Chapter VI

SUMMARY

The present investigations entitled ‘Variability analysis for root production and saponin content in Asparagus racemosus Willd.’ were undertaken with following objectives,

- To determine variability of various morphological traits in different seed sources of Asparagus racemosus
- To quantify variability for saponin content in different seed sources
- To study different genetic parameters and establish relationship with reference to saponin production
- To establish germplasm bank

The experimental material consisted of 20 seed sources, and their 42 progenies. Twenty seed sources of A. racemosus were collected from different geographical regions of India viz. Haryana, Chandigarh, Jammu and Kashmir, Himachal Pradesh, Rajasthan, Madhya Pradesh, Uttarakhand, New Delhi and Tamil Nadu.

The field trial of 20 seed sources was laid out in the month of February 2007 following randomized block design with three replications and nine plants in each replication at the Forest Research Institute, Dehradun.

Out of 20 seed sources, only eleven sources produced
sufficient seeds to take up the progeny trials. In total, therefore, the progeny trial consisted 42 progenies, which was laid-out in February 2009 following RBD with three replications and four plants in each replication at the Forest Research Institute, Dehradun. On the trials, the observations were collected for number of shoots, collar diameter, shoot dry weight, maximum shoot height, shoot height, number of tubers, tuber length, tuber dry weight and saponin content, and analyzed for following statistics,

- Analysis of variance (ANOVA) and correlations among important traits
- Genotypic, phenotypic and environmental coefficient of variations, and path coefficient analysis
- Heritability (broad sense) and genetic advance
- Genetic divergence analysis ($D^2$ analysis) and principal component of analysis

The salient results of study and conclusions drawn from 20 seed sources are summarized below.

- Statistically highly significant differences among 20 seed sources for most of the characters except number of shoots and collar diameter were observed. The most promising seed sources showing highest tuber dry weight with high performance for other characters were identified as FRI/A3, FRI/A7, FRI/A2, FRI/A1 and FRI/A17 while for saponin content, seed sources viz. FRI/A2, FRI/A1 and A15 were found to be promising.
ii The estimates of PCV were greater than the GCV for all the traits. The estimates indicated wide range of exploitable variations for these traits. The values of GCV were very close to their corresponding PCV for all the traits suggesting least influence of environment for the expression of these traits.

iii The estimates of heritability (bs) coupled with high genetic advance for the important traits suggested greater role of those traits in selection and further genetic improvement.

iv The phenotypic correlations studies for important traits indicated that tuber dry weight was positively influenced with shoot dry weight, maximum shoot height, tuber length and number of tubers. More or less similar pattern was observed for genotypic correlations baring few exceptions.

v The correlation coefficients suggested that shoot dry weight, maximum shoot height, number of tubers and tuber length had positive and highly significant association with tuber dry weight indicating that tuber dry weight could be increased indirectly through correlated characters.

vi Path coefficients analysis identified shoot dry weight as direct contributor trait to tuber dry weight. However, maximum shoot height, tuber length, number of shoots and number of tubers through shoot dry weight as indirect components as having high order positive
indirect effect on tuber dry weight. It is suggested that while formulating selection strategies for higher tuber yield weightage should be given to these component traits.

vii On the other hand, non-significant and negative associations for most of the traits with saponin content displayed this ultimately leads unusual partitioning of those correlations in the form of direct and indirect effects.

viii The Mahalanobis $D^2$ statistic grouped 20 seed sources into nine distinct clusters indicating existence of genetic diversity among the seed sources. Maximum number of seed sources were grouped in Cluster II (9) followed by in cluster I, III and VII (2 in each), and remaining clusters contained single seed source.

ix The maximum per cent contribution towards total genetic diversity was recorded with shoot dry weight followed by tuber weight and saponin content while minimum contribution was through number of shoots, collar diameter and shoot height.

Further, similar studies were carried out on 42 progenies which are summarized hereunder.

i The ANOVA clearly showed that the progenies possessed sufficient amount of variation. Progenies FRI/A9/3, FRI/A17/2, FRI/A2/1, FRI/A6/3 and FRI/A17/4 were identified to be the most promising progenies for high tuber dry weight.
Though it seemed that the traits have not fully expressed themselves at the age of 1.5 years, the GCV was close to their corresponding PCV values, this suggests least influence of environment in expression of traits.

The high heritability (bs) coupled with high genetic advance recorded for shoot dry weight, tuber dry weight and saponin content suggested that these characters could be further improved through selection.

The path analysis suggested that shoot dry weight was an important character with high direct effect on tuber dry weight.

The Mahalanobis $D^2$ statistic grouped 42 progenies into eight distinct clusters which indicated certain amount of existence of genetic diversity among the progenies, majority of progenies (36) assembled in just two clusters suggesting that characters have not yet been fully expressed.

The maximum contribution towards total genetic diversity was recorded from tuber dry weight followed by shoot dry weight and number of tubers.

The above mentioned salient findings which have emerged out of this investigation will pave the way for further genetic improvement of traits of economic value in this species of medicinal importance.