RINGKASAN

Kentang adalah tanaman sayuran penghasil umbi dari famili Solanacea. Tingkat konsumsi rumah tangga dan industri Indonesia lambat laun meningkat seiring pertumbuhan penduduk, sehingga peningkatan produktivitas kentang sangat dibutuhkan. Peningkatan produktivitas kentang dapat dilakukan menggunakan metode intensifikasi. Metode intensifikasi pada tanaman kentang dapat dilakukan dengan penggunaan bibit unggul. Sebagai syarat dalam perakitan kualitas unggul klon kentang, maka dibutuhkan adanya keragaman genetik yang luas. Penggunaan penanda morfologis berdasarkan kenampakan ciri tanaman dalam menganalisis keragaman kentang sangat dibutuhkan. Namun, pengaruh lingkungan dapat menyebabkan perbedaan identifikasi antarindividu walaupun susunan genetik yang sama. Hal ini yang mendasari perlunya analisis keragaman kentang dalam tingkat genetik. Penanda molekuler banyak digunakan dalam analisis keragaman genetik tanaman, salah satunya adalah *Random Amplified Polymorphic DNA* (RAPD), dan *Simple Sequence Repeat* (SSR).

Kegiatan penelitian ini dimulai dari pengumpulan semua koleksi plasma nutfah kentang (13 kultivar/sampel), kemudian dilanjutkan dengan kegiatan di Laboratorium. Pengambilan sampel daun kentang dilaksanakan di daerah Batur, Banjarnegara dan Dieng, Wonosobo. Analisis molekuler dilaksanakan di Laboratorium Pemuliaan Tanaman dan Bioteknologi Fakultas Pertanian Universitas Jenderal Soedirman. Penelitian ini dilaksanakan mulai bulan November 2016 sampai Juli 2017. Variabel pengamatan yang dilakukan pada penelitian ini berupa kualitatif dan kuantitatif. Variabel kualitatif berupa keberadaan pita DNA yang teramplifikasi, dan variabel kuantitatif berupa angka angka hasil pengukuran ladder saat elektroforesis dan spektrofotometer.

Hasil penelitian menunjukkan bahwa keragaman genetik dari 13 kultivar tanaman kentang yang digunakan, memiliki tingkat keragaman genetik yang tinggi dengan persentase polimorfik sebesar 67% - 100%, dan nilai PIC dengan keterangan sedang - sangat informatif. Analisis kekerabatan pada 13 kultivar dihasilkan dua klaster utama. Kelompok klaster pertama terdiri atas kultivar Merah, Margahayu, NH1, Gareta, Vega, Klon 17, Granola, MZ, Lokal Dieng, Ungu, NH2, dan Bliss. Kelompok klaster kedua dibentuk oleh kultivar X. Penggunaan primer RAPD dan SSR menghasilkan pita DNA yang beragam membuktikan bahwa primer RAPD dan SSR dapat digunakan secara spesifik dalam menganalisis hubungan kekerabatan antar kultivar.

SUMMARY

Potato was vegetable crops that produce tubers from Solanacea. Generally, there was still low productivity of Indonesia potato but household and industries consumption were keep increase alongside population growth, so that escalation of potato productivity were desperately needed. Escalation of potato productivity could be done by using intensification method. Intensification method for potato was optimizing available farmland. As a requirement for assembling high quality of potato cultivar, there was needed of wide genetic diversity. Genetic diversity limitedness was a problem for fulfill a requirement for assembling high quality of potato cultivar, so there were need many efforts to get the characters that expected. One of the ways to create genetic diversity on potato was hybridization between species as much as possible. Use of morphology marker which based from plant appearance was needed to analyzed genetic diversity. But environment can made different identification between individuals, even though had same genetic arrangement. So that there was need to use genetic marker for analyzed genetic diversity, such as Random Amplified Polymorphic DNA (RAPD) and Simple Sequence Repeat (SSR).

Scope of this research started from collecting all of potato germplasm (13 cultivars/samples), then continued with analyzing in laboratory. Leaf sampling was carried on Dieng, Banjarnegara. Molecular analyzing was carried in Laboratory of Plant Breeding and Biotechnology Faculty of Agriculture University of Jenderal Soedirman. This research was carried from November 2016 until July 2017. Observation variable divided by two kind, that were qualitative and quantitative. Qualitative variable was amplified DNA bands and quantitative variable was number showed from ladder.

The results showed from 13 potato's varieties, there were high genetic diversity that showed by 67% - 100% percentage of polymorphic and moderate – hingh informative PIC value. From genetic relationship analyzing of 13 cultivars, its generated two main clusters. First cluster group were Merah, Margahayu, NH1, Gareta, Vega, Klon 17, Granola, MZ, Lokal Dieng, Ungu, NH2, dan Bliss. Second cluster group were X. Used of RAPD and SSR primer produced diverse DNA bands. It proved that RAPD and SSR primer can used specifically for analyzed genetic relationship between varieties.