

## Oxidative DNA Damage, Oxidative Stress and Genetic Susceptibility-Prognostic Scores in 'Missing' COPD Cases

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**ABSTRACT** *In situ* identification of COPD cases at workplace and sample assessment for oxidative stress/ DNA damage as a function of metabolic/antioxidant genotypes (as susceptibility genotypes) offers a novel manner of hazardous workplace-identification for genotoxic/carcinogenic events. In this case-control study, blood/ sera samples of the COPD cases (n=32 identified spirometrically among the stone-crushing workers) and healthy controls (n=19) were assessed for 8-OHdG (DNA damage), glutathione and superoxide dismutase levels (oxidative stress) and genotyped for *GSTT1*, *M1*, *P1* and *MnSOD* variants. Significant increase in oxidative damage and lung-function decline were observed as a function of some genotypes. Predictors of genetic damage included tGSH, SOD and *GSTM1*. A prognostic index score based on prognostic factors was developed revealing cases were at high- (53.12%), intermediate- (34.37%) or low- (12.50%) risk for progressive DNA damage. These aberrant findings imply workplace exposure. This study provides insight on exposure-effect relationship in workers at stone-crushing sites.

### INTRODUCTION

Chronic Obstructive Pulmonary Disease (COPD) is an obstructive airway disorder characterized by the slowly progressive and irreversible decrease in forced expiratory volume in one second (FEV<sub>1</sub>), accompanied by emphysema and chronic bronchitis (Rabe et al. 2007; Cazzola et al. 2015); it develops with decreasing lung function as a function of age in the normal population (Ito and Barnes 2009). Despite the heritability of 40-77 percent, a host of other influences can also exacerbate this condition (Young et al. 2009). Rather the development and progression of COPD involves multiple genes, gene-gene and gene-environment interactions (•idzik et al. 2008; de Jong et al. 2015). Smoking exposure is considered as the most important risk factor for the development of COPD (Chan-Yeung et al. 2007; Kurmi et al.2015) with mild and moderate COPD cases having a three-fold risk of developing lung cancer within ten years, which increases to a ten-fold risk with severe COPD compared to the smokers with normal lung function (El-Zein et al. 2012). There also however exists COPD-

associated increased mortality from lung cancer in non-ever smokers (Turner et al. 2007; Kiri et al. 2010; Aldrich et al.2015).

Despite quarrying and mining activities as important occupational set-ups inducing COPD (Jhoncy et al. 2011; Iftikhar et al. 2009), yet workplace identification of this occupational disease has not come to attention on pursuing literature related to COPD. Also there is uncertainty in prognosis of COPD although a number of validated indices exist (Briggs et al. 2008). As these indices require in-puts from patients and the interpretation by the care-giver/physician, these may not be able to cater to disease-identification in the field. In the present study, the on-site disease-identification using the recommended spirometry evaluation (Briggs et al. 2008; Shiota et al. 2015) to recognize COPD cases at stone-crushing units (dust exposure) was carried out. Such an identification at the workplace gains importance as 50-80 percent of COPD are missed-out on the basis of misdiagnosis/co-current diagnosis due to relying on reported symptoms which are not sufficiently sensitive and / or because of failure of persons to report to the health provider (Levy et al. 2009).

The effect of various environmental stressors from occupational exposures needs to be assessed for prediction of cancer outcome(s) (Fenech 2002) as 90 percent of cancer is environmental in origin (Hemminki et al. 2006). COPD has also been identified as an independent risk

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factor for lung cancer with inflammation as the pathophysiologic factor for high risk of its progression (Sin et al. 2006; Hillas et al. 2015) and smoking-induced COPD associated with lung cancer has also been documented (Koshiol et al. 2009). While mechanisms governing the risk of developing neoplastic disease are not well known (Barreiro 2008), of the various theories, oxidative stress may be playing a pivotal role in its manifestation. In COPD, oxidative stress has been observed as ensuing from decreased FEV<sub>1</sub> (Kluchová et al. 2007), substantial inflammatory response increasing cytokines as triggered by exogenous dust particles (Yang et al. 2011) and decreased antioxidants because of depletions of glutathione peroxidase, superoxide dismutase (SOD), catalase, ascorbic acid and vitamin E (Borm et al. 2004).

The impaired oxidant-antioxidant status can cause cellular damage; DNA damage can result from the action of reactive oxygen species (Jackson and Loeb, 2001) and is the underlying cause of mutations leading to cancer (Bernstein, 2012). Chromosomal damage (increased micronuclei frequency) in peripheral blood lymphocytes has been extensively used for predicting risk of cancer (Fenech et al. 2011) and oxidative DNA damage is also implicated in carcinogenesis, ageing and age-related neurodegenerative diseases (Fortini et al. 2003, Nishigori et al. 2004). The major form of oxidative DNA damage is 8-hydroxy-2'-deoxyguanosine (8-OHdG) resulting from G→T and A→C base substitutions. It may lead to mutagenesis if unrepaired and is directly correlated with lung carcinogenesis (Gackowski et al. 2003). The lesion 8-OHdG is an established biomarker of oxidative stress/oxidative DNA damage and being potentially mutagenic, it is useful as an intermediate marker of a disease end-point like cancer (Cheng et al. 1992). Therefore in the present study, 8-OHdG level was assessed as a pre-lesion of neoplasia in peripheral blood leukocytes (PBL) of COPD-identified cases at stone-crushing units. Although the leukocytes are not the direct target of the exposure at this workplace, they may possibly be affected by the accumulated unmetabolized toxic compound(s) in the lung (Gackowski et al. 2003). This hence prompted the assessment of oxidative DNA damage in the peripheral blood leukocytes and also because of the non-accessibility of the target (lung) cells.

The biomarkers of exposure and effect, and clinical disease (cancer) may further be influ-

enced by susceptibility genotypes and their gene products as pre-dispositional factors (Their et al. 2003). Also as DNA damage and DNA repair have a major role in carcinogenesis and from occupational settings, the susceptible metabolic genotypes (gene products) may inherently be associated in causing genetic damage. Therefore genotyping of the occupational workforce was carried out for glutathione-S-transferase (*GST*) gene variants (both for disease susceptibility and genetic damage) since *GST* alleles have been documented to have an association with COPD (Young et al. 2011b). Furthermore, a reduced expression of these alleles has also been observed in the air passage of COPD patients (Imboden et al. 2007; Lakhdar et al. 2011) and hence the expression of glutathione-S-transferases was also estimated. Association of the *Val/Ala* variants of manganese superoxide dismutase (*MnSOD*) with lung cancer (Wang et al. 2001) further justified the genotyping of this allele and assessing its expression. Variant forms of these susceptible genes are generally common in the population. Due to their specificities for substrates they interact with during environmental exposures, they can increase the risk for disease-causation (Lan et al. 2000). Incidentally, *GST* and SOD enzymes are also involved in the metabolic and oxidative stress pathways (Borm et al. 2004), and since stone-crushing is an inflammation-triggering occupation (Vallyathan et al. 1995), the assessment of the amounts of these enzymes was thought appropriate.

The purpose of the present study was two-fold. On one hand to identify COPD cases from workplace exposure (occupation-related disease) and hence assist in identifying 'missing' COPD cases using recommended (spirometry) measurements (Briggs et al. 2008; Young et al. 2011a) and COPD categorizations (GOLD 2003). The other (main) purpose was to determine the propensity (Prognostic Index/score) for genetic damage and by extension an increased likelihood for carcinogenesis as ensuing from the combined effects/interactions of prognostic (risk) factors in COPD cases (the workers exposed to industrial-type prevalent conditions) at stone-crushing units. This entailed the evaluation for the presence of oxidative stress (GSH and SOD) and oxidative DNA damage in workers at stone-crushing units genotyped for the *GST* and *MnSOD* genes.

## Objective

The objective of the present study was to assess oxidative DNA damage (8-OHdG) and oxidative stress (glutathione and superoxide dismutase) along with molecular genotyping of *GSTT1*, *GSTM1*, *GSTP1* and *MnSOD* gene variants in COPD cases identified from stone-crushing units and in healthy controls.

## MATERIAL AND METHODS

### Study Design

The present study was carried out after obtaining approval from the Institutional Ethics Committee. In order to investigate for genetic damage from occupational exposures as from stone-crushing activities, villages near Pathankot (Sarna, Mirthal) and Gurdaspur (Babbehali) of Punjab, India where four stone-crusher units are located, were visited. The workforce comprised local Mazhbi Sikh and Scheduled Caste and Backward Class Hindu males primarily engaged in drilling, dressing and loading of stones (all dust-emitting activities) with an occupational exposure from five to 14 years. Most of the workers were staying on-site. No preventive or precautionary measures, as set-up in the guidelines by the government (CPCB 2009), were prevailing.

Group discussions were held with the workers and after voluntary written informed consent, their demographic details, medical, genetic and exposure-histories and information on their life-styles and dietary habits were recorded on a pre-designed questionnaire. Healthy male subjects with no occupational/incidental or accidental exposure(s), of similar ethnic and geographic origin, comprised the control group. Since many of the workers as well as the controls were smokers, the Brinkman index for smokers was calculated by multiplying the number of *bidis* (Indian cigarette) smoked daily with the number of years of smoking, that is, smoking years (Kojima et al. 2005). The higher the Brinkman index, more are the *bidis* smoked for longer period of time (years). Anthropometric measurements for height and weight were also taken for each subject using standard protocols (Weiner and Lourie, 1981) so as to calculate the body mass index (BMI, kg/m<sup>2</sup>) of the study participants.

### The Pulmonary Function Test

The Pulmonary Function Test (PFT) is performed to assess lung function, lung damage, lung disease diagnosis and whether lung function is affected at work place/ occupational exposure (Jhoncy et al. 2011). The Spiro Excel spirometer model (Medicaid Systems, India) was used for carrying out the PFT. The subjects were asked to breathe in and out through the mouth-piece to get familiarized with the equipment. The Forced Expiratory Volume per second (FEV<sub>1</sub>; l) and Forced Vital capacity (FVC; l) were recorded and the Forced Expiratory Ratio (FEV<sub>1</sub>/FVC) calculated. The value of body surface area (BSA, m<sup>2</sup>) was also recorded. The same instrument was used throughout the study and three successive readings were taken for each subject in a standing posture using the standard spirometric procedures. The best reading was used for calculation purposes as per the manufacturer's recommendations and the Global Initiative for Chronic Obstructive Lung Disease (GOLD) guidelines (GOLD, 2003). The best reading is when the flow curve (flow rate against volume of air exhaled) displayed is proper, without any artifact such as improper blow of air or leak from mouth piece and without coughing or closed glottis.

### Identification of COPD Cases

The FVC values are decreased in pulmonary obstruction, emphysema, pleural effusion, etc, and FEV<sub>1</sub> is low in obstructive lung disease and reduced lung volume. In fact, the FEV<sub>1</sub> decline is a convenient standard for identifying subjects with COPD and those exposed to environmental pollutants (Jhoncy et al. 2011). Therefore, based on the obtained values of FEV<sub>1</sub>, FVC, FEV<sub>1</sub>/FVC and the specific respiratory distress symptoms among the workers, they were categorized as those at-risk (FEV<sub>1</sub>/FVC 0.7-0.8, FEV<sub>1</sub> ≥ 80 percent predicted spirometry, cough, sputum production), mild (FEV<sub>1</sub>/FVC < 0.7, FEV<sub>1</sub> ≥ 80 percent predicted; with or without cough, sputum production) or moderate (FEV<sub>1</sub>/FVC < 0.7, FEV<sub>1</sub> between 50 and 80 percent predicted; with or without cough, sputum production) COPD cases following the criteria recommended by the Global Initiative for Chronic Obstructive Lung Disease (GOLD 2003). Since

spirometry-evaluation is recommended for COPD-identification, all these workers had varying stages of COPD and have been classified as COPD cases. Hence after disease-identification, this study design took the shape of a case-control study.

### Sample size-Power Calculation

Given that a  $p=0.05$  incremental increase in genetic damage is considered significant on Student's t-test analysis and taking the average base-line 8-OHdG levels of 0.21pg/ml (SD=0.39) obtained in a preliminary study of an ethnic-specific control group, the total sample size requirement for the study group was calculated (Sigma XL software) as 42 for a statistical power of 80 percent with  $\alpha=0.05$  (after (Albertini et al. 2000)). Hence, the sample size of 51 of the present study is justified at the required power of statistical analysis at 95 percent confidence interval.

### Oxidative DNA Damage Assessment

Serum levels of the 8-OHdG as the biomarker of oxidative damage was measured with the highly sensitive enzyme-linked immunosorbent assay (ELISA) using the EIA kit (Stress Marq Bioscience Inc, India). In tissues where this lesion is expected to have low levels (blood serum in the present study), the competitive *in vitro* ELISA is used. This technique is a valid and simple alternative tool to measure oxidative DNA damage with HPLC-EC or GC-MS techniques since a good correlation between ELISA and these methods has been obtained. The measurement of 8-OHdG in serum samples is reflective of overall oxidative damage in the body similar to that excreted in urine and includes damaged nuclear DNA (removed during base excision repair) as well as the damaged mitochondrial DNA and damaged DNA from the cytoplasmic nucleotide pools (Forlenza and Miller 2006).

For the present study, the manufacturer's instructions as given with the kit were followed. The serum samples were centrifuged, the samples and standards were added to 8-OHdG-coated microtitre plates followed by the addition of the 8-OHdG monoclonal antibodies. After an overnight incubation at 4 C, the plates were washed with a washing buffer, and a second enzyme-labeled antibody was added to each well. The chromogen was added after another

washing and the contents were allowed to incubate in the dark for 15min. The subsequent colour development was observed; it is proportional to the amount of antibody, being inversely related to the amount of 8-OHdG in the serum sample; low colour indicates higher amounts of 8-OHdG. The absorbance was read at 415 nm using a computerized ELISA reader (BioRad 680 XR, USA). Triplicate readings were taken and the results in pg/ml were recorded at the last absorbance.

### Oxidative Stress Analysis

The levels of oxidative stress biomarkers (glutathione and superoxide dismutase) were determined from blood sera samples using standard protocols as described below.

#### *Glutathione (GSH) and Glutathione Disulfide (GSSG) Assays*

Glutathione exists in the reduced (GSH) and oxidized (GSSG) forms and an optimal GSH: GSSG ratio is critical for cell survival and for an adequate oxidant-antioxidant balance (Gherghel et al. 2005). The total GSH (t-GSH) and GSSG levels were assessed using the GSSGR-DTNB (glutathione disulphide reductase-5, 5 dithiobis-2-nitrobenzoic acid)-recycling procedure (Rahman et al. 2007). In brief, for obtaining the standard curves for GSH and GSSG by linear regression, 0.50 nanomole increments (0-2nmoles) using GSH solution for the GSH and 0.025 nanomole increments (0-0.25 nmoles) for the GSSG assays, were prepared and their absorbance recorded at 412nm and 410nm, respectively on an ELISA reader (BioRad 680XR, USA). After adjusting with a blank, GSH and GSSG values were obtained in nmoles. Both, the GSH levels (GSH=t GSH-GSSG) and the redox index (ratio of GSH to GSSG) were calculated (Gherghel et al. 2005).

Glutathione (GSH) is a tripeptide thiol antioxidant and its intracellular concentration is an indicator of oxidative stress (Lushchak 2012). GSH neutralizes reactive oxygen species (ROS) and other radicals by detoxification involving the glutathione peroxidase (GPx), glutathione-S-transferase (GST) and glutathione reductase (GR). Normally in the cell, the ratio of GSH (reduced)/GSSG (oxidized) is 1:10 as GSH tends to be rapidly oxidized to GSSG with GSH ranging between 1-10 mM and GSSG representing <1 percent of the total cytoplasmic glutathione pool (Rahman and Adcock 2006). Glutathione reduc-

tase, in the presence of NADPH, recycles GSSG to GSH (Rahman and Adcock 2006). Hence the total amount of glutathione (tGSH) in the sample represents the sum of reduced and oxidized glutathione (tGSH=GSH+2GSSG). In the cells, both the reduced (GSH) and oxidized (GSSG) forms exist and oxidative stress leads to a reduced GSH/GSSG ratio (the Redox Index).

### **Superoxide Dismutase (SOD)**

Serum samples were mixed with NBT (nitroblue tetrazolium), tritonX-100 and hydroxylamine hydrochloride. The absorbance was recorded spectrophotometrically (Thermo Scientific, USA) at 560nm after calibration with Tris HCl (blank). The amount of SOD in the sample was calculated from the absorbance values and expressed as U/ml. SOD inhibits the reduction of NBT by superoxide generated from the peroxidation of hydroxylamine hydrochloride, and the inhibition of chromogenic reaction is measured (Kono et al. 1978). Superoxide anions assist in the regulation of oxidative stress as the free anions are the substrate for generation of ROS (Siedlinski et al. 2009). These anions are degraded by SOD to  $H_2O_2$ , which if not detoxified by  $GP_x$ , converts to the more toxic hydroxyl radical. Of the three forms of SOD, *MnSOD* (manganese superoxide dismutase) is expressed in the mitochondria and accounts for ~ 90 percent of total SOD activity (Mak et al. 2007). The Val-9Ala variant (rs 179972) arises from a T→C substitution. This causes the secondary structure of the protein to change and affects the transport of *MnSOD* into the mitochondria (Cai et al. 2004) and the Ala/Ala *MnSOD* has higher enzymatic activity (Siedlinski et al. 2009).

### **Genotyping for GST and MnSOD Polymorphisms**

Genomic DNA was isolated from whole blood using a standard protocol (*Sambrook and Russell, 2001*). Four polymorphic markers were genotyped using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP)/ PCR method (Applied Biosystems, India). The *GSTT1* (rs 17856199) and *GSTM1* (rs 366631) genotypes were determined by a multiplex PCR method (Vettriselvi et al. 2006) with intron 3 of HLADRB1 gene sequence as an internal control. The amplified *GSTM1* gene frag-

ment comprised 220bp and 450bp for *GSTT1* gene with which the internal control fragment of 796 bp was amplified. The absence of the amplified product was consistent with the null genotype. Genotyping of *GSTP1* (Ile/Val; rs 1695) was carried out by the PCR-RFLP method (Vedyakov and Tonevitskii 2006). An A→G transition in its exon 5 introduces an *Alw261* digestion site with 176bp representing the Ile/Ile genotype and 91bp and 85bp bands indicate the Val/Val genotype while the presence of all the three bands indicate heterozygosity (Ile/Val). The PCR-RFLP method was also employed for genotyping *MnSOD* (Val/Ala; rs179972) (Cai et al. 2004). A T→C transition in codon 9 of the gene produces the Val→Ala substitution. *NgoMIV* digested the PCR product (107bp) into two fragments 89bp and 18bp in case of Ala/Ala (rs 179972), whereas homozygosity for Val yielded no digested product and only the 107bp fragment.

### **Statistical Analysis**

The variables under study showed normal distribution on testing. The Chi-square analysis and the Student's t-test were used to compare the categorical and continuous demographic and clinical characteristics, respectively in the studied population. The statistical analysis of differences in oxidative DNA damage and oxidative stress biomarkers between workers (COPD) and controls was carried out using the two-tailed Student's t-test. Gene frequencies were estimated by the gene counting method/ Hardy-Weinberg equation and genotypic distribution was tested by Chi-square analysis. Hardy-Weinberg equilibrium was evaluated by the Chi-square test for goodness of fit. Effect of single and combined variants on COPD and on DNA damage and oxidative stress in workers and controls was investigated using odds ratio (OR) at 95 percent Confidence Interval (CI). As the cases and controls were matched for age, socio-economic status, smoking habit, alcohol drinking and BMI, no adjustment for these parameters was done. Correlations between different variables, both for oxidative stress and genotypes with oxidative damage, were determined by the Pearson's correlation and multiple linear regression analyses. In order to determine whether any of the demographical and clinically-relevant variables could be predictors for genetic damage, the standard Cox proportional hazard model was em-

ployed. On the basis of the significant prognostic factors for each subject, a prognostic index was developed based on survival analysis (Hoster et al. 2008) using the equation: Prognostic index =  $\beta_{1x} + \beta_{2y} + \dots$  (where x and y, etc are the significant prognostic factors). The differences in the prognostic scores in COPD categories were analyzed using the Student's t-test. The odds ratio and Chi-square analyses were performed using Medcalc software package and all other analyses were carried out using the SPSS version 16.00 for Windows. A p value  $\leq 0.05$  was considered significant.

## RESULTS AND DISCUSSION

As the assessment of a large number of variables adds to the significance of human biomonitoring studies because of the possibility of multiple comparisons (Ketelslegers et al. 2008), therefore in the present study, a multitude of end-points for genetic integrity, oxidative stress and genetic predisposition to COPD and genetic susceptibility to DNA damage in workers (engaged in crushing stones and related activities) have been studied. This is of significance as the cascade of genotoxic/carcinogenic events involves the associations between various genetic polymorphisms and intermediary molecular markers as well as individual susceptibility towards environmental and occupational carcinogens (Naccarati et al. 2006). Attempt has further been made to assimilate all the obtained observations and translate the results as factors into a prognostic index/score. The observations from the study reveal that both, oxidative DNA damage and oxidative stress levels, were significantly increased in all workers (COPD cases) compared to controls. Genotypic associations varied with respect to genetic damage and oxidative stress. Hereunder the observations on demographic and clinically-relevant variables are first described followed by the findings on DNA damage, oxidative stress, genotyping, their correlation analysis and the prognostic scores.

### Demographic Variables

The study group (Table 1) included workers (n=32, mean  $30.34 \pm 0.95$ y) of mixed Punjabi ethnicity (Mazbi Sikhs, Scheduled Caste and Backward Class Hindus) engaged at four stone-crushing units in the same occupation from five to 14

y (mean  $7.75 \pm 0.42$ y), and healthy controls (n=19, mean  $29.73 \pm 1.55$ y) with no workplace/incidental exposure(s). The participants were all males and matched for age, socio-economic status, tobacco chewing, smoking as well as alcohol drinking habits with low BMI. The BSA and abnormal pulmonary function were the significantly differing features in workers. All non-exposed participants had normal lung function and so formed the control group.

### On-site COPD Identification

The lung function parameters, FEV<sub>1</sub> (p=0.007), FVC (p=0.000) and FEV<sub>1</sub>/FVC (p=0.001), were significantly lowered in workers. These aberrant spirometry findings underpin the risk from occupational dust exposure and so, on the development of these lung-dysfunctional parameters. The workers were classified as those at-risk, mild and moderate COPD cases (GOLD 2003). On discoursing with these workers about their lung-function values, the workers disclosed that they had not sought any medical assistance for their respiratory problems (missing COPD cases) and considered these as a part of the occupational hazards. Various reported risk factors for respiratory distress and COPD include age, BMI, sex, low socio-economic status (SES) and smoking and poor diet (Koster et al. 2004; Jindal 2006; Bemt et al. 2010; Lee et al. 2015). There were 81.25 percent workers in the present study who were smokers with a Brinkman index ( $69.93 \pm 12.54$ , range 15-256) significantly (p $\leq 0.01$ ) higher. An almost similar number (81.25%) were in the continuous habit of tobacco and lime chewing. Alcohol-drinking was also prevalent (65.62%) and SES of most of the cases was low (87.49%) and hence could be important contributing factors for onset of COPD (Eisner et al. 2011; Crighton et al. 2015). Low BMI is another causal factor for COPD and the present group had 22% COPD cases who were underweight ( $< 18.00$  kg/m<sup>2</sup>) with the BSA also significantly (p=0.019) lowered.

Respiratory distress reported by the workers ranged from lung damage to lung disease in all probability from exposure to the dust-emitting activities. Inhaled dust can irritate airways, cause defective oxygen diffusion and lung function impairment during stone quarrying/crushing (Ghotkar et al. 1995; Chattopadhyay et al. 2006; Draid et al. 2015). It can lead to tubercu-

**Table1: Demographic and clinical characteristics of the study group**

Characteristics	COPD cases No. (%)	Controls No. (%)	χ <sup>2</sup> value	P value
Age (y) Mean± S.E.M. (Range)	30.34±0.95(20-45)	29.73±1.55(23-48)	-	-
<30	15(46.87)	13(68.42)	1.45	0.228
>30	17(53.13)	06(31.57)		
Occupational exposure (y) mean±S.E.M. (range )	7.75±0.42(5-14)	-	-	-
Diet - Veg/ Non-veg (occasional)	16(50.00)/ 16(50.00)	12(63.15)/07(36.84)	0.38	0.530
Smoking habit -Yes/ No	26(81.25)/ 06(18.75)	11(57.89)/ 08(42.10)	2.19	0.130
<sup>†</sup> Brinkman Index (bidis <sup>b</sup> smoked daily x smoking years)	69.93±12.54	25.05±7.87 <sup>a</sup>		<b>0.010</b>
<100	18(50.25)	10(52.63)	2.12	0.340
<200	06(18.75)	01(5.26)		
<300	02(6.25)	-		
Tobacco +lime chewing (continuous)-Yes/No	27(84.37)/ 05(15.62)	13(68.42)/ 06(31.57)	0.97	0.320
Alcohol drinking (750-900ml/week)- Yes/ None	21(65.62)/11(34.37)	10(52.63)/09(47.36)	0.38	0.530
<sup>c</sup> Socio-economic Status				
Upper lower	13(40.62)	07(36.84)	0.32	0.850
Lower middle	15(46.87)	09(47.36)		
Upper middle	02(6.25)	02(10.52)		
<sup>d</sup> Body Mass Index(kg/m <sup>2</sup> )				
<18.00 (underweight)	07(21.87)	-	11.12	<b>0.010</b>
18.00-22.90 (normal)	21(65.62)	10(52.63)		
23.00-24.90(overweight)	03(9.37)	04(21.05)		
>25.00(obese)	01(3.12)	05(26.31)		
Body Surface Area (m <sup>2</sup> )	1.58±0.16	1.66±0.03 <sup>a</sup>	-	<b>0.019</b>
<sup>e</sup> Pulmonary Function test-COPD identification				
Normal	-	19(100.00)	51.00	<b>0.0001</b>
At -risk	16(50.00)	-		
Mild	10(31.25)	-		
Moderate	06(18.75)	-		
<sup>††</sup> III-health Indicators(self-reported)				
Cough, Phlegm, Sputum	32(100.00)	-	-	-
Breathlessness	26(85.21)	-		
Eye irritation and watering	27(84.67)	-		
Skin irritation	21(65.62)	-		
Loss of appetite	17(53.12)	-		

<sup>a</sup> Student's t-test; <sup>b</sup> Tobacco (0.15-0.25g) loosely packed in a hand –rolled, dried leaf of Tendu tree (*Diisopyros melanoxylon*), smoked as a cigarette. <sup>†</sup> (Kojima et al. 2005); <sup>c</sup> (Kumar et al. 2007); <sup>d</sup> (WHO 2004)/(Misra et al. 2009); <sup>e</sup>(GOLD 2003); <sup>††</sup>Combinations with cough-phlegm-sputum indicators

losis, COPD, silicosis, emphysema, chronic bronchitis and laryngeal and lung cancers (Jhony et al. 2011; Iftikhar et al. 2009; Golbabaee et al. 2004; Tiwari et al. 2004; Sivacoumar et al. 2006). Respiratory and skin infections were observed in workers quarrying stones in a Nigerian study (Ugbogu et al. 2009), cough, dyspnea and wheezing in Peshawar (Pakistan) stone-crushing workers (Iftikhar et al. 2009) and respiratory distress including cough, phlegm and allergic disorders in those quarrying stones in

Iran (Golbabaee et al. 2004). Pulmonary dysfunctions were also reported in individuals engaged in building-demolition (Jhony et al. 2011). These symptoms are triggering factors for COPD and are inclusive of the criteria for COPD categorization (GOLD 2003).

**Oxidative DNA Damage**

An approximately two-fold significantly (p=0.010) elevated oxidative DNA damage (Table 2)

**Table 2: Oxidative DNA damage, oxidative stress and pulmonary function test in COPD cases and in non-exposed healthy controls**

Variables		COPD cases Mean $\pm$ S.E.M.		Controls Mean $\pm$ S.E.M.	P value			
Oxidative DNA damage		8-OHdG (pg/ml)		0.55 <sup>**</sup> $\pm$ 0.08	0.21 $\pm$ 0.09	<b>0.010</b>		
Oxidative Stress biomarkers		tGSH(nmol)		215.91 $\pm$ 3.51	225.40 <sup>*</sup> $\pm$ 0.89	<b>0.046</b>		
		GSSG(nmol)		26.80 $\pm$ 0.65	28.20 $\pm$ 0.78	0.187		
		GSH(nmol)		189.10 $\pm$ 3.39	197.20 $\pm$ 0.96	0.077		
		Redox Index		7.16 $\pm$ 0.21	7.09 $\pm$ 0.21	0.814		
		SOD(U/M)		94.47 $\pm$ 1.37	99.36 <sup>*</sup> $\pm$ 1.33	<b>0.021</b>		
Pulmonary Function Test parameters		FEV <sub>1</sub> (l)		2.07 $\pm$ 0.24	2.99 <sup>**</sup> $\pm$ 0.09	<b>0.007</b>		
		FVC(l)		3.05 $\pm$ 0.16	4.90 <sup>***</sup> $\pm$ 0.35	<b>0.000</b>		
		FEV <sub>1</sub> /FVC		0.57 $\pm$ 0.05	0.82 <sup>***</sup> $\pm$ 0.01	<b>0.001</b>		
		COPD cases (Mean $\pm$ S.E.M.)		Controls (Mean $\pm$ S.E.M.)				
Disease Status	N	8-OHdG (pg/ml)	tGSH (nmol)	SOD (U/M)	n	8-OHdG (pg/ml)	t GSH (nmol)	SOD (U/M)
Controls	Normal	-	-	-	19	0.21 $\pm$ 0.09	225.40 <sup>***</sup> $\pm$ 0.89 <sup>*c</sup>	99.36 <sup>*</sup> $\pm$ 1.33
<sup>†</sup> COPD categories								
	At-risk	16	0.58 <sup>*</sup> $\pm$ 0.13	218.56 $\pm$ 1.70 <sup>b</sup>	95.54 $\pm$ 1.97 <sup>d</sup>	-	-	-
	Mild	10	0.73 <sup>**</sup> $\pm$ 0.14 <sup>b</sup>	206.21 $\pm$ 10.53 <sup>c</sup>	93.22 $\pm$ 2.49 <sup>e</sup>	-	-	-
	Moderate	06	0.19 $\pm$ 0.17 <sup>b</sup>	225.00 $\pm$ 1.15 <sup>b</sup>	96.38 $\pm$ 3.31	-	-	-

Values in bold are significant ( $p \leq 0.05$ ), \*\*\*very highly significant ( $p \leq 0.001$ ), \*\*highly significant ( $p \leq 0.01$ ),

<sup>†</sup>significant ( $p < 0.05$ , Student's t-test) compared to controls; Values with similar letters are significant.

<sup>†</sup>(GOLD 2003); 8-OHdG-8-hydroxy-2'-deoxyguanosine, tGSH- total glutathione levels, GSSG- glutathione disulphide (oxidized form), GSH-glutathione (reduced form), SOD-superoxide dismutase, FEV<sub>1</sub>- Forced Expiratory Volume in one second, FVC- Forced Vital capacity, FEV<sub>1</sub>/FVC -Forced Expiratory Ratio.

was observed in all workers; the stratified at-risk ( $p=0.024$ ) and mild ( $p=0.004$ ) COPD cases also had significant DNA damage compared to controls while the mild COPD cases had more DNA damage ( $p=0.037$ ) compared to those with moderate COPD. The lower damage in moderate COPD cases may be because of fewer individuals in that group and their differing genotypes/lifestyles/habits. Moreover the common oxidized bases become reactive intermediates under conditions of oxidative stress (Burrows et al. 2002) and the 8-OHdG moiety has the tendency on further oxidation to form hydantoin products (which have the same mutagenic potential and are subject to the action of the same repair enzymes as the parental 8-OHdG). Since the moderate COPD subjects are under greater oxidative stress than those with the mild COPD, therefore, after processing of 8-OHdG by oxidants, there are probably fewer intact 8-OHdG groups in the moderate than in the mild COPD. The marked inflammation in COPD can further worsen the oxidant/antioxidant balance and in this way may

be promoting the disruption of genomic integrity (Boots et al. 2003).

Genetic damage has been observed in similar occupational environments: in road-tunnel construction workers, the micronuclei frequency in PBL was increased (Villarini et al. 2008), in calcite factory workers, higher micronuclei and nuclear abnormalities in buccal cells were observed (Diler and Ergene 2010), and in those involved in mining, stone-crushing, grinding and sandblasting, increased micronuclei, both in PBL and in nasal epithelial cells, were reported (Demircigil et al. 2010). Workers engaged in stone crushing, grinding, carrying chips, and extracting brick earths were reported to have increased genetic damage both in peripheral blood lymphocytes and the buccal mucosal cells (Halder and De 2012). Workers engaged in crushing and quarrying stones were also reported to have significant chromosomal damage in their urothelial cells (Kaur and Gandhi 2011a, 2011b) and an increase in chromosomal aberrations in the PBL had also been earlier documented (Sob-



ti and Bhardwaj 1991). The blood levels of 8-OHdG were significantly raised in lung cancer patients (Gackowski et al. 2003) while the cytokinesis block micronucleus assay in COPD disease showed increased micronuclei (MN) frequency (Maluf et al. 2007) though no increase in sister chromatid-exchanges (SCEs) or MN were observed in COPD cases (Casella et al. 2006). However, 8-OHdG levels were elevated in COPD cases (Caramori et al. 2001; Tzortzaki et al. 2012) with increase in DNA strand breaks (Ceylan et al. 2006) and damage index (da Silva et al. 2013b); oxidative damage in RNA and DNA in COPD cases has also been reported (Drost et al. 2005; MacNee 2005; Yoshida and Tudor 2007). The observations on DNA damage in the present study hence are similar to those in literature.

### Oxidative Stress

All workers had significantly lowered total GSH ( $p=0.046$ ) and SOD ( $p=0.021$ ) levels implying the presence of oxidative stress (Table 2). As also observed for oxidative DNA damage, the at-risk and mild COPD cases, respectively had significantly decreased tGSH ( $p=0.001$ ,  $p=0.018$ ) and SOD ( $p=0.046$ ,  $p=0.024$ ) levels from controls. In the moderate COPD cases significantly ( $p=0.038$ ) elevated tGSH levels in comparison to those at-risk for COPD were observed. The group comprised fewer individuals; they may have higher antioxidant levels and variant life-styles accounting for the comparatively lesser oxidative-stress vis-à-vis in mild cases.

In the literature also oxidative stress has been documented in COPD cases. Low erythrocyte glutathione peroxidase ( $GP_x$ ) activity and higher serum malondialdehyde levels in severe COPD cases were reported (Kluchová et al. 2007) in comparison to values in moderate COPD cases, but there were no differences in the erythrocyte SOD and CAT activities between the patients differing for severity of COPD. Oxidative stress in COPD and in lung dysfunction was observed as decreased levels of glutathione, superoxide dismutase, catalase, antioxidants (ascorbic acid, vitamin E) and increased lipid peroxidation (Kluchová et al. 2007; Borm et al. 2004; Tug et al. 2005; da Silva et al. 2013a).

Disease pathogenesis involves cell damage induced by superoxide radical ( $O_2^{\cdot-}$ ) and related oxygen species (Mak et al. 2007). The enzymes SOD, CAT and  $GP_x$  neutralize free radicals and

prevent the transformation of the superoxide to hydroxyl radicals (Borm et al. 2004). SOD converts  $O_2^{\cdot-}$  to hydrogen peroxide, while  $GP_x$  (using reduced GSH as hydrogen donor) and catalase transform it to water (Mak et al. 2007). Changes in activities of these enzymes or their absence can hence cause oxidative stress. In fact oxidative stress is among the pathological hallmarks in the development of COPD (Boots et al. 2003); this was also observed in COPD cases of present study as decreased SOD and GSH levels. The detrimental effects of oxidative stress include impairment of membrane functions, inactivation of membrane-bound receptors and enzymes, and increased tissue permeability (Kluchová et al. 2007). In addition to these, oxidative stress aggravates inflammatory processes in lungs and worsens the oxidant/antioxidant balance (Boots et al. 2003).

### Oxidative DNA Damage and Oxidative Stress

A significant inverse association of enzymatic levels (tGSH:  $r=-0.353$ ,  $p=0.047$ ; SOD:  $r=-0.721$ ,  $p=0.000$ ) with oxidative DNA damage (8-OHdG levels) in COPD cases was apparent on correlation and multiple linear regression analyses (Table 6). This association also extended to levels of GSSG ( $r=-0.299$ ,  $p=0.033$ ) and GSH ( $r=-0.362$ ,  $p=0.009$ ) verifying that with decreased enzymatic levels, oxidative stress is not neutralized and manifests as the observed oxidative DNA damage.

Both oxidative DNA damage and oxidative stress have together also been earlier documented in literature which substantiates that oxidative stress in all probability is causing oxidative DNA damage. DNA damage and oxidative stress were markedly increased in COPD cases (Ceylan et al. 2006) while increased apoptosis because of excessive genetic damage from prolonged oxidative stress in lymphocytes from airways of COPD patients was also reported (Segura-Valdez et al. 2000; Majo et al. 2001; Hodge et al. 2003).

### Genotyping

Since besides oxidative stress, the development and progression of COPD also involves multiple genes, gene-gene and gene-environment interactions (•idzik et al. 2008), genotyping of three allelic variants of the *GST* multigene

family (phase II enzymes) and one of *MnSOD* was carried out (Table 3). The reactive oxygen species generated by phase I enzymes get converted to inactive derivatives by phase II enzymes (*GST* multigene family). The *GSTT1* and *GSTM1* null genotypes show no enzyme activity and the *GSTP* Val allele has reduced enzyme activity (Hiragi et al. 2011). The *MnSOD* precursor protein with Ala signal peptide is essential for its efficient mitochondrial transport and it accounts for ~90 percent of the total SOD activity while the Val substitution causes reduced SOD activity (Mak et al. 2007).

The frequencies obtained of the variant genotypes were generally low, viz. *GSTT1*+/- (75.00%, 25.00%), M1+/- (56.25%, 43.75%) and P1+/-+/- (87.50%, 3.12%, 9.37%) and of *MnSOD* (Val/Val-53.12%; Ala/Val-31.25%; Ala/Ala-6.12%) in COPD cases. In literature, a range of frequencies of these genotypes exist for COPD cases from China (Chan-Yeung et al. 2007), Turkey (Çalikoglu et al. 2006) and in Caucasians (Siedlinski et al. 2009). Rather, the frequency of

*GSTM1* null genotype is within the reported range of 40-50 percent in Caucasians (Moretti et al. 2007). On comparison of the genotypes in COPD cases and controls, no significant differences were forthcoming implying that these genotypes showed no association with disease occurrence and/or lung dysfunction. Combination- genotypes also failed to yield any genetic predisposition to COPD. This is at variance with some results in literature for lung function/COPD. The presence of microsomal epoxide hydroxylase (EPHX1) His113- His113 variant and *GSTM1* null genotype was a significant predictor for increased susceptibility to COPD in the Slovak population (Zidzik et al. 2008). The *GSTT1* null genotype (alone or in combination with *GSTM1* null genotype) was associated with decline in FEV<sub>1</sub> in SAPALDIA cohort study comprising European caucasian ethnicity and Swiss nationality (Imboden et al. 2007). In central Tunisia, the *GSTM1* null/Val/Val *GSTP1* combination genotype was associated with COPD (Lakhdar et al. 2011). However other reports match with those

**Table 3: Distribution of genotypes and allele frequencies in the study group**

Genetic Polymorphism	COPD cases n (%)	Controls n (%)	$\chi^2$ value	P value
<i>Genotypes</i>				
<i>GSTT1</i> ( <sup>†</sup> rs17856199)				
Present	24(75.00)	16(84.21)	0.170	0.67
Null	08(25.00)	03(15.78)		
<i>GSTM1</i> ( <sup>†</sup> rs366631)				
Present	18(56.25)	13(68.42)	0.310	0.57
Null	14(43.75)	06(31.57)		
<i>GSTP1</i> (Ile/Val) ( <sup>†</sup> rs1695)				
Ile/Ile	28(87.5)	15(78.94)	2.790	0.24
Ile/Val	01(3.12)	03(15.78)		
Val/Val	03(9.37)	01(5.26)		
<i>MnSOD</i> (Val/Ala)( <sup>†</sup> rs179972)				
Val/Val	17(53.12)	13(68.42)	1.150	0.56
Ala/Val	10(31.25)	04(21.05)		
Ala/Ala	05(16.12)	02(10.52)		
<i>Alleles</i>				
<sup>**</sup> <i>GSTT1</i>				
Present	32(50.00)	23(60.52)	0.680	0.41
Null	32(50.00)	15(39.47)		
<sup>**</sup> <i>GSTM1</i>				
Present	22(34.37)	17(44.73)	0.690	0.41
Null	42(65.62)	21(55.26)		
<i>GSTP1</i> (Ile/Val)				
Ile	57(89.06)	33(86.80)	0.000	0.98
Val	07(10.93)	05(13.15)		
<i>MnSOD</i> (Val/Ala)				
Val	44(68.75)	30(78.94)	0.780	0.37
Ala	20(31.25)	08(21.05)		

Significant at p value <0.05, <sup>†</sup>SNP database Id(Gene cards). <sup>\*\*</sup>Hardy-Weinberg equation  
*GSTT1*-glutathione S-transferase theta-1, *GSTM1*-glutathione S-transferase mu 1, *GSTP1*-glutathione S-transferase pi, *MnSOD*- manganese superoxide dismutase;  
*GSTT1* and *GSTM1*: present (wild-type homozygous or heterozygous) and null (homozygous gene deletion).

in the present study: in Koreans no association of *GST1* and *GSTM1* was observed with COPD (Yim et al. 2000). The Ala variant of *MnSOD* in the Chinese exhibited increased risk for lung cancer but not for COPD (Wang et al. 2001), and in Hong Kong Chinese similarly, both *MnSOD* and catalase genes did not show predisposition for COPD (Mak et al. 2007).

### Genetic Polymorphism and Oxidative DNA Damage

Significantly elevated 8-OHdG levels (Table 4) were obtained in COPD cases with the *GSTM1* null ( $p=0.000$ ), *GSTP1* Val/Val ( $p=0.000$ ) and *MnSOD* Val/Ala, Ala/Ala ( $p=0.000$ ) genotypes.

Studies from literature have also revealed that the *GST* and *MnSOD* variants are associated with increased genetic damage. The *GSTM1* null genotype was associated with higher levels of 8-OHdG (Mirzaei et al. 2014). The *GSTP1* (Val/Val) genotype was associated with increased DNA tail moment (Liu et al. 2006) and the *MnSOD* Val/Ala or Ala/Ala genotypes with MPO G/G genotype had higher urinary 8-OHdG concentrations on PAH exposure (Park et al. 2006).

### Genetic Polymorphism and Oxidative Stress

The t GSH levels were significantly ( $p=0.003$ ) lower in COPD cases with *GSTP1* Val/Val genotype compared to those with the Ala/Ala genotype. Significantly lower SOD levels were also observed in COPD cases with *GSTT1* null ( $p=0.002$ ) and *GSTM1* null ( $p=0.004$ ) compared respectively with those having these alleles. As expected, the cases with *MnSOD* Val/Ala or the *MnSOD* Ala/Ala genotypes had significantly ( $p=0.000$ ) lowered SOD levels compared to those with the *MnSOD* Val/Val genotype (Table 4).

In reports in literature, an association of increased oxidative stress with genetic polymorphism has been documented. Significant lower GP<sub>x</sub>, GR, SOD, GSH and TAS levels were observed in COPD patients and their correlation was observed with the double null *GSTM1/GSTT1*, and *GSTM1*null/*GSTP1* Val/Val combination genotypes (Lakhdar et al. 2011).

### Oxidative DNA Damage, Oxidative Stress and Genotype Interactions

In order to study the association of different genotypes with oxidative DNA damage, only the *GSTT1/GSTM1* combinations and those with

sufficient study participants were analyzed (Table 4). COPD cases with *GSTT1*present/*GSTM1* null genotypes had significantly ( $p=0.000$ ) elevated 8-OHdG levels compared to the *GSTT1/MI* present genotypes. A significant increase in oxidative DNA damage was also observed in COPD cases with the *GSTT1* null/*GSTM1* null genotype compared to those with *GSTT1* null/*GSTM1* present genotype ( $p=0.054$ ). Significantly lowered t GSH levels were observed in COPD cases with *GSTT1* null/*GSTM1* null ( $p=0.000$ ) and *GSTT1* present/*GSTM1*null ( $p=0.021$ ). For SOD, low levels were observed in COPD cases with *GST* (*GSTT1*present/*GSTM1*null ( $p=0.000$ ), *GSTT1*null/*GSTM1*present ( $p=0.049$ ) and *GSTT1*null/*GSTM1* null ( $p=0.000$ ) combination genotypes in comparison to those with the *GSTT1* present/*GSTM1*present combination genotype.

Studies in literature also showcase such observations. The *MnSOD* Val/Ala had less DNA damage and lower lipid peroxidation (Miranda-Vilela et al. 2010) while the *MnSOD* Val/Val genotype was more frequent in COPD patients and showed lower expression of *MnSOD* mRNA (Pietras et al. 2010). Both 8-OHdG in DNA and 8-OHdGuanine in RNA were increased in lung diseases (Deslee et al. 2010).

### Genetic Predisposition to COPD

To assess whether the genetic variants of *GST* and *MnSOD* genes could be predictors for pre-disposition to COPD (Table 5), the odds ratio was calculated (without adjustment for sex, age and SES since these variables were matched for cases and controls) taking the wild type genotypes as referents. None of the genotypes in the study group showed any significance or likelihood for developing COPD.

Reports in literature for COPD cases are lacking. However, children with asthma having the *GSTM1* null and Val/Val *GSTP1* genotypes had abnormal pulmonary functions (Gilliland et al. 2002) and the *GSTP1* Ile/Ile genotype showed association with chronic lung disease (Manar et al. 2004).

### Predictive factors for Genetic Damage

Taking 8-OHdG as a dependent variable, the analysis of correlation and multiple linear regression revealed that genetic damage was signifi-

Table 4: Oxidative DNA damage and oxidative stress as functions of genetic polymorphisms in COPD cases and healthy subjects

Genetic polymorphism	COPD cases				Controls			
	n	8-OHdG (Mean±S.E.M.)	tGSH <sup>†</sup> (Mean ± S.E.M.)	SOD (Mean±S.E.M.)	n	8-OHdG (Mean±S.E.M.)	tGSH <sup>†</sup> (Mean±S.E.M.)	SOD (Mean±S.E.M.)
<i>MnSOD</i>								
Val/Val	17	0.27 <sup>*</sup> ± 0.09 <sup>a</sup>	221.63± 1.31	100.10± 0.5 <sup>a</sup>	13	0.04± 0.00 <sup>b</sup>	226.74 <sup>**</sup> ± 0.84 <sup>a</sup>	101.39± 0.43 <sup>a</sup>
Val/Ala	10	0.87± 0.15 <sup>b</sup>	217.45± 2.28	88.53± 2.45 <sup>a</sup>	04	0.30± 0.24 <sup>b</sup>	223.84± 2.35 <sup>b</sup>	100.42 <sup>**</sup> ± 0.80 <sup>a</sup>
Ala/Ala	5	0.85± 0.17 <sup>b</sup>	193.37± 20.27	87.23± 2.04 <sup>b</sup>	02	1.12± 0.009 <sup>b</sup>	219.76± 0.64	84.08± 4.60 <sup>b</sup>
<i>GSTP1</i>								
Ile/Ile	28	0.52 <sup>**</sup> ± 0.09	218.88± 1.21 <sup>a</sup>	94.74± 1.42	15	0.11± 0.07 <sup>a</sup>	226.26 <sup>***</sup> ± 0.95 <sup>a</sup>	100.59 <sup>**</sup> ± 0.94 <sup>a</sup>
Ile/Val	1	0.02± 0.00 <sup>a</sup>	228.33± 0.00	102.34± 0.00	03	0.755± 0.33 <sup>b</sup>	221.00± 1.63 <sup>b</sup>	93.12± 6.82 <sup>b</sup>
Val/Val	3	1.06 <sup>***</sup> ± 0.00 <sup>b</sup>	183.99± 35.85 <sup>b</sup>	89.39± 5.64	01	0.078± 0.00	225.67± 0.00	99.68± 0.00
<i>GSTT1</i>								
Present	24	0.51 <sup>*</sup> ± 0.10	219.54± 1.20	95.28± 1.52 <sup>a</sup>	16	0.17± 0.08	225.87 <sup>***</sup> ± 0.96	100.43 <sup>**</sup> ± 0.87 <sup>a</sup>
Null	8	0.69± 0.15	205.02± 13.50	92.06± 3.02 <sup>b</sup>	03	0.42± 0.35	222.28± 2.29	93.68± 7.16 <sup>b</sup>
<i>GSTM1</i>								
Present	18	0.24 <sup>*</sup> ± 0.08 <sup>a</sup>	221.97± 1.54	97.97± 1.38 <sup>a</sup>	13	0.03± 0.005 <sup>a</sup>	227.16 <sup>**</sup> ± 0.84 <sup>a</sup>	101.60 <sup>*</sup> ± 0.43
Null	14	0.95± 0.10 <sup>b</sup>	208.12± 7.42	89.97± 2.06 <sup>b</sup>	06	0.59± 0.22 <sup>b</sup>	221.59± 1.10 <sup>b</sup>	94.51± 3.50
<sup>††</sup> Gene-Gene Combinations								
<i>GSTT1</i> (+)/ <i>GSTM1</i> (+)	13	0.16± 0.08 <sup>a</sup>	223.63± 1.18 <sup>a</sup>	99.63± 1.04 <sup>a</sup>	11	0.03± 0.005 <sup>a</sup>	227.60 <sup>**</sup> ± 0.89 <sup>a</sup>	101.75± 0.45 <sup>a</sup>
<i>GSTT1</i> (+)/ <i>GSTM1</i> (-)	10	0.91± 0.14 <sup>b</sup>	214.48± 1.04 <sup>b</sup>	89.21± 2.32 <sup>b</sup>	6	0.59± 0.22 <sup>b</sup>	221.59 <sup>***</sup> ± 1.10	94.51± 3.50
<i>GSTT1</i> (-)/ <i>GSTM1</i> (+)	5	0.46± 0.18 <sup>c1</sup>	217.63± 4.37	93.65± 3.78 <sup>b</sup>	2	0.06± 0.00 <sup>c1</sup>	224.74± 2.29	100.79± 1.61
<i>GSTT1</i> (-)/ <i>GSTM1</i> (-)	3	1.06± 0.00 <sup>c2</sup>	183.99± 35.85 <sup>b</sup>	89.39± 5.64 <sup>b</sup>	1	1.13± 0.00 <sup>c2</sup>	219.12± 0.00 <sup>b</sup>	79.48± 0.00 <sup>b</sup>

<sup>\*\*\*</sup>very highly significant (p≤0.001), <sup>\*\*</sup>highly significant(p≤0.01), <sup>\*</sup>significant (p<0.05, Student's t-test) compared to controls.

Values with different letters and number (gene-gene combination) are significant within group.

*GSTT1*-glutathione S-transferase theta-1, *GSTM1*-glutathione S-transferase mu 1, *GSTP1*-glutathione S-transferase pi, *MnSOD*- manganese superoxide dismutase; *GSTT1* and *GSTM1*: + (present; wild-type homozygous or heterozygous) and - (null; homozygous gene deletion).

<sup>a</sup>only tGSH significantly lower in COPD cases than the controls so analysed;

<sup>††</sup>*GST* (*T1*, *M1* and *P1*) and *MnSOD* combinations not analysed because of lesser number in the groups.

**Table 5: Predictor assessment for COPD on the basis of genetic polymorphisms**

Genetic Polymorphism		COPD Con-	Refe-		Odds Ratio	P value
		cases	trols	rent	(95% CI)	
<i>GSTT1</i>	Present	24	16	1.00	0.56 (0.12-2.44)	0.440
	Null	8	3			
<i>GSTM1</i>	Present	18	13	1.00	0.59 (0.18-1.95)	0.390
	Null	14	6			
<i>GSTP1</i> (Ile/Val)	Ile/Ile	28	15	1.00	5.6 (0.53-58.63)	0.150
	Ile/Val	1	3			
	Val/Val	03	01		0.62 (0.05-6.51)	0.690
	Ile/Ile+Ile/Val	29	18	1.00		
	Val/Val	03	01		1.611 (0.29-8.86)	0.580
<i>MnSOD</i> (Val/Ala)	Val/Val	17	13	1.00	0.52 (0.13-2.05)	0.350
	Val/Ala	10	04			
	Ala / Ala	05	02		0.52 (0.08-3.13)	0.470
	Val/Val + Val/Ala	27	17	1.00	0.63 (0.11-3.65)	0.610
	Ala/Ala	05	02			
<i>Gene-Gene Combinations</i>						
<i>GSTT1/GSTM1</i>	Present / Present	13	11	1.00		
	Present / Null	11	04		0.429 (0.106-1.73)	0.230
	Null / Present	04	02		0.59 (0.09-3.86)	0.580
	Null / Null	03	01		0.39 (0.03-4.34)	0.440
<i>GSTT1</i> (+), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Val		11	10	1.00		
<i>GSTM1</i> (-), <i>GSTT1</i> (-), <i>GSTP1</i> Val/Val, <i>MnSOD</i> Ala / Ala		01	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Val		03	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Ala		07	01		0.15(0.01-1.51)	0.100
<i>GSTM1</i> (-), <i>GSTT1</i> (-), <i>GSTP1</i> Val/Val, <i>MnSOD</i> Val/Val		02	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Ala / Ala		01	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Ala / Ala		01	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Ala		01	01		1(0.06-20.01)	0.948
<i>GSTT1</i> (-), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Ala		01	-		-	
<i>GSTT1</i> (-), <i>GSTM1</i> (+), <i>GSTP1</i> Val/Val, <i>MnSOD</i> Ala / Ala		02	-		-	
<i>GSTT1</i> (-), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Ala / Ala		01	-		-	
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Ala / Ala		01	01		1(0.06-20.01)	0.948
<i>GSTT1</i> (-), <i>GSTM1</i> (+), <i>GSTP1</i> Ile/Ile, <i>MnSOD</i> Val/Val		-	02		-	-
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Val/Val, <i>MnSOD</i> Val/Ala		-	01		-	-
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/ Val, <i>MnSOD</i> Val/Val		-	01		-	-
<i>GSTT1</i> (+), <i>GSTM1</i> (-), <i>GSTP1</i> Ile/ Val, <i>MnSOD</i> Val/Ala		-	01		-	-
<i>GSTM1</i> (-), <i>GSTT1</i> (-), <i>GSTP1</i> Ile/ Val, <i>MnSOD</i> Ala / Ala		-	01		-	-
<i>Allelic distribution</i>						
<sup>†</sup> <i>GSTT1</i>						
	Present	32	23	1.00	0.65(0.28-1.47)	0.300
	Null	32	15			
<sup>†</sup> <i>GSTM1</i>						
	Present	22	17	1.00	0.65(0.28-1.47)	0.290
	Null	42	21			
<i>GSTP1</i>						
	Ile	57	33	1.00	1.23(0.36-4.20)	0.730
	Val	07	05			
<i>MnSOD</i>						
	Val	44	30	1.00	0.58(0.22-1.50)	0.260
	Ala	20	08			

p<0.05 is significant, CI- confidence interval. † Hardy-Weinberg equation  
*GSTT1*-glutathione S-transferase theta-1, *GSTM1*-glutathione S-transferase mu 1, *GSTP1*-glutathione S-transferase pi, *MnSOD*- manganese superoxide dismutase; *GSTT1* and *GSTM1*: + (present; wild-type homozygous or heterozygous) and - (null; homozygous gene deletion).

cantly associated with the levels of tGSH and GSSG, GSH, SOD as well as the *GSTM1*, *GSTP1* and *MnSOD* genotypes (Table 6). Hence these can all be also considered as predictive factors

for genetic damage in the studied population. Of these, the *GSTM1* and *MnSOD* genotypes as well as the SOD enzyme were highly significant (p=0.000) predictors.

Table 6: Predictive factors for genetic damage (8-OHdG level<sup>a</sup>)

Variables	COPD cases				Controls				Total study group			
	Pearson Correlation	Multiple linear regression	P value	t	Pearson Correlation	Multiple linear regression	P value	t	Pearson Correlation	Multiple linear regression	P value	t
tGSH	-0.353	-0.353	<b>0.047</b>	-2.068	-0.681	-0.681	<b>0.001</b>	-3.839	-0.413	-0.413	<b>0.003</b>	-3.174
GSSG	-0.285	-0.285	0.115	-1.626	-0.185	-0.185	0.448	-0.776	-0.299	-0.299	<b>0.033</b>	-2.192
GSH	-0.311	-0.311	0.083	-1.793	-0.486	-0.486	<b>0.035</b>	-2.292	-0.362	-0.362	<b>0.009</b>	-2.719
Redox Index	0.015	0.015	0.935	0.083	0.062	0.062	0.801	0.256	0.037	0.037	0.796	0.260
SOD	-0.721	-0.721	<b>0.000</b>	-5.691	-0.801	-0.801	<b>0.000</b>	-5.517	-0.769	-0.769	<b>0.000</b>	-8.417
GSTT1(-)vs GSTT1(+)	0.157	0.157	0.392	0.8691	0.237	0.237	1.005	1.005	0.204	0.204	0.151	1.459
GSTMI(-)vs GSTT1(+)	0.703	0.703	<b>0.000</b>	5.407	0.667	0.667	<b>0.002</b>	3.687	0.684	0.684	<b>0.000</b>	6.570
GSTP(Ile/Ile and Ile/Val vs Val/Val)	0.187	0.187	0.306	1.042	0.499	0.499	2.374	2.374	0.234	0.234	0.098	1.688
MnSOD(Val/Val and Val/Ala vs Ala/Ala )	0.593	0.593	<b>0.000</b>	4.030	0.650	0.650	<b>0.003</b>	3.522	0.616	0.616	<b>0.000</b>	5.472

<sup>a</sup>dependent variable is leukocyte DNA 8-OHdG level. values in bold are significant (p<0.05).  
 GSTT1-glutathione S-transferase theta-1, GSTMI-glutathione S-transferase mu 1, GSTP1-glutathione S-transferase pi,  
 MnSOD- manganese superoxide dismutase; 8-OHdG-8-hydroxy-22 -deoxyguanosine,  
 tGSH- total glutathione levels, GSSG- glutathione disulphide (oxidized form), GSH-glutathione (reduced form), SOD-superoxide dismutase.  
 GSTT1 and GSTMI: + (present; wild-type homozygous or heterozygous) and - (null; homozygous gene deletion).

**Prognostic factors for DNA Damage–  
Calculation of Hazard Ratio**

In Table 7, the significant prognostic factors for both oxidative stress and genetic damage are shown. Of these, FEV<sub>1</sub> among the lung function values (HR16.48, 95% CI 238.32-100.9), SOD levels (HR 1.351, 95%CI 1.07-1.69) among oxidative stress parameters, the *GSTM1* genotype (HR 0.091, 95% CI 0.001-0.374%) and alcohol drinking habit (HR 0.178, 95%CI 0.031-1.033) were revealed to be significant (p≤0.05) prognostic factors. As oxidative stress and oxidative DNA damage are correlated (p≤0.05), the observed significantly(p≤0.05) raised 8-OHdG level in COPD cases has probably occurred because of the cellular oxidative stress arising from the decreased GSH, GSSG, SOD levels. In the literature also, greater levels of oxidative stress were observed to show greatest oxidative damage to leukocytic DNA (Liu et al. 2009). The 8-OHdG results from the oxidation of DNA (on interaction of hydroxyl ions with guanine) and becomes pro-mutagenic (Gackowski et al. 2003; Kasai

1997). The oxidative mechanisms produce reactive oxygen species (ROS) and exacerbate the generation of molecular oxygen and the superoxide and hydroxyl radicals. The 8-OHdG resulting from the oxidation of DNA as hydroxyl radicals interact with guanine makes it pre-mutagenic (Valavanidis et al. 2009). This oxidized DNA product has been documented to further promote/exacerbate oxidative stress and result in ageing, malignancy, tumors and neurodegenerative disease (Rahman 2007; Valko et al. 2007). Both alcohol drinking and FEV<sub>1</sub> depicted an increased hazard risk for oxidative stress and oxidative DNA damage. Alcohol intake has been observed to increase chromosomal damage (Kalaiselvi et al. 2002) and its association with oxidative stress and oxidative DNA damage in the present study, matches reports in literature: alcohol consumption elevated genetic damage (Fenech et al. 2007), oxidative stress (Albano 2006) and was associated with decline in lung function (Siu et al. 2010). Among the genotypes, the *GSTM1* variant in the ethnic group of the present study with very highly significant (p=0.001) HR (0.091, 95%CI

**Table 7: Prognostic factors for oxidative stress and genetic damage and prognostic score of COPD cases**

<i>Prognostic factors</i>	<i>Hazards ratio (95%CI)</i>	<i>β</i>	<i>P value</i>	<i>Prognostic score of COPD cases Mean±S.E.M.(range)</i>
FEV <sub>1</sub>	16.48 (1.54 - 175.54)	2.802	<b>0.020</b>	42.46±0.95(31.94 - 49.81)
SOD	1.351 (1.07 - 1.69)	0.301	<b>0.009</b>	
<i>GSTM1</i>	0.091 (0.001- 0.374)	3.973	<b>0.009</b>	-
Alcohol drinking	0.178 (0.031- 1.033)	1.726	<b>0.054</b>	
Age	0.924 (0.793- 1.076)	-0.079	0.309	
BMI	0.850 (0.411- 1.757)	-0.162	0.661	
BI	1.004 (0.977- 1.032)	0.004	0.773	
Smoking	0.174 (0.014- 2.164)	-1.748	0.174	
Tobacco	1.604 (0.126- 20.42)	0.472	0.716	
FVC	1.240 (0.344- 4.476)	0.215	0.742	
FEV <sub>1</sub>	0.346 (0.00 - 217.519)	-4.994	<b>0.000</b>	
tGSH	0.584 (0.709- 1.839)	0.133	0.584	
GSSG	0.498 (0.012- 8.593)	-1.136	0.321	
<i>GSTT1</i>	0.298 (0.031- 2.911)	-1.209	0.298	
<i>GSTP1</i> (Ile/Val)	1.239 (0.154- 9.965)	0.214	0.841	
<i>MnSOD</i> (Val/Ala)	2.897 (0.075- 112.274)	1.064	0.569	
<i>COPD status</i>	<i>Prognostic Score Mean± S.E.M.Student's t-test</i>		<i>P-value</i>	
At-risk	45.74±0.76	At-risk versus Mild	<b>0.015</b>	
Mild	41.25±1.81	At-risk versus Moderate	<b>0.000</b>	
Moderate	35.88±0.39	Mild versus Moderate	<b>0.042</b>	

Values in bold are significant (P<0.05; multiple Cox proportional hazards model, Student's t-test), CI- confidence interval, BMI-body mass index, FEV<sub>1</sub>- Forced Expiratory Volume in one second, BMI-body mass index, BI-brinkman index, FVC-forced vital capacity, tGSH- total glutathione levels, GSSH- glutathione disulphide (oxidized form), SOD-superoxide dismutase, *GSTM1*-glutathione S-transferase mu 1.

0.001-0.374) is also a strong prognostic factor for DNA damage following SOD (HR 1.351, 95% CI 1.07-1.69) and FEV<sub>1</sub> (HR 16.48, 95% CI 1.54-175.54). The *GSTM1* null genotype has also been associated with increased genetic damage viz. increased DNA tail moment (Singh et al. 2012) and 8-OHdG levels (Kim et al., 2003). The former is the product of length of tail of DNA and the percentage of DNA in the tail. If damage/ breaks in DNA have occurred and the cells are subjected to electrophoresis, fragmented DNA will move out of the nucleoid causing tail formation (comet), which is observable using the single cell gel electrophoresis assay.

### Prognostic Score/Index for Oxidative DNA Damage

A prognostic score (Table 7) as a liability index for genetic damage was developed as this was the main purpose of the present study. Such an index can by extension be used for cancer risk susceptibility since genetic damage (especially 8-OHdG) is an earlier indicator of cancer. For the formulation of the index it was required that the independent COPD prognostic risk factors deterministic for genetic damage be considered based on the model (survival analysis) proposed for Mantle Cell International Prognostic Index (MIPI) (Hoster et al. 2008). The significant prognostic risk factors obtained (Table 7) in the present study were considered for developing the prognostic index using the Cox proportional hazard model. The median prognostic score was 42.56 (range 31.94-49.81) with a mean score of

42.46±0.95. Considering that 10% of the score values were below 41.94 and 90% below 43.41, potential cut-off points were set between 41.93 and 43.43 in steps of 0.05 were assessed for increased likelihood for genetic damage. On this basis, a high risk group of 17 COPD cases (53.12%, score ≥42.60) was identified. There were 11 cases (34.37%) at intermediate risk (37.07 ≤ score < 42.60) and the remaining four COPD cases (12.5%, score < 37.07) belonging to the low risk group for genetic damage.

### Stone-crushing Sites and Genetic Damage

The settled dust on the top-layer of the soil from stone-crushing units was collected and outsourced for analysis (Atomic Absorption Spectrophotometer and X-ray diffraction). Soil samples from all units contained lead, cadmium, copper, zinc, chromium and silica (personal communication). There was no statistically significant differences for oxidative DNA damage and oxidative stress in workers stratified for different stone-crushing units (Table 8). The concentration of various metals also varied only somewhat because of matching geochemical profile in these parts of Punjab indicating an almost similar kind of probable contributors to oxidative stress and DNA damage in the studied group.

As documented in literature, the heavy metals- sulphhydryl group interactions in the enzymes result in structural enzyme deficiency /inhibition / disruption contributing to oxidative stress

**Table 8: Genetic damage and oxidative stress in COPD cases as stratified for different stone-crushing units**

Variables	COPD cases					
	Sarna (n=15)	Gurdaspur (n=5)	Pathankot I (n=7)	Pathankot II (n=5)	Controls	
Oxidative DNA Damage	8-OHdG (Mean± S.E.M.)	0.55 <sup>a</sup> ±0.13 <sup>a</sup>	0.43±0.19	0.71 <sup>**</sup> ±0.21 <sup>a</sup>	0.4728±0.25	0.214±0.09 <sup>b</sup>
Oxidative Stress Parameters	tGSH (Mean ± S.E.M.)	213.38±7.36	216.25±2.87 <sup>a</sup>	220.14±2.84 <sup>a</sup>	217.23±2.88 <sup>a</sup>	225.40 <sup>***</sup> / <sup>*</sup> ±0.89 <sup>b</sup>
Parameters	SOD (Mean ±S.E.M.)	93.978±2.04 <sup>a</sup>	91.730±3.72 <sup>a</sup>	94.820±3.25	98.240±2.68	99.364 <sup>a</sup> ±1.33 <sup>b</sup>

\*\*\*very highly significant (p≤0.001), \*\*highly significant (p≤0.01), \*significant (p<0.05, Student's t-test) compared to controls. Values with different letters are significant from controls.

8-OHdG-8-hydroxy-2'-deoxyguanosine, tGSH- total glutathione levels, SOD-superoxide dismutase. Values with different letters are significant (p<0.05; Student's t-test)



(Hall 2002) and these, via free radicals can alter the structure of proteins, lipids and nucleic acids (Calderón et al. 2003) forming lesions, strand breaks, and base-modifications and so causing metal-induced carcinogenesis (Leonard et al. 2004). Heavy metal genotoxicity has also been documented: lead was genotoxic in peripheral blood lymphocytes and urine (Hengstler et al. 2003), cadmium in blood (Valverde et al. 2001), chromium in body fluids (Eastmond et al. 2008), cadmium and lead were genotoxic in bronchial epithelial cells (Glahn et al. 2008) and cadmium in urine was associated with 8-OHdG levels in non-smokers (Ketelslegers et al. 2008). Silica dust is also a proven genotoxicant (Basaran et al. 2003; Kim et al. 2010) and is carcinogenic (IARC 1997). The dust-particles containing silica and particulate matter (PM) from stone-crushing activities induce oxidative stress and lung damage (Villarini et al. 2008; Demircigil et al. 2010); silica dust, talc and particulate matter are both genotoxic and carcinogenic (Fatima et al. 2001; Albrecht et al. 2009). The dust and continued presence of these metals across the stone-crushing units hence makes them potential contributors towards oxidative stress and DNA damage observed in the workers.

The significantly increased DNA damage in the workers is a cause for concern in the light of associated potential risk for cancer documented in literature. Cancer etiology is linked to consequences of DNA modifications/DNA damage (apurinic/apyrimidinic sites, oxidized purines or pyrimidines and strand breaks) and replication errors in somatic cells that give rise to mutations and subsequently cause promotion and development of the malignant tumour (Valavanidis et al. 2009). Unrepaired DNA lesions in the cell cycle manifest as aneuploidy, chromosomal rearrangement and breakage-fusion-bridge cycles (Fenech 2002) and can trigger oncogenesis/DNA amplification. The unrepaired DNA lesions can also further promote oxidative stress and cause ageing, malignancy, tumors and neurodegenerative diseases (Valko et al. 2007). Diminished DNA repair capacity (from damaged DNA) can in turn cause transcription arrest, replication errors and genomic instability and initiate carcinogenesis (Jackson and Loeb 2001).

The observations of the present study corroborate those in the literature. The inhalation of air-borne dust at stone-crushing/quarrying and other dust-emitting occupations has been

reported to cause ill-health such as respiratory distress (cough, phlegm, allergic disorders) and skin infections (Golbabaei et al. 2004; Ugboqu et al. 2009), as well as lung injury and inflammation (Vallyathan et al. 1995), tuberculosis (Tiwari et al. 2011), COPD (Jhoney et al. 2011, Iftikhar et al. 2009), chronic renal and autoimmune diseases and even lung cancer (Gottesfeld et al. 2008).

Of the various mechanisms proposed in the pathogenesis of lung cancer and COPD, the shared pathways include oxidative stress, altered DNA replication, inflammation, angiogenesis and cellular proliferation/anti-apoptosis and epigenetic modifications including DNA methylation and histone modifications (Yang et al. 2011). From among these, the results of the present study have shown oxidative stress, DNA damage and genetic susceptibility in COPD cases. In the literature, there are not many reports on genetic damage assessment from exposure at this occupation (stone-crushing). The few studies have reported higher frequency of chromosomal aberrations and sister-chromatid-exchanges (Sobti and Bhardwaj 1991) and increased micronuclei (Kaur and Gandhi 2011a, 2011b) in stone crusher-unit workers. Some reports on elevated micronuclei frequency and increased comet tail length in PBL have also been presented, but in building-construction workers and in those with occupational exposure to silica dust (Demircigil et al. 2010; Sellappa et al. 2010; Halder and De 2012). The presence of oxidative stress from stone-crushing associated activities (as in the present study for tGSH and SOD) has also been documented (Tiwari et al. 2004). The *GSTM1* null genotype was also ascertained as a strong predictor for COPD in the present study as was also observed among the Slovaks (Šidzik et al. 2008) and in Tunisians (Lakhdar et al. 2011); the *GSTM1* locus displayed loss of heterozygosity with a 15kb homozygous deletion (*GSTM1* null allele) in lung and bladder cancers (Ford et al. 2000; Lee et al. 2010). Genetic predisposition and/or a combination of susceptible genes and exposures including environmental factors (gene-environment) are known to contribute to cancer development and evidences suggest that COPD or impaired lung function is associated with lung cancer (Kiri et al. 2010). In the present study, *GSTM1*, FEV1, SOD, and alcohol drinking were significant prognostic factors for genetic damage. In the literature,

the *GSTM1* genotype has shown association with lung cancer (Carlston et al. 2008; Young et al. 2011b) and with FEV<sub>1</sub> decline (Imboden et al. 2007). As the 8-OHdG is pro-mutagenic (Gackowski et al. 2003; Kasai 1997) and is present in considerable amounts in malignancy and tumors (Rahman 2007; Valko et al. 2007), its increased level in the COPD cases of the present study make it a strong contender for initiating carcinogenesis. Furthermore, increased oxidative stress (SOD, t GSH, antioxidant depletion, etc.) as also observed in the present study, has been linked to cancer (Dincer et al. 2007; Abdalla 2011).

### CONCLUSION

In conclusion, this is the first study to provide insights and exposure-effect relationship in workers exposed from occupational contaminants at stone-crushing sites. Despite the small study group, an effort nonetheless has been made to quantify at least, part of the inter-individual differences in relation to occupational exposure (thus enabling the identification of more susceptible groups for COPD 'missing cases'), genetic damage and eventually, future cancer-risk.

### RECOMMENDATIONS

Similar studies with a greater number of samples can further elaborate on this. The knowledge about and targeting of common pathogenic mechanisms for lung cancer and COPD can provide potential diagnostic and therapeutic applications for patients with lung diseases as well as for those at-risk and also for establishing an effective surveillance. Also the investigations for changes at the genome level (as in the present study) are crucial in view of the possible implication(s) in progression from genetic damage, mutagenesis to neoplasia. The developing of prognostic scores and a prognostic index (based on survival analysis) for genetic damage (8-OHdG) risk and progression is a novel concept, albeit requiring validation in larger sample groups. Such an index has potential for wider ramifications for a host of other genetic damage end-points and can find applications, by extension for cancer-risk since all neoplasia have a genetic etiology.

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