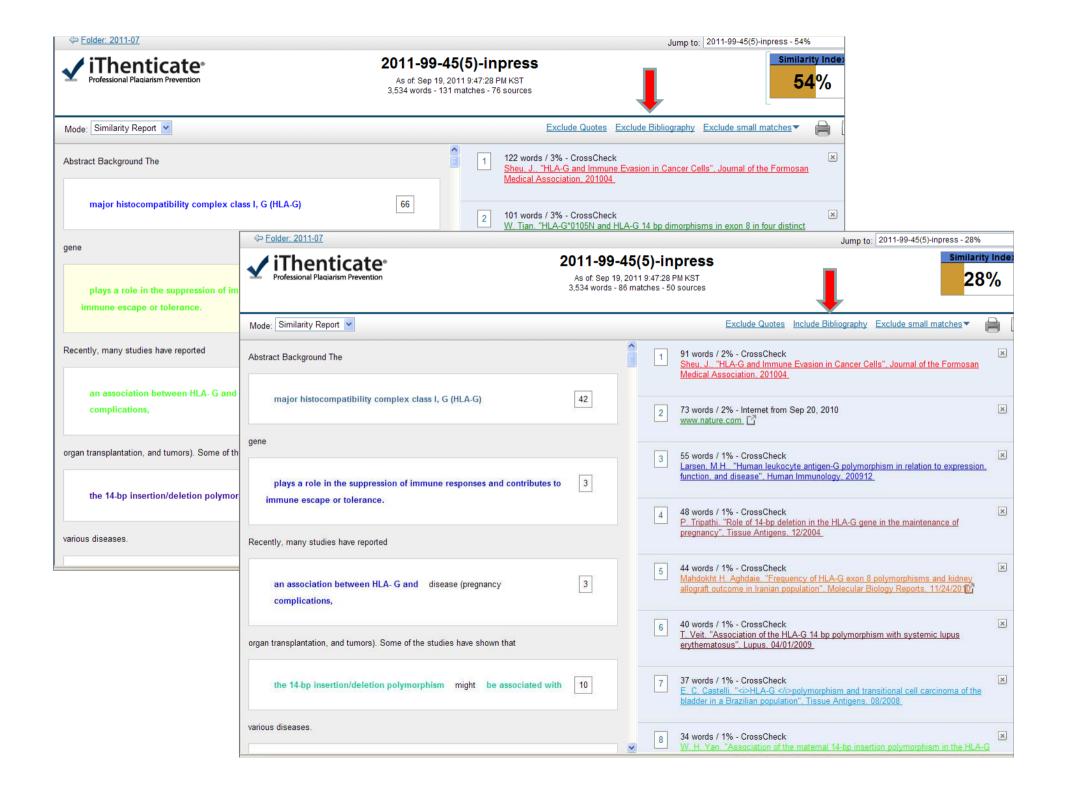


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Clinical evidence in support of the role of H is primarily derived from studies that have level of HLA.G expression and clinical outcon transplantation, which represent two major conself tissues

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HLA-G is an important immunotolerant mole

Key words:

HLA-G; polymorphism; recurrent spontaneous abortion; 14 bp del

Acknowledgments:

This work was supported by Department of Science and Technology, New Delhi. Authors are thankful to Sanjay Gandhi Post Graduate Institute of Medical Sciences Lucknow for providing various lab facilities and other assistance.

Abstract: Differential expression of human leukocyte antigens (HLAs) on trophoblast has been the focus of many studies, specially on extravillous cytotrophoblast cells, which migrates into the maternal uterine tissues. These invading cells do not express classical major histocompatibility complex class I (–A and –B) and class II molecules, along with low expression of HLA-C. HLA-G is the predominantly expressed antigen along with HLA-E. Hence, it is believed that expressed antigens may be involved in materno-fetal tolerance. In the present study, we have studied 14-bp deletion polymorphism in the exon-8 of the non-classical HLA-G antigen. There was no difference in the frequency of deletion/insertion polymorphism in fertile normal women and recurrent spontaneous abortion (RSA) women. However, the number of heterozygotes (–14b/+14b) were increased in RSA women. The probable mechanism for the increase of heterozygotes in recurrent fetal loss is discussed in light of soluble HLA-G.

Human leukocyte antigen (HLA)-G, a non-classical major histocompatibility complex (MHC) class I molecule, plays an important role in the regulation of the immune response. Although it is structurally similar to the classical HLA class I gene products (1), HLA-G also exhibits some unique features. There are seven protein isoforms of HLA-G, and it exhibits limited polymorphism. HLA-G expression varies in different pathological conditions (2–5). The mRNA profile and protein show differences (6). This may be due to regulated gene

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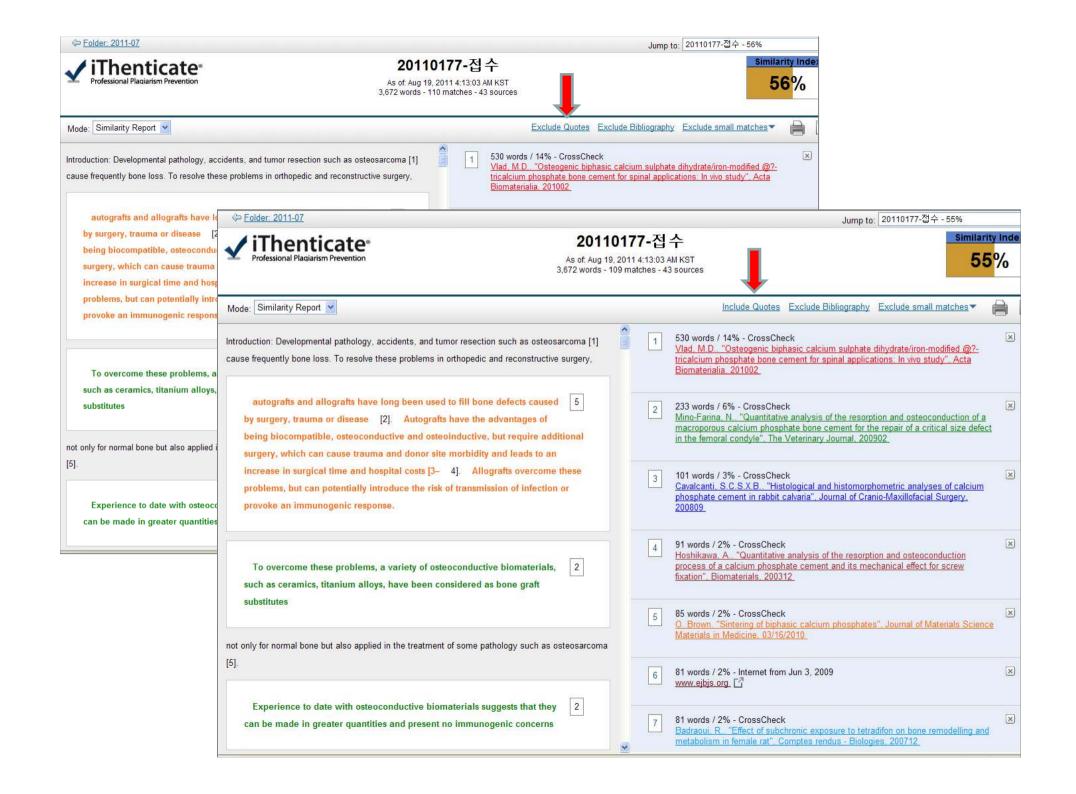
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HLA-G has a restricted distribution on normal tissue cells, being primarily expressed in the thymus, pancreas and intestines. HLA-G is also abundantly expressed in placental tissue, particularly in the extravillous cytotrophoblast, being implicated in the inhibition of the cytotoxic function of maternal NK cells. The HLA-G gene generates multiple protein isoforms by alternative splicing of a single mRNA, giving rise to four membrane-bound isoforms (HLA-G1mb to -G4mb), and three soluble isoforms (HLA-G5s to -G7s) generated by the presence of a stop codon in intron 4.9 HLA-G transcripts are also expressed at low levels in a variety of normal humanadult tissues; 10 however, normal cervical cells do not express HLA-G. 11 HLA-G expression may be upregulated in inflammatory and neoplastic tissues, 12 and in viral infections. 13, 14, 15 The membrane-bound variant HLA-G1 suppresses the proliferation of T CD4+ cells, and the soluble variant HLA-G5 may induce apoptosis of activated T CD8+ cells. 16, 17 Several polymorphic sites have been described for the HLA-G locus. Nucleotide substitutions mainly in exons 2, 3 and 4 may discriminate 42 confirmed alleles clustered into nine distinct allele groups, and generating only 15 different proteins due to the presence of several synonymous substitutions among HLA-G alleles (Anthony Nolan Research Institute, February 2009). 18 HLA-G alleles may influence the plasma levels of soluble HLA-G (sHLA-G). 19 In addition, a 14bp insertion/deletion polymorphism has been reported in the 3'-untranslated region (UTR) of exon 8.20 HLA-G alleles exhibiting the 14bp insertion (+14bp) undergo an alternative splicing that removes 92 bases from 3' LITE 21 influencing the atability of LILA C mDNA 22 Although removal of the 02



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of the cancer tissues and/or moderately stained, and (+++) tissue specimens:
positive parenchyma cell with more than 75% of the cancer tissues and/or strongly
stained. Statistical analysis

Statistical comparisons for significance were variables. Significance of differences was as was performed using the SPSS for Windows immunohistochemistry (IHC) method, we de paraffin-embedded tissues with receptor exp sections were Basal-like subtype (n=36) (Fig (n=144) (Figure 2). From Normal breast subt

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Statistical analysis

Association between *TSPAN1* gene expression and other clinicopathological factors of the tumor were assessed by the Fisher's exact test (two-sided) for categorical variables and c² test were used to compare ordinal variables. The grading-related data was analysed by Spearman test. Overall survival was defined as the period from the date of diagnosis to the date of death. Survival curves were determined according to the Kaplan-Meier method, and compared using Log-rank test statistical differences. Multivariate survival analysis was performed with SPSS version 11.0 Software (Chicago, IL, USA).

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