1. INTRODUCTION

1. Wheat is the most important foodgrain of India next to rice and is the staple food of millions of Indians, particularly in the northern and north-western parts of the country. It is rich in proteins, vitamins and carbohydrates and provides balanced food. Approximately one-sixth of the total arable land in the world is cultivated with wheat. Worldwide, wheat occupied an area of 219 million hectares with production of 735.3 million tonnes (Anonymous 2015). In India, it ranks second with the production of 93.5 million tonnes and area of 29.5 million hectares (Anonymous 2015) and in Himachal Pradesh, it covers an area of 356 thousand hectares with production of 568 thousand tonnes (Anonymous 2014).

The logarithmically growing population however, has put pressure on the breeders to meet the continuously raising demand which is to be doubled by 2030. Steadily changing climatic scenario has further worsened the situation by complicating the stresses whether abiotic and biotic. The pre-requisite for sustainable wheat improvement without compromising with its quality attributes is to develop elite genotypes with better resistance for biotic and abiotic stresses. But continuous monoculture of elite cultivars over wide area since times has narrowed down the genetic base of wheat. Narrowing down of genetic diversity in wheat has made it vulnerable to number of biotic and abiotic stresses especially rusts and drought. Further, genetic improvement should be based on the exploration and exploitation of the genetic diversity in the existing and untapped germplasm resources, making diversity studies imperative for future breeding endeavours. The major goal in front of wheat breeders today is to broaden its genetic background by introgressing novel genes from alien sources and fix them. For fixation of the introgressed genes, wide hybrids of wheat x alien donor species are subjected to haploid induction followed by chromosome doubling through colchicine treatment. Doubled haploidy (DH) breeding using androgenesis mediated approach (Chu et al. 1973; Ouyang et al. 1973), bulbosum technique (Barclay 1975), wheat x maize (Laurie and Bennett 1986; Laurie and Bennett 1988) and wheat x Imperata cylindrica (Chaudhary et al. 2005; 2
Chaudhary 2007; 2008a & b; 2009; 2010 a & b; 2011; 2012; Chaudhary 2013a & b; Kaila et al. 2012; Rather 2012; Rather et al. 2013; Badiyal et al. 2014) mediated chromosome elimination approaches have proved to be the efficient systems of doubled haploid production. Following wheat x maize system a number of doubled haploids have been developed from winter x spring wheat derivatives in the Molecular Cytogenetics and Tissue culture Lab (Singh et al. 2002; Sharma et al. 2005) and the system has been further explored in wheat x rye (Kishore et al. 2011) and triticale x wheat derivatives (Pratap et al. 2005) but significant success was lacking. This led to the invention of a dynamic and highly efficient Imperata cylindrica- mediated chromosome elimination system (Chaudhary et al. 2005) for haploid induction in wheat x wheat (Chaudhary et al. 2005), wheat x rye (Kishore et al. 2011) and triticale x wheat (Pratap et al. 2005; Badiyal et al. 2014) derivatives. The system has been efficiently used for the generation of DHs in the MCT Lab and has taken advantage over wheat x maize system, especially in triticale x wheat derivatives (Kishore et al. 2011). Since then, a large number of DHs have been developed in the MCT Lab following these approaches.

The understanding of the genetic diversity and knowledge of correlation combined with path analysis for the morphological characters along with the grain yield provides a rational approach for planning more efficient improvement programme. The genetic diversity among the populations is evaluated by using morpho-physiological, biochemical and molecular markers. Knowledge about genetic diversity and relationships is an invaluable aid in plant breeding and for the assessment of genetic diversity, various multivariate analytical techniques are being widely used. Among these, D2 Mahalanobis, Principal Component Analysis (PCA) and molecular markers are useful methods for diversity analysis. Morpho-physiological markers are often environmentally influenced in their manifestation and express low degree of polymorphism and to overcome these limitations, biochemical and molecular markers offer a rapid and reliable method of characterization. Biochemical markers (especially isoenzymes) also display limited polymorphism and are stage specific in their expression. These limitations are overcome by molecular markers which can be utilized as potent and reliable tools for the estimation of genetic variability. Molecular markers may or may not correlate with phenotypic expression of a genomic trait. They offer numerous advantages over conventional, phenotype-based alternatives as they are stable and detectable in all tissues regardless of growth, differentiation and development. DNA markers are widely used to assess the genetic diversity as they are distributed over whole genome and are not affected by environmental conditions. Simple sequence repeat (SSR) markers, which are also known as microsatellite markers offer a number of advantages such as high level of polymorphism, locus specificity, co-dominance, reproducibility, random and uniform distribution throughout the genome (Roder et al. 2002). SSR markers have been useful for integrating the genetic, physical and sequence-based physical maps in plant species, and simultaneously have provided breeders and geneticists with an efficient tool to link phenotypic and genotypic variation. SSR markers remain one of the best marker systems for wheat research because of their chromosome specificity and high polymorphism (Huang et al. 2002; Roder et al. 1998). Hence, the present investigation was undertaken to study the genetic and morphological variability among the doubled haploids produced from various elite wheat and triticale cultivars keeping in view the following objectives: To 1. assess the variability amongst wheat doubled haploids using various morpho-physiological traits and SSR markers, 2. infer genetic relationship between the pedigree of the doubled haploids together with the potential bread wheat varieties and 3. identify the doubled haploids of bread wheat with targeted traits like yield, resistance to biotic (yellow rust and powdery mildew) and abiotic (drought) stresses.